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<400> 2622
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<210> 2623
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<212> DNA
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<400> 2623
ttttaagct tttttgtaag tcagccagca agaacacagg aagaaatact c 51

<210> 2624
<211> 51
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<210> 2625
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tcccgggtgg gaagaggaac agcctatgtg ggcttccacg gagggctgtg g

51

<210> 2626

<211> 51

<212> DNA

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<223> Accession number cg41085637

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51

<210> 2627

<211> 51

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<223> 1 of 2 allelic variants (2628 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg41088106

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51

<210> 2628

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<223> 2 of 2 allelic variants (2627 is other entry)

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<223> Accession number cg41088106

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51

<210> 2629

<211> 51

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<223> 1 of 2 allelic variants (2630 is other entry)

<221> misc_feature
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<223> Accession number cg41090658

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aaaggctgaa acacagcatg tgatgcgagt caaggtagtt gatgcccaac t 51

<210> 2630
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (2629 is other entry)

<221> misc_feature
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<223> Accession number cg41090658

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aaaggctgaa acacagcatg tgatgtgagt caaggtagtt gatgcccaac t 51

<210> 2631
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<223> 1 of 2 allelic variants (2632 is other entry)

<221> misc_feature
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<223> Accession number cg41362674

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cagggtcatt tattttggcc aagagaggcc tccaacgccc cgaaatgctt c 51

<210> 2632
<211> 51
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<221> misc_feature
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<223> Accession number cg41362674

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<210> 2633
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<223> 1 of 2 allelic variants (2634 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg41389761

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tgatggtgtc gtagaacccg aagaaacgga cctgcgagta caacgacagc a 51

<210> 2634
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<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (2633 is other entry)

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<223> Accession number cg41389761

<400> 2634
tgatggtgtc gtagaacccg aagaacggac ctgcgagtac aacgacagca 50

<210> 2635
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (2636 is other entry)

<221> misc_feature
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<223> Accession number cg41389761

<400> 2635

tcgtagaacc cgaagaaacg gacctgagac tacaacgaca gcatgatcga t

51

<210> 2636

<211> 50

<212> DNA

<213> Homo sapiens

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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

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tcgtagaacc cgaagaaacg gacctcgagt acaacgacag catgatcgat

50

<210> 2637

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (2638 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg41394528

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gattttttct ttactcaaga atatagatct aaaaaaaaaa aacacttctg c

51

<210> 2638

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

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<223> Accession number cg41394528

<400> 2638
gattttttct ttactcaaga atatacatct aaaaaaaaaa aacacttctg c 51

<210> 2639
<211> 51
<212> DNA
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<221> misc_feature
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<223> Accession number cg41394528

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actcaagaat atagatctaa aaaaaaaaaa cacttctgca tctcaaaagc a 51

<210> 2640
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<223> 2 of 2 allelic variants (2639 is other entry)

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<400> 2640
actcaagaat atagatctaa aaaaacaaaa cacttctgca tctcaaaagc a 51

<210> 2641
<211> 51
<212> DNA
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2642 is other entry)

<221> misc_feature
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<223> Accession number cg41394528

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<210> 2642
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<213> Homo sapiens

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<223> Accession number cg41394528

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51

<210> 2643

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (2644 is other entry)

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<223> Accession number cg41394528

<400> 2643

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51

<210> 2644

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (2643 is other entry)

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<223> Accession number cg41394528

<400> 2644

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51

<210> 2645

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 1 of 2 allelic variants (2646 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg41567419

<400> 2645
ggctcaagta atctaccac ctcagcctcc caaagtgctg ggattacaag g 51

<210> 2646
<211> 51
<212> DNA
<213> Homo sapiens

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<222> (26)...(0)
<223> 2 of 2 allelic variants (2645 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg41567419

<400> 2646
ggctcaagta atctaccac ctcagtcctcc caaagtgctg ggattacaag g 51

<210> 2647
<211> 51
<212> DNA
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2648 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg41618657

<400> 2647
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<210> 2648
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (2647 is other entry)

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51

<210> 2649

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<223> 1 of 2 allelic variants (2650 is other entry)

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<222> (0)...(0)

<223> Accession number cg41622706

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51

<210> 2650

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (2649 is other entry)

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<222> (0)...(0)

<223> Accession number cg41622706

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<223> Accession number cg41628365

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51

<210> 2652

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (2651 is other entry)

<221> misc_feature
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<223> Accession number cg41628365

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atggctcact gcagcctcaa cctcccaggc tcaagcgatc ctctctcag c 51

<210> 2653
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (2654 is other entry)

<221> misc_feature
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<223> Accession number cg41628365

<400> 2653
ccaagtagct gggaccacag gcacacgccca ccatgcctgg ctaatttttt a 51

<210> 2654
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (2653 is other entry)

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<222> (0)...(0)
<223> Accession number cg41628365

<400> 2654
ccaagtagct gggaccacag gcacatgccca ccatgcctgg ctaatttttt a 51

<210> 2655
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (2656 is other entry)

<221> misc_feature
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<223> Accession number cg41640016

<400> 2655
gctgggtggg cgtggaggca ggagggggccc cagcaaggcc agggcaggca g 51

<210> 2656
<211> 51
<212> DNA
<213> Homo sapiens

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<222> (26)...(0)
<223> 2 of 2 allelic variants (2655 is other entry)

<221> misc_feature
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<223> Accession number cg41640016

<400> 2656
gctgggtggg cgtggaggca ggaggagccc cagcaaggcc agggcaggca g 51

<210> 2657
<211> 51
<212> DNA
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2658 is other entry)

<221> misc_feature
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<223> Accession number cg41640016

<400> 2657
ggcaggaggg gccccagcaa ggccagggca ggcaggaggc tgccttccca t 51

<210> 2658
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (2657 is other entry)

<221> misc_feature
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<223> Accession number cg41640016

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ggcaggaggg gccccagcaa ggccacggca ggcaggaggc tgccttccca t 51

<210> 2659
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (2660 is other entry)

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ttacacggat actaaaatga gaagaatccg cactttttgg tttggccact t 51

<210> 2660
<211> 51
<212> DNA
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2659 is other entry)

<221> misc_feature
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<223> Accession number cg41643464

<400> 2660
ttacacggat actaaaatga gaagagtcg cactttttgg tttggccact t 51

<210> 2661
<211> 51
<212> DNA
<213> Homo sapiens

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<222> (26)...(0)
<223> 1 of 2 allelic variants (2662 is other entry)

<221> misc_feature
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<223> Accession number cg41650847

<400> 2661
ctccccacag tcatggtggc tgaaagctgg tgtgcaacct tgttctcga g 51

<210> 2662
<211> 50
<212> DNA
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<223> 2 of 2 allelic variants (2661 is other entry)

<221> misc_feature
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<223> Accession number cg41650847

<400> 2662
ctccccacag tcatggtggc tgaaactggt gtgcaacctt gttcctcgag 50

<210> 2663
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (2664 is other entry)

<221> misc_feature
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<223> Accession number cg41672460

<400> 2663
gcagctcagc tgggtggccgg gtggccggcc cgggcaaccc cagtgaacct g 51

<210> 2664
<211> 50
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (2663 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
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<223> Accession number cg41672460

<400> 2664
gcagctcagc tgggtggccgg gtggccggccc gggcaacccc agtgaacctg 50

<210> 2665
<211> 51
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<213> Homo sapiens

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<223> 1 of 2 allelic variants (2666 is other entry)

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51

<210> 2666

<211> 51

<212> DNA

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<223> Accession number cg42036034

<400> 2666

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51

<210> 2667

<211> 51

<212> DNA

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<223> 1 of 2 allelic variants (2668 is other entry)

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<222> (0)...(0)

<223> Accession number cg42162412

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gtggtgtaat ctcagctcac tgcaaactct gcctcctggg ttcaagccat t

51

<210> 2668

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2667 is other entry)

<221> misc_feature
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<223> Accession number cg42162412

<400> 2668
gtggtgtaat ctcagctcac tgcaacctct gcctcctggg ttcaagccat t 51

<210> 2669
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2670 is other entry)

<221> misc_feature
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<400> 2669
gcctcagcct cccaagtagc tgggactaca ggcgcccgcc accacgcca g 51

<210> 2670
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<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2669 is other entry)

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<400> 2670
gcctcagcct cccaagtagc tgggattaca ggcgcccgcc accacgcca g 51

<210> 2671
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<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2672 is other entry)

<221> misc_feature
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<223> Accession number cg42176262

<400> 2671

ggtggatcac ttgaggtcag gagttcgaga ccaacctggc caacatggtg a

51

<210> 2672

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2671 is other entry)

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<223> Accession number cg42176262

<400> 2672

ggtggatcac ttgaggtcag gagtttgaga ccaacctggc caacatggtg a

51

<210> 2673

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2674 is other entry)

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<223> Accession number cg42180672

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gccccggctt tcctttgctt tcccgttggt tcaaggtttg agcgcttgcc g

51

<210> 2674

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2673 is other entry)

<221> misc_feature

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<223> Accession number cg42180672

<400> 2674

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51

<210> 2675

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (0)...(0)
<223> Accession number cg42186156

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<210> 2676
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2675 is other entry)

<221> misc_feature
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<223> Accession number cg42186156

<400> 2676
aacaataact ttcaccattt ataaatcttt caaattaagg ttttgagtag a 51

<210> 2677
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2678 is other entry)

<221> misc_feature
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<223> Accession number cg42282817

<400> 2677
ggtgggcagc tcttcatccc tctgatttgt catcatatct tcttcttcca g 51

<210> 2678
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (2677 is other entry)

<221> misc_feature
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<223> Accession number cg42282817

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ggtagggcagc tcttcacccc tctgacttgt catcatatct tcttcttcca g 51

<210> 2679
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2680 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42283789

<400> 2679
tgtcacccca gaaagtgaac tctcagtctt cccagccagt ctctttctta t 51

<210> 2680
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2679 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42283789

<400> 2680
tgtcacccca gaaagtgaac tctcactctt cccagccagt ctctttctta t 51

<210> 2681
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2682 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42283789

<400> 2681
ataggctactc ttttgtgtct gctttgttct gctcaacacc atgtttctga a 51

<210> 2682
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2681 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42283789

<400> 2682
ataggtactc ttttgtgtct gctttattct gctcaacacc atgtttctga a 51

<210> 2683
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (2684 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42283789

<400> 2683
ttctgaaatc attaccattg ttgtatgggt ctctaactcc atcatttcca t 51

<210> 2684
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2683 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42283789

<400> 2684
ttctgaaatc attaccattg ttgtacgggt ctctaactcc atcatttcca t 51

<210> 2685
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2686 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42306901

<400> 2685
ggcgcgggcg ggtggggaga gtgagctcgc gccgcggctg gggcgaggct a 51

<210> 2686
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (2685 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42306901

<400> 2686
ggcgcgggcg ggtggggaga gtgagttcgc gccgcggctg gggcgaggct a 51

<210> 2687
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2688 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42313384

<400> 2687
tcctggagga ctacgccttc gtggtgcggg gcctgctgga cctgtatgag g 51

<210> 2688
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (2687 is other entry)

<221> misc_feature

<222> (0)...(0)
<223> Accession number cg42313384

<400> 2688
tcctggagga ctacgccttc gtggttcggg gcctgctgga cctgtatgag g 51

<210> 2689
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2690 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42322469

<400> 2689
gagctaccgt gcccggttg aggtgctttt ttaactaata cattgtagca c 51

<210> 2690
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2689 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42322469

<400> 2690
gagctaccgt gcccggttg aggtgttttt ttaactaata cattgtagca c 51

<210> 2691
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2692 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42322469

<400> 2691
gagacaaggt ttcaccatgt tggccaggct ggtctgacgc tcctgacttc a 51

<210> 2692

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2691 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42322469

<400> 2692

gagacaaggt ttcacccatgt tggccgggct ggtctgacgc tcctgacttc a

51

<210> 2693

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2694 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42329503

<400> 2693

tcactctcca gaccttccta attaacgtct tctcagaatc gaccttctgt c

51

<210> 2694

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2693 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42329503

<400> 2694

tcactctcca gaccttccta attaatgtct tctcagaatc gaccttctgt c

51

<210> 2695

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2696 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42330545

<400> 2695
ccggcggccg cctgaccag tccacctgca ccagtgggggt gtggcatcag t 51

<210> 2696
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2695 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42330545

<400> 2696
ccggcggccg cctgaccag tccacttgca ccagtgggggt gtggcatcag t 51

<210> 2697
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2698 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42330545

<400> 2697
acatttctgc ccctaagtta gagaaccacc ttttagagtg gcgatctcat g 51

<210> 2698
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2697 is other entry)

<221> misc_feature
<222> (0)...(0)

<223> Accession number cg42330545

<400> 2698

acattttctgc ccctaagtta gagaatcacc ttttagagtg gcgatctcat g

51

<210> 2699

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2700 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42330545

<400> 2699

agttagagaa ccacctttta gaggggcgat ctcatgggag tggcagcttg a

51

<210> 2700

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2699 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42330545

<400> 2700

agttagagaa ccacctttta gagggacgat ctcatgggag tggcagcttg a

51

<210> 2701

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2702 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42330545

<400> 2701

ccacctttta gaggggcgat ctcatgggag tggcagcttg actctgcagg a

51

<210> 2702

<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2701 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42330545

<400> 2702
ccacctttta gagtggcgat ctcataggag tggcagcttg actctgcagg a 51

<210> 2703
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2704 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42330545

<400> 2703
caggaaatgt ggggtgctatg agtgcagaac agaaactctt acgcgtnctg a 51

<210> 2704
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2703 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42330545

<400> 2704
caggaaatgt ggggtgctatg agtgcggaac agaaactctt acgcgtnctg a 51

<210> 2705
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature

<222> (26)...(0)
<223> 1 of 2 allelic variants (2706 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42330545

<400> 2705
gctctttgaa ttgaataaag gcaccgctgg gattcgaacc caggatctcc t 51

<210> 2706
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2705 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42330545

<400> 2706
gctctttgaa ttgaataaag gcaccactgg gattcgaacc caggatctcc t 51

<210> 2707
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2708 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42335352

<400> 2707
gaaaagaaca tctccagagg aactgctgaa tgaccacgcc cgagagaaca g 51

<210> 2708
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2707 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42335352

<400> 2708
gaaaagaaca tctccagagg aactggtgaa tgaccacgcc cgagagaaca g 51

<210> 2709
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2710 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42340076

<400> 2709
ggttctagct cctgtgtag ctgttcccaa gtctctcttc ctaacgtggc t 51

<210> 2710
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2709 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42340076

<400> 2710
ggttctagct cctgtgtag ctgtttccaa gtctctcttc ctaacgtggc t 51

<210> 2711
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2712 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42340076

<400> 2711
tggtgctggc acaggccctt ccaggcggga ggctgcgtct caggctggag a 51

<210> 2712
<211> 51

<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2711 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42340076

<400> 2712
tgggtgctggc acaggccctt ccaggtggga ggctgcgtct caggctggag a 51

<210> 2713
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2714 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42340076

<400> 2713
agcaggaaca gggctcagca ccatgcccgg cactcttcat gcattactgc g 51

<210> 2714
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2713 is other entry)

<221> misc_feature
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<223> Accession number cg42340076

<400> 2714
agcaggaaca gggctcagca ccatgtccgg cactcttcat gcattactgc g 51

<210> 2715
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)

<223> 1 of 2 allelic variants (2716 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42340076

<400> 2715

actagctagc aaggggaagg ctgggcccaa ggagataagg aaactgggcc a

51

<210> 2716

<211> 50

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (2715 is other entry)

<221> misc_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42340076

<400> 2716

actagctagc aaggggaagg ctgggcccaag gagataagga aactgggcca

50

<210> 2717

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2718 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42340076

<400> 2717

taaggaaact gggccagggt ctcccagctt gagcttgag acgggggttc a

51

<210> 2718

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2717 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42340076

<400> 2718
taaggaaact gggccagggt ctcccggctt gagcttggag acggggtttc a 51

<210> 2719
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2720 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42340165

<400> 2719
gatttttatc taaatgaata aatttctctg tattgttaaa accattctac t 51

<210> 2720
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2719 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42340165

<400> 2720
gatttttatc taaatgaata aatttatctg tattgttaaa accattctac t 51

<210> 2721
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2722 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42342525

<400> 2721
ttccgggaag ggatcacggt gattgatgtg aaagcctcca tcgaccccggt c 51

<210> 2722
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2721 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42342525

<400> 2722
ttccggaag ggtacacggt gattggtgtg aaagcctcca tcgaccccg c 51

<210> 2723
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2724 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42343432

<400> 2723
ctggatggca agtgctaccc agcacagcag ccgtgaggac ctttcttggg c 51

<210> 2724
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2723 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42343432

<400> 2724
ctggatggca agtgctaccc agcacggcag ccgtgaggac ctttcttggg c 51

<210> 2725
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2726 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42344264

<400> 2725
tacagttgac ttacttaaag tgatgtttaa tgctgtttca tgtattcaga 50

<210> 2726
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2725 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42344264

<400> 2726
tacagttgac ttacttaaag tgatgattta atgctgtttc atgtattcag a 51

<210> 2727
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2728 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42344264

<400> 2727
ttaatgctgt ttcattgatt cagagttgta caaccatcac aatcaatttc a 51

<210> 2728
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature

<222> (26)...(0)
<223> 2 of 2 allelic variants (2727 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42344264

<400> 2728
ttaatgctgt ttcatgtatt cagaggtgta caaccatcac aatcaatttc a 51

<210> 2729
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2730 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42344264

<400> 2729
atcaatttca gagcatcctc ataagcgcac ccaaaagaaa ccctgtactc a 51

<210> 2730
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2729 is other entry)

<221> misc_feature
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<223> Accession number cg42344264

<400> 2730
atcaatttca gagcatcctc ataagtgac ccaaaagaaa ccctgtactc a 51

<210> 2731
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2732 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42344264

<400> 2731
gcgcacccaa aagaaaccct gtactcatta gcagtgaatc tccatttcct c 51

<210> 2732
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2731 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42344264

<400> 2732
gcgcacccaa aagaaaccct gtacttatta gcagtgaatc tccatttcct c 51

<210> 2733
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2734 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42344264

<400> 2733
cctgtactca ttagcagtga atctccattt cctcgcaaac ctctcccag t 51

<210> 2734
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2733 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42344264

<400> 2734
cctgtactca ttagcagtga atctctattt cctcgcaaac ctctcccag t 51

<210> 2735
<211> 51

<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2736 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42347810

<400> 2735
taaaatgaat acgtctatatt atgcgtttaa agaataccat gtagtagacg c 51

<210> 2736
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2735 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42347810

<400> 2736
taaaatgaat acgtctatatt atgcgcttaa agaataccat gtagtagacg c 51

<210> 2737
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2738 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42351001

<400> 2737
aagggtcatc tgaagtcgtg attgggtcac taataacacc aggacaaagt t 51

<210> 2738
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (2737 is other entry)

<221> misc_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42351001

<400> 2738

aagggtcatc tgaagtcgtg attgggtcact aataacacca ggacaaaagtt

50

<210> 2739

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2740 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42356003

<400> 2739

cgtagttaca aatgcttact gatttgcata attatatattt cattggaaga c

51

<210> 2740

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

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<223> 2 of 2 allelic variants (2739 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42356003

<400> 2740

cgtagttaca aatgcttact gatttacata attatatattt cattggaaga c

51

<210> 2741

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<223> 1 of 2 allelic variants (2742 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42356206

<400> 2741
gagggcgagg cagagggcggc ggtagctggc cagagcaagc acgagcagcg g 51

<210> 2742
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (2741 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42356206

<400> 2742
gagggcgagg cagagggcggc ggtagtggcc agagcaagca cgagcagcgg 50

<210> 2743
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (2744 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42369735

<400> 2743
ttcaggtgac catgaaggca cagctgctac ttctgggccc ggggtgatat t 51

<210> 2744
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2743 is other entry)

<221> misc_feature
<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42369735

<400> 2744

ttcaggtgac catgaaggca cagctctact tctgggccgg gggatgatt

50

<210> 2745

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2746 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42370741

<400> 2745

aaaaggcaat ctacatcatc tggaaaattg taacttagta attaattagg a

51

<210> 2746

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

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<223> 2 of 2 allelic variants (2745 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42370741

<400> 2746

aaaaggcaat ctacatcatc tggaagattg taacttagta attaattagg a

51

<210> 2747

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

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<223> 1 of 2 allelic variants (2748 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42370741

<400> 2747
aatctacatc atctggaaaa ttgtaactta gtaattaatt aggataattt c 51

<210> 2748
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (2747 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42370741

<400> 2748
aatctacatc atctggaaaa ttgtacctta gtaattaatt aggataattt c 51

<210> 2749
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (2750 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42381740

<400> 2749
tattcttctgtg ggtgcctgga ggtggagtga ggccaccacc cctgggctgt c 51

<210> 2750
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2749 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42381740

<400> 2750
tattcttctgtg ggtgcctgga ggtggggtga ggccaccacc cctgggctgt c 51

<210> 2751
<211> 51
<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2752 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42385141

<400> 2751

tattaaaaga attctaattt gcatgtttgt agcctgttct ggagagttgg g

51

<210> 2752

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (2751 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42385141

<400> 2752

tattaaaaga attctaattt gcatgcttgt agcctgttct ggagagttgg g

51

<210> 2753

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 1 of 2 allelic variants (2754 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42387697

<400> 2753

gcaggaaagg cagcccaagg aatagcagga gatgttggtt gggtttcacc a

51

<210> 2754

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2753 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42387697

<400> 2754
cgaggaaagg cagcccaagg aatagtagga gatgttggtt gggtttcacc a 51

<210> 2755
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2756 is other entry)

<221> misc_feature
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<223> Accession number cg42387697

<400> 2755
tgctgaatct gtgcttttgg aatagtttga ctcacaatgc tatttgctgc a 51

<210> 2756
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (2755 is other entry)

<221> misc_feature
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<223> Accession number cg42387697

<400> 2756
tgctgaatct gtgcttttgg aatagattga ctcacaatgc tatttgctgc a 51

<210> 2757
<211> 51
<212> DNA
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<220>
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<223> 1 of 2 allelic variants (2758 is other entry)

<221> misc_feature
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<223> Accession number cg42387697

<400> 2757

tgtgcttttg gaatagtttg actcacaatg ctatttgctg catgtgtatt c

51

<210> 2758

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2757 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42387697

<400> 2758

tgtgcttttg gaatagtttg actcataatg ctatttgctg catgtgtatt c

51

<210> 2759

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2760 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42392985

<400> 2759

gagaaccagc tgaaaaagct gtggctcgca tcctggttcc cgtgacgacg g

51

<210> 2760

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2759 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42392985

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gagaaccagc tgaaaaagct gtggcccgca tcctggttcc cgtgacgacg g

51

<210> 2761

<211> 51

<212> DNA

<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (2762 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42458827

<400> 2761
cacccgtggg cactgccggc tcttctgtca cagttcatct tcattgacct g

51

<210> 2762
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2761 is other entry)

<221> misc_feature
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<223> Accession number cg42458827

<400> 2762
cacccgtggg cactgccggc tcttccgtca cagttcatct tcattgacct g

51

<210> 2763
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2764 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42458827

<400> 2763
ggcactgccg gctcttctgt cacagttcat cttcattgac ctgcctatgt t

51

<210> 2764
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2763 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42458827

<400> 2764
ggcaactgccg gctcttctgt cacagctcat cttcattgac ctgcctatgt t 51

<210> 2765
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2766 is other entry)

<221> misc_feature
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<223> Accession number cg42458827

<400> 2765
gttcaccttc attgacctgc ctatgtttct taccgcccc acagcggaac c 51

<210> 2766
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2765 is other entry)

<221> misc_feature
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<223> Accession number cg42458827

<400> 2766
gttcaccttc attgacctgc ctatgtttct taccgcccc acagcggaac c 51

<210> 2767
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2768 is other entry)

<221> misc_feature
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<223> Accession number cg42458827

<400> 2767
tcattgacct gcctatgttt cttaccgcc ccacagcgga accttttgct g 51

<210> 2768

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (2767 is other entry)

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<223> Accession number cg42458827

<400> 2768

tcattgacct gcctatgttt cttactgccc ccacagcgga accttttgct g

51

<210> 2769

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2770 is other entry)

<221> misc_feature

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<223> Accession number cg42458827

<400> 2769

gtttcttacc gccccacag cggaaccttt tgctgagaat gatgaggagg c

51

<210> 2770

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2769 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42458827

<400> 2770

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51

<210> 2771

<211> 51

<212> DNA

<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2772 is other entry)

<221> misc_feature
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<223> Accession number cg42458827

<400> 2771
ccccacagcg gaaccttttg ctgagaatga tgaggaggcc cacgacgaag g 51

<210> 2772
<211> 51
<212> DNA
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<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2771 is other entry)

<221> misc_feature
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<223> Accession number cg42458827

<400> 2772
ccccacagcg gaaccttttg ctgaggatga tgaggaggcc cacgacgaag g 51

<210> 2773
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2774 is other entry)

<221> misc_feature
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<223> Accession number cg42458827

<400> 2773
accttttgct gagaatgatg aggaggccca cgacgaaggc caggcccgcg a 51

<210> 2774
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2773 is other entry)

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<222> (0)...(0)
<223> Accession number cg42458827

<400> 2774
accttttgct gagaatgatg aggagtccca cgacgaaggc caggcccgcg a 51

<210> 2775
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
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<223> 1 of 2 allelic variants (2776 is other entry)

<221> misc_feature
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<223> Accession number cg42458827

<400> 2775
cgaagatcag gcctcctttg cggacggttt catagtcgta ctogaaggga t 51

<210> 2776
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2775 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42458827

<400> 2776
cgaagatcag gcctcctttg cggactgttt catagtcgta ctogaaggga t 51

<210> 2777
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2778 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42458827

<400> 2777
ctcctttgcg gacggtttca tagtcgtact cgaagggaatt ctctgtcccc t 51

<210> 2778
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2777 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42458827

<400> 2778
ctcctttgcg gacggtttca tagtcatact cgaaggatt ctctgtcccc t 51

<210> 2779
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2780 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42460243

<400> 2779
gagtccgaga ctgcttgagc gctgcgacac cccctctcgt gggcccccca c 51

<210> 2780
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2779 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
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<223> Accession number cg42460243

<400> 2780
gagtccgaga ctgcttgagc gctgccacac cccctctcgtg ggccccccac 50

<210> 2781
<211> 50

<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (2782 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42462239

<400> 2781
cacaggagag agctgaaggt ggggtgccag gccagggtgt gaactttctc

50

<210> 2782
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (2781 is other entry)

<221> misc_feature
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<223> Accession number cg42462239

<400> 2782
cacaggagag agctgaaggt ggggtggcca ggccagggtg tgaactttct c

51

<210> 2783
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2784 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42462775

<400> 2783
gtgactcctt gttcatgaga gcagaatttt aacaagacaa gtatgaaagg a

51

<210> 2784
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2783 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42462775

<400> 2784
gtgactcctt gttcatgaga gcagatTTTT aacaagacaa gtatgaaagg a 51

<210> 2785
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2786 is other entry)

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<222> (0)...(0)
<223> Accession number cg42466107

<400> 2785
aaataccaac cggctctgtag tgtgtactca cctaatact tctgttatcg a 51

<210> 2786
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2785 is other entry)

<221> misc_feature
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<223> Accession number cg42466107

<400> 2786
aaataccaac cggctctgtag tgtgtgtca cctaatact tctgttatcg a 51

<210> 2787
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2788 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42469263

<400> 2787
aaatgtggca cccagaggga gtggcctaata agccagttac caataatata t 51

<210> 2788
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2787 is other entry)

<221> misc_feature
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<223> Accession number cg42469263

<400> 2788
aaatgtggca cccagaggga gtggcataata agccagttac caataatata t 51

<210> 2789
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2790 is other entry)

<221> misc_feature
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<223> Accession number cg42473468

<400> 2789
cacaatctca gctcactgca acctccacct cccaggttca agcgattctc c 51

<210> 2790
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (2789 is other entry)

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<223> Accession number cg42473468

<400> 2790
cacaatctca gctcactgca acctctacct cccaggttca agcgattctc c 51

<210> 2791
<211> 51
<212> DNA
<213> Homo sapiens

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<222> (26)...(0)
<223> 1 of 2 allelic variants (2792 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42481310

<400> 2791
gctggaaata taaacatggc attttcaggt aaagtttctt ccactagttg a 51

<210> 2792
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2791 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42481310

<400> 2792
gctggaaata taaacatggc atttttaggt aaagtttctt ccactagttg a 51

<210> 2793
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2794 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42481963

<400> 2793
gagatcgtgc cactgcactc cagcctgggg gacaaagcaa gactccctct c 51

<210> 2794
<211> 51
<212> DNA
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2793 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42481963

<400> 2794
gagatcgtgc cactgcactc cagcccgggg gacaaagcaa gactccctct c 51

<210> 2795
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (2796 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42491212

<400> 2795
gcctcaggag cggtggctgg atttgagaga gaaaattggg ttagcatca a 51

<210> 2796
<211> 51
<212> DNA
<213> Homo sapiens

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<222> (26)...(0)
<223> 2 of 2 allelic variants (2795 is other entry)

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<223> Accession number cg42491212

<400> 2796
gcctcaggag cggtggctgg atttgggaga gaaaattggg ttagcatca a 51

<210> 2797
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (2798 is other entry)

<221> misc_feature

<222> (0)...(0)
<223> Accession number cg42491212

<400> 2797
catcaaggag gtaaccgcc cgccccgga cttacatcgt cgccactcgc t 51

<210> 2798
<211> 51
<212> DNA
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2797 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42491212

<400> 2798
catcaaggag gtaaccgcc cgccccgga cttacatcgt cgccactcgc t 51

<210> 2799
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (2800 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42495105

<400> 2799
tttcaactgac gcctaggctt gtcactgctg caggtgagag tggtgtggtt g 51

<210> 2800
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (2799 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42495105

<400> 2800
tttcaactgac gcctaggctt gtcatactgg caggtgagag tggtgtggtt g 51

<210> 2801
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2802 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42500135

<400> 2801
agccacatc tgcctctggc cctcaggggc gctggggaaa ggaaggccaa a 51

<210> 2802
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2801 is other entry)

<221> misc_feature
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<221> misc_feature
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<400> 2802
agccacatc tgcctctggc cctcagggcg ctggggaaaag gaaggccaaa 50

<210> 2803
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2804 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42500135

<400> 2803
ctcctcagca cgtgtctggt gggccaggcg tgcagtgatg tgggccaggt c 51

<210> 2804
<211> 51

<212> DNA
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<223> 2 of 2 allelic variants (2803 is other entry)

<221> misc_feature
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<400> 2804
ctcctcagca cgtgtctggt gggccgggcg tgcagtgatg tgggccaggt c 51

<210> 2805
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (2806 is other entry)

<221> misc_feature
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<223> Accession number cg42500135

<400> 2805
gcacgtgtct ggtgggccag gcgtgcagtg atgtgggccca ggtccgcggc c 51

<210> 2806
<211> 50
<212> DNA
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<223> 2 of 2 allelic variants (2805 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
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<400> 2806
gcacgtgtct ggtgggccag gcgtgagtga tgtgggccag gtccgcggcc 50

<210> 2807
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2808 is other entry)

<221> misc_feature
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<223> Accession number cg42500135

<400> 2807
gggccaggcg tgcagtgatg tgggccagggt ccgcggcctt gtccagcttg a 51

<210> 2808
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2807 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42500135

<400> 2808
gggccaggcg tgcagtgatg tgggcgagggt ccgcggcctt gtccagcttg a 51

<210> 2809
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2810 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42501567

<400> 2809
gcctcagtgc cctcagcgcc ttctgtcttc tggctggatt cagagtcccg g 51

<210> 2810
<211> 51
<212> DNA
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<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2809 is other entry)

<221> misc_feature
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<223> Accession number cg42501567

<400> 2810
gcctcagtgc cctcagcgcc ttctgccttc tggctggatt cagagtcccg g 51

<210> 2811
<211> 51
<212> DNA
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2812 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42510617

<400> 2811
agcctaggag tttagagacca gcctagacaa catagtgaga aatccatctc a 51

<210> 2812
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (2811 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42510617

<400> 2812
agcctaggag tttagagacca gcctaaacaa catagtgaga aatccatctc a 51

<210> 2813
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2814 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42513366

<400> 2813
gtggacgctg ttctgcctg agagtctctt agaggaaggc tgggaacact g 51

<210> 2814
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2813 is other entry)

<221> misc_feature
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<223> Accession number cg42513366

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gtggacgctg ttcctgctg agagtttctt agaggaaggc tgggaacact g 51

<210> 2815
<211> 51
<212> DNA
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<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2816 is other entry)

<221> misc_feature
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<223> Accession number cg42513366

<400> 2815
ggacgctgtt cctgcctgag agtctcttag aggaaggctg ggaacactgt g 51

<210> 2816
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2815 is other entry)

<221> misc_feature
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<223> Accession number cg42513366

<400> 2816
ggacgctgtt cctgcctgag agtcttttag aggaaggctg ggaacactgt g 51

<210> 2817
<211> 51
<212> DNA
<213> Homo sapiens

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<222> (26)...(0)
<223> 1 of 2 allelic variants (2818 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42513366

<400> 2817
tttttttgga gaaagtttgc tttttgtttt ttttttttta agacaaggtc t 51

<210> 2818
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (2817 is other entry)

<221> misc_feature
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<223> Accession number cg42513366

<400> 2818
tttttttgga gaaagtttgc tttttttttt ttttttttta agacaaggtc t 51

<210> 2819
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (2820 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42513366

<400> 2819
aaagtttgc ttttggtttt ttttttttaa gacaaggctc cattctgtca c 51

<210> 2820
<211> 50
<212> DNA
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<223> 2 of 2 allelic variants (2819 is other entry)

<221> misc_feature

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<400> 2820
aaagtttgct tttgtttttt tttttttaag acaaggtctc attctgtcac 50

<210> 2821
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (2822 is other entry)

<221> misc_feature
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<223> Accession number cg42513366

<400> 2821
aagtttgctt tttgtttttt tttttttaag acaaggtctc attctgtcac c 51

<210> 2822
<211> 50
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2821 is other entry)

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<400> 2822
aagtttgctt tttgtttttt ttttttaaga caaggtctca ttctgtcacc 50

<210> 2823
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (2824 is other entry)

<221> misc_feature
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<223> Accession number cg42513366

<400> 2823
agtttgcttt ttgttttttt tttttaaga caaggtctca ttctgtcacc c 51

<210> 2824
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (2823 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
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<223> Accession number cg42513366

<400> 2824
agtttgcttt ttgttttttt tttttaagac aaggtctcat tctgtcacc 50

<210> 2825
<211> 51
<212> DNA
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<220>
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<223> 1 of 2 allelic variants (2826 is other entry)

<221> misc_feature
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<223> Accession number cg42513533

<400> 2825
gcagcctctc agctgccacc atggagcacc tggcggcaga acgcagacct c 51

<210> 2826
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2825 is other entry)

<221> misc_feature

<222> (0)...(0)
<223> Accession number cg42513533

<400> 2826
gcagcctctc agctgccacc atggaccacc tggcggcaga acgagacct c 51

<210> 2827
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2828 is other entry)

<221> misc_feature
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<223> Accession number cg42513533

<400> 2827
agcctctcag ctgccaccat ggagcacctg gcggcagaac gcagacctct a 51

<210> 2828
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2827 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42513533

<400> 2828
agcctctcag ctgccaccat ggagcgctg gcggcagaac gcagacctct a 51

<210> 2829
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2830 is other entry)

<221> misc_feature
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<223> Accession number cg42513533

<400> 2829
caccatggag cacctggcgg cagaacgcag acctctagct ctctttgcca g 51

<210> 2830
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2829 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42513533

<400> 2830
caccatggag cacctggcgg cagaaagcag acctctagct ctctttgccca g 51

<210> 2831
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2832 is other entry)

<221> misc_feature
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<223> Accession number cg42513533

<400> 2831
accatggagc acctggcggc agaacgcaga cctctagctc tctttgccag c 51

<210> 2832
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2831 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42513533

<400> 2832
accatggagc acctggcggc agaaccaga cctctagctc tctttgccag c 51

<210> 2833
<211> 51
<212> DNA
<213> Homo sapiens

<220>

<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2834 is other entry)

<221> misc_feature
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<223> Accession number cg42513533

<400> 2833
gaacgcagac ctctagctct ctttgccagc ctcttggtta gacctgcgtt c 51

<210> 2834
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2833 is other entry)

<221> misc_feature
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<223> Accession number cg42513533

<400> 2834
gaacgcagac ctctagctct ctttgacagc ctcttggtta gacctgcgtt c 51

<210> 2835
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2836 is other entry)

<221> misc_feature
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<223> Accession number cg42513533

<400> 2835
tgccagcctc ctggctagac ctgcgttcac tgcgcaccct ggctgacgtg c 51

<210> 2836
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2835 is other entry)

<221> misc_feature
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<223> Accession number cg42513533

<400> 2836

tgccagcctc ctggctagac ctgcgctcat tgcgcaccct ggctgacgtg c

51

<210> 2837

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (2838 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42513533

<400> 2837

ttagtcaaag cctggagaat agttacatct cctggatgat cagttcagaa a

51

<210> 2838

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2837 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42513533

<400> 2838

ttagtcaaag cctggagaat agttatatct cctggatgat cagttcagaa a

51

<210> 2839

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2840 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42513533

<400> 2839

agtgcagaga tatatcaciaa tgtcccctgt acaaaaagcc tggaaatgat t

51

<210> 2840

<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2839 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42513533

<400> 2840
agtgcagaga tatatcaciaa tgtccgctgt acaaaaagcc tggaaatgat t 51

<210> 2841
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2842 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42521007

<400> 2841
aaggtgggtg ggttggtcca gtaaatgac tgcaccatca cacaagccaa g 51

<210> 2842
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2841 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42521007

<400> 2842
aaggtgggtg ggttggtcca gtaaatgac tgcaccatca cacaagccaa g 51

<210> 2843
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature

<222> (26)...(0)
<223> 1 of 2 allelic variants (2844 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42527623

<400> 2843
gaagcaaact cccaaatggg gcacaaagggt aataaaaagc agctgagaga t 51

<210> 2844
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2843 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42527623

<400> 2844
gaagcaaact cccaaatggg gcacagagggt aataaaaagc agctgagaga t 51

<210> 2845
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2846 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42527623

<400> 2845
aaacactgga acaccaggtc tctcagatgc ccgcgggagg ggccccaggg a 51

<210> 2846
<211> 51
<212> DNA
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<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2845 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42527623

<400> 2846
aaacactgga acaccagggtc tctcacatgc ccgcgggagg ggccccaggg a 51

<210> 2847
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2848 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42528323

<400> 2847
ccccagaaac ctgggaattg agagcacaag catatgggtc acaaggcccc g 51

<210> 2848
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2847 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42528323

<400> 2848
ccccagaaac ctgggaattg agagctcaag catatgggtc acaaggcccc g 51

<210> 2849
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2850 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42528323

<400> 2849
acctgggaat tgagagcaca agcatatggc tcacaaggcc ccgccctgcc a 51

<210> 2850
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51

<210> 2851
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (2852 is other entry)

<221> misc_feature
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<223> Accession number cg42528323

<400> 2851
cctgggaatt gagagcacao gcatatggct cacaaggccc cgcacctgcca g

51

<210> 2852
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (2851 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42528323

<400> 2852
cctgggaatt gagagcacao gcataaggct cacaaggccc cgcacctgcca g

51

<210> 2853
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (2854 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42528323

<400> 2853

aattgagagc acaagcatat ggctcacaag gccccgccct gccagcggcc c

51

<210> 2854

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (2853 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42528323

<400> 2854

aattgagagc acaagcatat ggctctcaag gccccgccct gccagcggcc c

51

<210> 2855

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (2856 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42528323

<400> 2855

attgagagca caagcatatg gctcacaagg ccccgccctg ccagcgcccc c

51

<210> 2856

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (2855 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42528323

<400> 2856
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<210> 2857
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (2858 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42528323

<400> 2857
ccctgccagc ggccccgccc cacctttcat tcattgctgg ctgctaggag c 51

<210> 2858
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (2857 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
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<223> Accession number cg42528323

<400> 2858
ccctgccagc ggccccgccc caccttcatt cattgctggc tgctaggagc 50

<210> 2859
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (2860 is other entry)

<221> misc_feature
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<223> Accession number cg42528323

<400> 2859
cctgccagcg gccccgcccc accttcatt cattgctggc tgctaggagc t 51

<210> 2860
<211> 50
<212> DNA
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<223> 2 of 2 allelic variants (2859 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
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<223> Accession number cg42528323

<400> 2860
cctgccagcg gccccgcccc accttcattc attgctggct gctaggagct

50

<210> 2861
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (2862 is other entry)

<221> misc_feature
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<223> Accession number cg42528509

<400> 2861
agaaaaaagc tccagagttt cctatgttgg agaagcagaa ctggttgatt c

51

<210> 2862
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (2861 is other entry)

<221> misc_feature
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<223> Accession number cg42528509

<400> 2862
agaaaaaagc tccagagttt cctatgttgg agaagcagaa ctggttgatt c

51

<210> 2863

<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (2864 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42532779

<400> 2863
tgtgaaactt gctttctttt ttttttttga gacggagtct gctctgtcg c 51

<210> 2864
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2863 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
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<223> Accession number cg42532779

<400> 2864
tgtgaaactt gctttctttt ttttttttgag acggagtctc gctctgtcgc 50

<210> 2865
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2866 is other entry)

<221> misc_feature
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<223> Accession number cg42532779

<400> 2865
gtgaaacttg ctttctttt ttttttttgag acggagtctc gctctgtcgc c 51

<210> 2866
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<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (2865 is other entry)

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<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

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<222> (0)...(0)

<223> Accession number cg42532779

<400> 2866

gtgaaacttg cttctcttttt ttttttgaga cggagtctcg ctctgtcgcc

50

<210> 2867

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2868 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42532779

<400> 2867

tgaaacttgc tttctcttttt ttttttgaga cggagtctcg ctctgtcgcc c

51

<210> 2868

<211> 50

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (2867 is other entry)

<221> misc_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42532779

<400> 2868

tgaaacttgc tttctcttttt tttttgagac ggagtctcgc tctgtcgccc

50

<210> 2869

<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2870 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42537030

<400> 2869
ggtgcccctg ccctttgccg gcttcgtggc gcaggcgcct aacaactacc g 51

<210> 2870
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2869 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42537030

<400> 2870
ggtgcccctg ccctttgccg gcttcttggc gcaggcgcct aacaactacc g 51

<210> 2871
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2872 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42537030

<400> 2871
agttcgggcc cggggtcacg gagaaccccc agtaccceaa cccggcactg c 51

<210> 2872
<211> 51
<212> DNA
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<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2871 is other entry)

<221> misc_feature
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<223> Accession number cg42537030

<400> 2872
agttcggggcc cggggtcacg gagaatcccc agtaccctcaa cccggcactg c 51

<210> 2873
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2874 is other entry)

<221> misc_feature
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<223> Accession number cg42539286

<400> 2873
ggtggcaggt tggtccttaa agggacatct tgctttagaa atacgataaa t 51

<210> 2874
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2873 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42539286

<400> 2874
ggtggcaggt tggtccttaa agggatatct tgctttagaa atacgataaa t 51

<210> 2875
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2876 is other entry)

<221> misc_feature
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<223> Accession number cg42542592

<400> 2875
tagagaaggg gtttcaccgt gttggccagg ctggtcttaa actgccaacc t 51

<210> 2876
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2875 is other entry)

<221> misc_feature
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<223> Accession number cg42542592

<400> 2876
tagagaaggg gtttcaccgt gttggtcagg ctggtcttaa actgccaacc t 51

<210> 2877
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2878 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42543610

<400> 2877
attcatcaat ttcaaacttt ccctgcaagt aatactggat gaaaattaac t 51

<210> 2878
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (2877 is other entry)

<221> misc_feature
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<223> Accession number cg42543610

<400> 2878
attcatcaat ttcaaacttt ccctgaaagt aatactggat gaaaattaac t 51

<210> 2879
<211> 51

<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2880 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42543610

<400> 2879
aataaaacat aaatttcctt aatttgatac tgtaaatgga gtaatttggt g 51

<210> 2880
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2879 is other entry)

<221> misc_feature
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<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42543610

<400> 2880
aataaaacat aaatttcctt aatttatact gtaaatggag taatttggtg 50

<210> 2881
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2882 is other entry)

<221> misc_feature
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<223> Accession number cg42544183

<400> 2881
cctcccaaag tgctgggatt acaggcgtga gcttctgtgc ccagccataa g 51

<210> 2882
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2881 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42544183

<400> 2882
cctcccaaag tgctgggatt acaggtgtga gtttctgtgc ccagccataa g 51

<210> 2883
<211> 50
<212> DNA
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<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2884 is other entry)

<221> misc_feature
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<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42546822

<400> 2883
gtattctgtg ttcttaagaa aaaaagaatt tctgagcttc acgaccttct 50

<210> 2884
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2883 is other entry)

<221> misc_feature
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<223> Accession number cg42546822

<400> 2884
gtattctgtg ttcttaagaa aaaaagaat ttctgagctt cagaccttc t 51

<210> 2885
<211> 51
<212> DNA
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<220>

<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2886 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42547288

<400> 2885
aagactttca gaccagtctg ggcaatgtgg cgagaccgtc tctacaaaaa a 51

<210> 2886
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2885 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42547288

<400> 2886
aagactttca gaccagtctg ggcaacgtgg cgagaccgtc tctacaaaaa a 51

<210> 2887
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2888 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42548835

<400> 2887
gattacaggc gtgagccact gtgcctgggc attttaattt tttaaagcc t 51

<210> 2888
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2887 is other entry)

<221> misc_feature
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<223> Accession number cg42548835

<400> 2888

gattacaggc gtgagccact gtgcccggtc attttaattt tttaaatgcc t

51

<210> 2889

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 1 of 2 allelic variants (2890 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42549000

<400> 2889

ctcacggaac gtcagcaacg atcccgatgt catcaagttg caagagattc c

51

<210> 2890

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2889 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42549000

<400> 2890

ctcacggaac gtcagcaacg atcccatgt catcaagttg caagagattc c

51

<210> 2891

<211> 50

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2892 is other entry)

<221> misc_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42560726

<400> 2891
tcccgcggtg agccaggtgt ggtgggtcacg cctgtaatct cagcactctg 50

<210> 2892
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2891 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42560726

<400> 2892
tcccgcggtg agccaggtgt ggtgggtcac gcctgtaatc tcagcactct g 51

<210> 2893
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2894 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42563045

<400> 2893
gaacaaaaat acaggaaaaa aaaaaatata acaggttcgc acaacatcca g 51

<210> 2894
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2893 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42563045

<400> 2894
gaacaaaaat acaggaaaaa aaaaatacaa caggttcgca caacatccag 50

<210> 2895
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2896 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42563666

<400> 2895
atgatctcat caaagagata acggagatct tcccacggga cctggggagg g 51

<210> 2896
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (2895 is other entry)

<221> misc_feature
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<223> Accession number cg42563666

<400> 2896
atgatctcat caaagagata acggacatct tcccacggga cctggggagg g 51

<210> 2897
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2898 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42566605

<400> 2897
gtcaaataagg atggtggctg gggccagggc tctggggact ccttctgccc c 51

<210> 2898
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2897 is other entry)

<221> misc_feature
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<223> Accession number cg42566605

<400> 2898
gtcaaataagg atggtggctg gggccggggc tctggggact ccttctgccc c 51

<210> 2899
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2900 is other entry)

<221> misc_feature
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<223> Accession number cg42647678

<400> 2899
acaaccctt atcttaaccc agacactccc ttctattgat tctaggtctt t 51

<210> 2900
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2899 is other entry)

<221> misc_feature
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<223> Accession number cg42647678

<400> 2900
acaaccctt atcttaaccc agacattccc ttctattgat tctaggtctt t 51

<210> 2901
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2902 is other entry)

<221> misc_feature

<222> (0)...(0)
<223> Accession number cg42653839

<400> 2901
acttttaaat taaataagag tatttggtat ggaggattac tctaaagcca a 51

<210> 2902
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2901 is other entry)

<221> misc_feature
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<223> Accession number cg42653839

<400> 2902
acttttaaat taaataagag tattttattat ggaggattac tctaaagcca a 51

<210> 2903
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2904 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42655636

<400> 2903
ttatttttgt agtttcaatg cttttcttcc ccgaggaaag ggaggagctc a 51

<210> 2904
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2903 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42655636

<400> 2904
ttatttttgt agtttcaatg cttttgttcc ccgaggaaag ggaggagctc a 51

<210> 2905
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2906 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42655636

<400> 2905
ttgtagtttc aatgcttttc ttccccgagg aaaggaggga gctcaggaga a 51

<210> 2906
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
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<223> 2 of 2 allelic variants (2905 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42655636

<400> 2906
ttgtagtttc aatgcttttc ttccccgagg aaaggaggga gctcaggaga a 51

<210> 2907
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2908 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42655636

<400> 2907
gggaggagct caggagaaca gtgtcatcaa aatttcctgg tggttggtta a 51

<210> 2908
<211> 51
<212> DNA
<213> Homo sapiens

<220>

<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2907 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42655636

<400> 2908
gggaggagct caggagaaca gtgtcgtcaa aatttcctgg tggttgttta a

51

<210> 2909
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (2910 is other entry)

<221> misc_feature
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<223> Accession number cg42655636

<400> 2909
ttcctggtgg ttgtttaatc acagcagcag agtaggtcag gaaactcttc c

51

<210> 2910
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2909 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42655636

<400> 2910
ttcctggtgg ttgtttaatc acagccgcag agtaggtcag gaaactcttc c

51

<210> 2911
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (2912 is other entry)

<221> misc_feature
<222> (0)...(0)

<223> Accession number cg42655636

<400> 2911

ctggtggttg tttaatcaca gcagcagagt aggtcaggaa actcttcag a

51

<210> 2912

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (2911 is other entry)

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<222> (0)...(0)

<223> Accession number cg42655636

<400> 2912

ctggtggttg tttaatcaca gcagccgagt aggtcaggaa actcttcag a

51

<210> 2913

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2914 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42660192

<400> 2913

ggagagcagt ttctcataaa agcttgtgga ttcaactgta aaagtggcaa t

51

<210> 2914

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (2913 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42660192

<400> 2914

ggagagcagt ttctcataaa agcttttggga ttcaactgta aaagtggcaa t

51

<210> 2915

<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2916 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42660573

<400> 2915
tcacatcttg gcacatttaa gagacagtca cccaggact caaaaatagg g 51

<210> 2916
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2915 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42660573

<400> 2916
tcacatcttg gcacatttaa gagactgtca cccaggact caaaaatagg g 51

<210> 2917
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2918 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42663908

<400> 2917
tcagctgata tgaaattata aaattccaca agtctgagta ttgaaactt a 51

<210> 2918
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature

<222> (26)...(0)
<223> 2 of 2 allelic variants (2917 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42663908

<400> 2918
tcagctgata tgaaattata aaatttcaca agtctgagta ttgaaactt a 51

<210> 2919
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2920 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42663908

<400> 2919
cagctgatat gaaattataa aattccacaa gtctgagtat ttgaaactta t 51

<210> 2920
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2919 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42663908

<400> 2920
cagctgatat gaaattataa aattctacaa gtctgagtat ttgaaactta t 51

<210> 2921
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2922 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42664168

<400> 2921
ttgatccac ctaacaccaa atgggactcc caaatagcgt ttgttggtta t 51

<210> 2922
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2921 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42664168

<400> 2922
ttgatccac ctaacaccaa atggggctcc caaatagcgt ttgttggtta t 51

<210> 2923
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2924 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42667019

<400> 2923
cagataattc tcaagaaacg tgaagagctc ttttaatttaa tattaagtga g 51

<210> 2924
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2923 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42667019

<400> 2924
cagataattc tcaagaaacg tgaaggctc ttttaatttaa tattaagtga g 51

<210> 2925
<211> 51

<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2926 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42667523

<400> 2925
cgggtgcagg gggaggagag aacagagaag tgcattgtct caccagctgg c 51

<210> 2926
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2925 is other entry)

<221> misc_feature
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<223> Accession number cg42667523

<400> 2926
cgggtgcagg gggaggagag aacagggaag tgcattgtct caccagctgg c 51

<210> 2927
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2928 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42667523

<400> 2927
gcagcccagg accctgctgg ggcgagcatt ccttttagaa aagaaaaccc a 51

<210> 2928
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)

<223> 2 of 2 allelic variants (2927 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42667523

<400> 2928

gcagcccagg accctgctgg ggcgaacatt ccttttagaa aagaaaaccc a

51

<210> 2929

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2930 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42667523

<400> 2929

tggggcgagc attcctttta gaaaagaaaa cccatcagca ggtatgaagc c

51

<210> 2930

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2929 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42667523

<400> 2930

tggggcgagc attcctttta gaaaaaaaaa cccatcagca ggtatgaagc c

51

<210> 2931

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2932 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42667523

<400> 2931
tttttagaaaa gaaaacccat cagcaggtat gaagccctca ggtctggta t 51

<210> 2932
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2931 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42667523

<400> 2932
tttttagaaaa gaaaacccat cagcaagtat gaagccctca ggtctggta t 51

<210> 2933
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2934 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42667523

<400> 2933
aaaacccatc agcaggtatg aagccctcag ggtctggat caaaggtggg t 51

<210> 2934
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2933 is other entry)

<221> misc_feature
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<223> Accession number cg42667523

<400> 2934
aaaacccatc agcaggtatg aagccctcag ggtctggat caaaggtggg t 51

<210> 2935
<211> 51
<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2936 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42667523

<400> 2935

tctggtatca aaggtgggtg gattgcacct tggcctctta tgtcattagg a

51

<210> 2936

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2935 is other entry)

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<222> (0)...(0)

<223> Accession number cg42667523

<400> 2936

tctggtatca aaggtgggtg gattgtacct tggcctctta tgtcattagg a

51

<210> 2937

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2938 is other entry)

<221> misc_feature

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<223> Accession number cg42667523

<400> 2937

aaggtgggtg gattgcacct tggcctctta tgtcattagg aaaggggttt c

51

<210> 2938

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2937 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42667523

<400> 2938
aaggtgggtg gattgcacct tggccccctta tgtcattagg aaaggggttt c 51

<210> 2939
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2940 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42667523

<400> 2939
ccagagccca ggacaaatcc atggacaaat aatggggaga tgtggtcagg c 51

<210> 2940
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2939 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42667523

<400> 2940
ccagagccca ggacaaatcc atggataaat aatggggaga tgtggtcagg c 51

<210> 2941
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2942 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42669434

<400> 2941

caagcatagc ttcttaactt tcacagccat tcagtagatt tagtggatgc c

51

<210> 2942

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (2941 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42669434

<400> 2942

caagcatagc ttcttaactt tcacaacccat tcagtagatt tagtggatgc c

51

<210> 2943

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2944 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42669440

<400> 2943

aaaattcatt gagggggggg ctcgcattgt acaaagaaaa tcagaccac c

51

<210> 2944

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2943 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42669440

<400> 2944

aaaattcatt gagggggggg ctcgcgttgt acaaagaaaa tcagaccac c

51

<210> 2945

<211> 51

<212> DNA

<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2946 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42669876

<400> 2945
catgtcatga gaatatcacg aacacacatt aaacatgaat taggtacctg c 51

<210> 2946
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2945 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42669876

<400> 2946
catgtcatga gaatatcacg aacactcatt aaacatgaat taggtacctg c 51

<210> 2947
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2948 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42669876

<400> 2947
atatcacgaa cacacattaa acatgaatta ggtacctgcc ttgtggcaag t 51

<210> 2948
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2947 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42669876

<400> 2948
atatcagcaa cacacattaa acatgtatta ggtacctgcc ttgtggcaag t 51

<210> 2949
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2950 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42669876

<400> 2949
gtcaggcaac cctaggaaaa gccctaactg aaagggggaa aagacacaca c 51

<210> 2950
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2949 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42669876

<400> 2950
gtcaggcaac cctaggaaaa gcccttactg aaagggggaa aagacacaca c 51

<210> 2951
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2952 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42669876

<400> 2951
gtaaacagga atacacacac aggtaaacac aatgctgcgc aagagcccag a 51

<210> 2952
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2951 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42669876

<400> 2952
gtaaacagga atacacacac aggtacacac aatgctgcgc aagagcccag a 51

<210> 2953
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2954 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42670494

<400> 2953
cctgtcctct aagttttcag tcctcgtctca ccctggaagg agacctgaaa t 51

<210> 2954
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2953 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42670494

<400> 2954
cctgtcctct aagttttcag tcctcgtctca ccctggaagg agacctgaaa t 51

<210> 2955
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2956 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42670494

<400> 2955
ctcgcctcacc ctggaaggag acctgaaatc acaggacaac ggcagtggtga c 51

<210> 2956
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2955 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42670494

<400> 2956
ctcgcctcacc ctggaaggag acctggaatc acaggacaac ggcagtggtga c 51

<210> 2957
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2958 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42670494

<400> 2957
gtacaggaga gcagagcctc ccattccagg caccagagt tccattccag 50

<210> 2958
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2957 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42670494

<400> 2958
gtacaggaga gcagagcctc ccattcccag gcacccagag ttccattcca g 51

<210> 2959
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2960 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42670494

<400> 2959
tctttcttct ggcaccaaatt ctgtagagtt tgctgaacac caagcaattc t 51

<210> 2960
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2959 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42670494

<400> 2960
tctttcttct ggcaccaaatt ctgtaaagtt tgctgaacac caagcaattc t 51

<210> 2961
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2962 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42670494

<400> 2961
tgctgaacac caagcaattc tccaacacta acacattgtc taacatttga a 51

<210> 2962
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2961 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42670494

<400> 2962
tgctgaacac caagcaattc tccaaaacta acacattgtc taacatttga a 51

<210> 2963
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2964 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42670494

<400> 2963
agtgggggtct gttatcagag ctctctgtcct ctaagttttc agtcctcgct c 51

<210> 2964
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2963 is other entry)

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<223> Accession number cg42670494

<400> 2964
agtgggggtct gttatcagag ctctcttcct ctaagttttc agtcctcgct c 51

<210> 2965
<211> 51

<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (2966 is other entry)

<221> misc_feature
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<223> Accession number cg42670545 ,

<400> 2965
gaatacatct taatgttctc accatacaca caaaaaaggt aattatgtga g 51

<210> 2966
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2965 is other entry)

<221> misc_feature
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<223> Accession number cg42670545

<400> 2966
gaatacatct taatgttctc accatgcaca caaaaaaggt aattatgtga g 51

<210> 2967
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2968 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42670658

<400> 2967
aaagaaagta atttgaatgg ttctagtact agggccatta ttaactagta a 51

<210> 2968
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (2967 is other entry)

<221> misc_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42670658

<400> 2968

aaagaaagta atttgaatgg ttctatacta gggccattat taactagtaa

50

<210> 2969

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (2970 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42672418

<400> 2969

tggaaccgtt tcatagactg aagtgtgaac gtaggagggg atggatatca g

51

<210> 2970

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

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<221> misc_feature

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<223> Accession number cg42672418

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tggaaccgtt tcatagactg aagtgcgaac gtaggagggg atggatatca g

51

<210> 2971

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (2972 is other entry)

<221> misc_feature
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<223> Accession number cg42676483

<400> 2971
gttacgaagg cagcattttc tgctgtcctt gggagaaggc aggcacggag c 51

<210> 2972
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (2971 is other entry)

<221> misc_feature
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<223> Accession number cg42676483

<400> 2972
gttacgaagg cagcattttc tgctgtcctt gggagaaggc aggcacggag c 51

<210> 2973
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2974 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42685163

<400> 2973
ttactatcct caagggtttg tgactaaact ggaattacta ttgtaaagca g 51

<210> 2974
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (2973 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42685163

<400> 2974
ttactatcct caagggtttg tgactcaact ggaattacta ttgtaaagca g 51

<210> 2975
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2976 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42688225

<400> 2975
actaggaatg tcaggtgatg gtttgacaat tatcacactg cctctctaaa a 51

<210> 2976
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2975 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42688225

<400> 2976
actaggaatg tcaggtgatg gtttggcaat tatcacactg cctctctaaa a 51

<210> 2977
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2978 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42695541

<400> 2977
cgcttttcac aggttgggga gatgggcgcc tggagaaggg aaatccagtt a 51

<210> 2978
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2977 is other entry)

<221> misc_feature
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<223> Accession number cg42695541

<400> 2978
cgctttttcac aggttgggga gatggacgcc tggagaaggg aaatccagtt a 51

<210> 2979
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2980 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42698411

<400> 2979
ctcccagcac agggtcctct ggcccaatgt tgcagagctc cagccctaga g 51

<210> 2980
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2979 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42698411

<400> 2980
ctcccagcac agggtcctct ggcccgatgt tgcagagctc cagccctaga g 51

<210> 2981
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2982 is other entry)

<221> misc_feature

<222> (0)...(0)
<223> Accession number cg42698411

<400> 2981
ccacggacca ccccttttcc ccaaccacac tggggtgtct ggggtgaggc t 51

<210> 2982
<211> 51
<212> DNA
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<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2981 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42698411

<400> 2982
ccacggacca ccccttttcc ccaactacac tggggtgtct ggggtgaggc t 51

<210> 2983
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2984 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42704233

<400> 2983
ggtaagagcc ctctctccca gcctctgtcc tccagccct ggagtccttg g 51

<210> 2984
<211> 51
<212> DNA
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<220>
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<223> 2 of 2 allelic variants (2983 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42704233

<400> 2984
ggtaagagcc ctctctccca gcctccgtcc tccagccct ggagtccttg g 51

<210> 2985
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2986 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42708153.

<400> 2985
cccgcggttc gtagcatgtc ccccaaaact cggggagcgc aggcaggaca g 51

<210> 2986
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2985 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42708153

<400> 2986
cccgcggttc gtagcatgtc ccccagaact cggggagcgc aggcaggaca g 51

<210> 2987
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2988 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42708452

<400> 2987
atgaggttg aacagaagtt taataagcaa aagaagaaag ctctccccag c 51

<210> 2988
<211> 51
<212> DNA
<213> Homo sapiens

<220>

<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2987 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42708452

<400> 2988
atgagggttg aacagaagtt taatatgcaa aagaagaaag ctctccccag c 51

<210> 2989
<211> 51
<212> DNA
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<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2990 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42712591

<400> 2989
tgactgtggg gccaccccag agggaccag cgggcgaatc cctgctagga a 51

<210> 2990
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (2989 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42712591

<400> 2990
tgactgtggg gccaccccag agggaaccag cgggcgaatc cctgctagga a 51

<210> 2991
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (2992 is other entry)

<221> misc_feature
<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42713200

<400> 2991

tgacagagct ttggggggccg tgatgattgc agctcctgag gtggcctgct

50

<210> 2992

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2991 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42713200

<400> 2992

tgacagagct ttggggggccg tgatggattg cagctcctga ggtggcctgc t

51

<210> 2993

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2994 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42714904

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51

<210> 2994

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (2993 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42714904

<400> 2994
gtgccccccc gtgccccggg gccgctcgcc cgcccttctg gacagccact t 51

<210> 2995
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2996 is other entry)

<221> misc_feature
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<223> Accession number cg42718881

<400> 2995
cagggctgct ggacaacggg ccagacgcag cccagtggtg gatccagagg t 51

<210> 2996
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (2995 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42718881

<400> 2996
cagggctgct ggacaacggg ccagatgcag cccagtggtg gatccagagg t 51

<210> 2997
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (2998 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42718881

<400> 2997
ctggtctgca cttctgacct ggggctctgg ctgtgcggtt ctgctgagct c 51

<210> 2998
<211> 51
<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2997 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42718881

<400> 2998

ctggtctgca cttctgacct ggggccctgg ctgtgcggtt ctgctgagct c

51

<210> 2999

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (3000 is other entry)

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<222> (0)...(0)

<223> Accession number cg42718881

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51

<210> 3000

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2999 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42718881

<400> 3000

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51

<210> 3001

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (3002 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42718881

<400> 3001
gaatgcttcc caacatgagg gcatctcagg ccagcaggcg gggcccagag a 51

<210> 3002
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3001 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42718881

<400> 3002
gaatgcttcc caacatgagg gcatcccagg ccagcaggcg gggcccagag a 51

<210> 3003
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3004 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42718933

<400> 3003
atcttataaa gaaaagcccc ataatgaaat taggctctgt gataccatc c 51

<210> 3004
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3003 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42718933

<400> 3004

atcttataaa gaaaagcccc ataattaaat taggctctgt gatacccatc c

51

<210> 3005

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (3006 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42719773

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atctttctcc tcaagttgta gccaacatctt tgtccgtaac tgatttcagg g

51

<210> 3006

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (3005 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42719773

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atctttctcc tcaagttgta gccaaaatctt tgtccgtaac tgatttcagg g

51

<210> 3007

<211> 50

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (3008 is other entry)

<221> misc_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42719781

<400> 3007

ggagaatcca gcaaaaggaa aaaaaggaca gttgaagatg acttactgct

50

<210> 3008
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3007 is other entry)

<221> misc_feature
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<223> Accession number cg42719781

<400> 3008
ggagaatcca gcaaaaggaa aaaaaaggac agttgaagat gacttactgc t 51

<210> 3009
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3010 is other entry)

<221> misc_feature
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<223> Accession number cg42719781

<400> 3009
aaaggaaaaa aaggacagtt gaagatgact tactgctcca aaaaccattt c 51

<210> 3010
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3009 is other entry)

<221> misc_feature
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<223> Accession number cg42719781

<400> 3010
aaaggaaaaa aaggacagtt gaagacgact tactgctcca aaaaccattt c 51

<210> 3011
<211> 51
<212> DNA
<213> Homo sapiens

<220>

<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3012 is other entry)

<221> misc_feature
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<223> Accession number cg42719781

<400> 3011
gtgcggcagg ggcacggga cctgtcctgc agcggctctc tcaggccgtg g 51

<210> 3012
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3011 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42719781

<400> 3012
gtgcggcagg ggcacggga cctgtgctgc agcggctctc tcaggccgtg g 51

<210> 3013
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3014 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42719906

<400> 3013
cagatgcaga aaatgccttt aaagtaagac ttagcatcag agcagctctt g 51

<210> 3014
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3013 is other entry)

<221> misc_feature
<222> (0)...(0)

<223> Accession number cg42719906

<400> 3014

cagatgcaga aaatgccttt aaagtgagac ttagcatcag agcagctctt g

51

<210> 3015

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (3016 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42722181

<400> 3015

atttgattat tagttcaata tacataattg aaacgtcata ctgtgccata a

51

<210> 3016

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (3015 is other entry)

<221> misc_feature

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<223> Accession number cg42722181

<400> 3016

atttgattat tagttcaata tacattattg aaacgtcata ctgtgccata a

51

<210> 3017

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (3018 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42722181

<400> 3017

tatattcaaa aagaaatggg gacaggatta tcctgatgtt ttactcattc c

51

<210> 3018

<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
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<223> 2 of 2 allelic variants (3017 is other entry)

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<223> Accession number cg42722181

<400> 3018
tatattcaaa aagaaatggg gacagcatta tcctgatggt ttactcattc c 51

<210> 3019
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (3020 is other entry)

<221> misc_feature
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<223> Accession number cg42722181

<400> 3019
attgcctaatt gtccattatt aacagaagct gacctcaaaa aaaaagagga a 51

<210> 3020
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3019 is other entry)

<221> misc_feature
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<223> Accession number cg42722181

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<210> 3021
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<210> 3024
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<210> 3025
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actatggtgg accccaattc ccccttcca ttcgatcctg gctcctctc t 51

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<210> 3027
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<210> 3028
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<210> 3030
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<210> 3031
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<223> Accession number cg42729221

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<210> 3032

<211> 50

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<210> 3035
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<210> 3036
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<223> Accession number cg42751082

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<210> 3038

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<210> 3039

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<212> DNA

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<223> 1 of 2 allelic variants (3040 is other entry)

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<223> Accession number cg42833326

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<210> 3040

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<223> Accession number cg42833326

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<210> 3042
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<210> 3044
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<223> 2 of 2 allelic variants (3043 is other entry)

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<223> Accession number cg42840564

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<223> 1 of 2 allelic variants (3046 is other entry)

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<223> Accession number cg42846342

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51

<210> 3046

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<223> 2 of 2 allelic variants (3045 is other entry)

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<222> (0)...(0)

<223> Accession number cg42846342

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aaggaagcaa acggctaaat taccacaacc gggatacttc ttgctatcaa

50

<210> 3047

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature
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<210> 3050
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<210> 3051
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<223> Accession number cg42846342

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tggatgccac aagccctctc ctaggaaaaa aaggaaacgc gtgcgcatac          50

<210> 3052
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<212> DNA
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<210> 3053
<211> 51
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<210> 3054
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<210> 3055
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<223> Accession number cg42865804

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<210> 3056
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<210> 3057
<211> 51
<212> DNA
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51

<210> 3058
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50

<210> 3059
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<210> 3060
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<210> 3061
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<210> 3062
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<223> 2 of 2 allelic variants (3061 is other entry)

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<210> 3064
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<210> 3065
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<212> DNA
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<210> 3066
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51

<210> 3067

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51

<210> 3068

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<212> DNA

<213> Homo sapiens

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<210> 3069

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (3070 is other entry)

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<210> 3070
<211> 51
<212> DNA
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<210> 3072
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<210> 3073
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<210> 3074
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<210> 3075
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<210> 3076
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<212> DNA
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3075 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42884893

<400> 3076
accaggcaga cccctgcctg ccaacccct ctcagctggg cttaactctg g 51

<210> 3077
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3078 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42884893

<400> 3077
gggttttaag acctttgccc agaccctgc aaccaactta gaactgacat c 51

<210> 3078
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3077 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42884893

<400> 3078
gggttttaag acctttgccc agaccactgc aaccaactta gaactgacat c 51

<210> 3079
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3080 is other entry)

<221> misc_feature

<222> (0)...(0)
<223> Accession number cg42885383

<400> 3079
ttttattatt ttgtagagat ggggttttgc catgttgccc aggctggtct c 51

<210> 3080
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3079 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42885383

<400> 3080
ttttattatt ttgtagagat ggggtcttgc catgttgccc aggctggtct c 51

<210> 3081
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3082 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42885676

<400> 3081
cctgcaattg tactgcggac tccacgagtt cttttctggt gggaggacta t 51

<210> 3082
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3081 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42885676

<400> 3082
cctgcaattg tactgcggac tccacaagtt cttttctggt gggaggacta t 51

<210> 3083
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3084 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42892295

<400> 3083
cttagtagga ccaccaacga ttattttttt cttttactaa attatacaat a 51

<210> 3084
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3083 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42892295

<400> 3084
cttagtagga ccaccaacga ttattctttt cttttactaa attatacaat a 51

<210> 3085
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3086 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42893310

<400> 3085
tggtggcacc ttctgtgtcc tctctcacct tgctgtgag ccttccagt g 51

<210> 3086
<211> 51
<212> DNA
<213> Homo sapiens

<220>

<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3085 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42893310

<400> 3086
tggtggcacc ttctgtgtcc tctcttacct tgctgtgag cctccagtg g 51

<210> 3087
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3088 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42894278

<400> 3087
tcagtattac tcgtgttttg tttttgtttt tgttttttgt tttctttttc c 51

<210> 3088
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3087 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42894278

<400> 3088
tcagtattac tcgtgttttg tttttttttt tgttttttgt tttctttttc c 51

<210> 3089
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3090 is other entry)

<221> misc_feature
<222> (0)...(0)

<223> Accession number cg42895269

<400> 3089

ggagagcagc ctgggaggcc tggcttggtg cccacgcggg ggaagtaggg g

51

<210> 3090

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (3089 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42895269

<400> 3090

ggagagcagc ctgggaggcc tggctgggtg cccacgcggg ggaagtaggg g

51

<210> 3091

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (3092 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42896570

<400> 3091

aagttttcca ttttcttaaa gtaggaaaaa atgaacagta ataattatga t

51

<210> 3092

<211> 50

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (3091 is other entry)

<221> misc_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42896570

<400> 3092
aagttttcca ttttcttaaa gtaggaaaaa tgaacagtaa taattatgat 50

<210> 3093
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3094 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42905189

<400> 3093
ttacattctc tttagtaatt atggctcagc aagcatgccca ccaaaatcat c 51

<210> 3094
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3093 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42905189

<400> 3094
ttacattctc tttagtaatt atggcccagc aagcatgccca ccaaaatcat c 51

<210> 3095
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3096 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42906789

<400> 3095
actactggat tacatccaat agcatttacc tggcccagc aggtactctg t 51

<210> 3096
<211> 51
<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (3095 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42906789

<400> 3096

actactggat tacatccaat agcatctacc tggcccgcgc aggtactctg t

51

<210> 3097

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (3098 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42909493

<400> 3097

agtgagacat tgagaatgaa agcactatta ataattatcc aagaacagca g

51

<210> 3098

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (3097 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42909493

<400> 3098

agtgagacat tgagaatgaa agcaccatta ataattatcc aagaacagca g

51

<210> 3099

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (3100 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42912759

<400> 3099
agggctttat ttgaggacag aatcacccag acaaaagggc cagaaagaga g 51

<210> 3100
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3099 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42912759

<400> 3100
agggctttat ttgaggacag aatcagccag acaaaagggc cagaaagaga g 51

<210> 3101
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3102 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42912759

<400> 3101
atttgaggac agaatcaccc agacaaaagg gccagaaaga gagtgcagct_t 51

<210> 3102
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3101 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42912759

<400> 3102

atttgaggac agaatcaccc agacagaagg gccagaaaga gagtgcagct t

51

<210> 3103

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (3104 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42913480

<400> 3103

gagatcaaat tgttactgtg tctgtgtaga aagaagtaga cataggagac t

51

<210> 3104

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (3103 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42913480

<400> 3104

gagatcaaat tgttactgtg tctgtataga aagaagtaga cataggagac t

51

<210> 3105

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (3106 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42913480

<400> 3105

atattgttat gtgctaagaa aaattattct gccttgagat tctgttaatc t

51

<210> 3106

<211> 51

<212> DNA

<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3105 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42913480

<400> 3106
atattgttat gtgctaagaa aaattcttct gccttgagat tctgttaatc t 51

<210> 3107
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3108 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42917270

<400> 3107
gcgtgctgaa gagaatttgg aaaaaaaaaa aagaaattaa aaatcgtctc t 51

<210> 3108
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3107 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42917270

<400> 3108
gcgtgctgaa gagaatttgg aaaaacaaaa aagaaattaa aaatcgtctc t 51

<210> 3109
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3110 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42918135

<400> 3109
gagggatact ggagtcttct ggtgtgatgt gcagtcaaac cacaggaaag g 51

<210> 3110
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3109 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42918135

<400> 3110
gagggatact ggagtcttct ggtgtaatgt gcagtcaaac cacaggaaag g 51

<210> 3111
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3112 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42918135

<400> 3111
ttccattcct tacctaagtc tcgtttgtct aatacacctg ccagctactg a 51

<210> 3112
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3111 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42918135

<400> 3112
ttccattcct tacctaagtc tcgttggtct aatacacctg ccagctactg a 51

<210> 3113
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3114 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42918135

<400> 3113
ttgactccta aggccacact gtttccatcc catagatttc acagaggtga t 51

<210> 3114
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3113 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42918135

<400> 3114
ttgactccta aggccacact gtttctatcc catagatttc acagaggtga t 51

<210> 3115
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3116 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42919304

<400> 3115
tacgcgtcag agcagtgact ttgatacgca gtcaggtttt tccattaata g 51

<210> 3116
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3115 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42919304

<400> 3116
tacgcgtcag agcagtgact ttgatgcgca gtcaggtttt tccattaata g 51

<210> 3117
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3118 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42919304

<400> 3117
gaaagataaa gaaggggacc gggcctctga ggaaggcaaa cagaaaggca a 51

<210> 3118
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3117 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42919304

<400> 3118
gaaagataaa gaaggggacc gggcccctga ggaaggcaaa cagaaaggca a 51

<210> 3119
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3120 is other entry)

<221> misc_feature

<222> (0)...(0)
<223> Accession number cg42919821

<400> 3119
acgacgtggtt tgtgaatctg gcagagagtg agatcaccat cgctccactt g 51

<210> 3120
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3119 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42919821

<400> 3120
acgacgtggtt tgtgaatctg gcagacagtg agatcaccat cgctccactt g 51

<210> 3121
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3122 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42920238

<400> 3121
atgaatccag tttaatttta actttgtggc ttgtctaaca cattttcagt t 51

<210> 3122
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3121 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42920238

<400> 3122
atgaatccag tttaatttta actttttggc ttgtctaaca cattttcagt t 51

<210> 3123
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3124 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42920238

<400> 3123
cagtttaatt ttaactttgt ggcttgctta acacattttc agttaagagt t 51

<210> 3124
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3123 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42920238

<400> 3124
cagtttaatt ttaactttgt ggcttttcta acacattttc agttaagagt t 51

<210> 3125
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3126 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42920603

<400> 3125
tcgagaccag cctggccaac atggtaaaac cccgtctcta ctaaaaatac a 51

<210> 3126
<211> 51
<212> DNA
<213> Homo sapiens

<220>

<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3125 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42920603

<400> 3126
tcgagaccag cctggccaac atggtgaaac cccgtctcta ctaaaaatac a 51

<210> 3127
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3128 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42920603

<400> 3127
agcctggcca acatggtaaa acccgtctc tactaaaaat acaaaaatta g 51

<210> 3128
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3127 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42920603

<400> 3128
agcctggcca acatggtaaa accccatctc tactaaaaat acaaaaatta g 51

<210> 3129
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3130 is other entry)

<221> misc_feature
<222> (0)...(0)

<223> Accession number cg42922107

<400> 3129

cctcctgctg tgcaccctgg atcctagcag gccacagacc agtaccagtc c

51

<210> 3130

<211> 50

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (3129 is other entry)

<221> misc_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42922107

<400> 3130

cctcctgctg tgcaccctgg atcctgcagg ccacagacca gtaccagtcc

50

<210> 3131

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (3132 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42924228

<400> 3131

tctaagcaat gtcctcattg gcaggggtgg agtgggggag tttcttaaaa a

51

<210> 3132

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (3131 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42924228

<400> 3132
tctaagcaat gtcctcattg gcaggagtgg agtgggggag tttcttaaaa a 51

<210> 3133
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3134 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42924993

<400> 3133
caggagttag agaccagcct ggccaacatg gtgaaacccc gtctctacta a 51

<210> 3134
<211> 51
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<221> misc_feature
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<223> Accession number cg42924993

<400> 3134
caggagttag agaccagcct ggccagcatg gtgaaacccc gtctctacta a 51

<210> 3135
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (3136 is other entry)

<221> misc_feature
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<223> Accession number cg42925042

<400> 3135
cctcagcagc cagctccctt gtatacacag tatacacagc ccagccagca c 51

<210> 3136
<211> 51
<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (3135 is other entry)

<221> misc_feature

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<223> Accession number cg42925042

<400> 3136

cctcagcagc cagctccctt gtataaacag tatacacagc ccagccagca c

51

<210> 3137

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (3138 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42925336

<400> 3137

cgaagaaggg gttgtcgtcc gcctcgatgc catagtactc caggacatt c

51

<210> 3138

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (3137 is other entry)

<221> misc_feature

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<223> Accession number cg42925336

<400> 3138

cgaagaaggg gttgtcgtcc gcctcaatgc catagtactc caggacatt c

51

<210> 3139

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (3140 is other entry)

<221> misc_feature
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<223> Accession number cg42927064

<400> 3139
gagctctaag atctccttta gagggcacag tgaggtgggc tgttgggatg g 51

<210> 3140
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (3139 is other entry)

<221> misc_feature
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<223> Accession number cg42927064

<400> 3140
gagctctaag atctccttta gagggcacag tgaggtgggc tgttgggatg g 51

<210> 3141
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (3142 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42929433

<400> 3141
ctcatttga aaaggacact gggatgaaca cgtaagcggt gcaagcacag g 51

<210> 3142
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (3141 is other entry)

<221> misc_feature
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<223> Accession number cg42929433

<400> 3142

ctcatttgga aaaggacact gggatcaaca cgtaagcggtt gcaagcacag g

51

<210> 3143

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (3144 is other entry)

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<222> (0)...(0)

<223> Accession number cg42933706

<400> 3143

gcgtggggct gcctatcacc ctgctgtcgt cggcgctggg cgggccccac a

51

<210> 3144

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (3143 is other entry)

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<223> Accession number cg42933706

<400> 3144

gcgtggggct gcctatcacc ctgctatcgt cggcgctggg cgggccccac a

51

<210> 3145

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (3146 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg42936190

<400> 3145

tttcacacta atgaaatgcc tgagatatta aaggtctaaa tgtaaaatta a

51

<210> 3146

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (3145 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42936190

<400> 3146
tttcacacta atgaaatgcc tgagagatta aaggtctaaa tgtaaaatta a 51

<210> 3147
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<212> DNA
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<220>
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<223> 1 of 2 allelic variants (3148 is other entry)

<221> misc_feature
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<223> Accession number cg42936190

<400> 3147
aaacagaata atatatatgt accctcggtt tgaaatagac tttaagcact a 51

<210> 3148
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<212> DNA
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<223> 2 of 2 allelic variants (3147 is other entry)

<221> misc_feature
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<223> Accession number cg42936190

<400> 3148
aaacagaata atatatatgt acccttggtt tgaaatagac tttaagcact a 51

<210> 3149
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3150 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42937265

<400> 3149
gacaatgatt ttatcaggct aaaggtgaaa tcagctcagt gacacagagt g 51

<210> 3150
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (3149 is other entry)

<221> misc_feature
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<223> Accession number cg42937265

<400> 3150
gacaatgatt ttatcaggct aaaggggaaa tcagctcagt gacacagagt g 51

<210> 3151
<211> 51
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<223> 1 of 2 allelic variants (3152 is other entry)

<221> misc_feature
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<223> Accession number cg42940691

<400> 3151
ggaggaagga agcagtgtgt tgattgatac cttagcccaa gctccttatt t 51

<210> 3152
<211> 51
<212> DNA
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<220>
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<223> 2 of 2 allelic variants (3151 is other entry)

<221> misc_feature
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<223> Accession number cg42940691

<400> 3152
ggaggaagga agcagtgtgt tgatttatac cttagcccaa gctccttatt t 51

<210> 3153
<211> 51
<212> DNA
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<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3154 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg42942726

<400> 3153
gtcacttcat tgtctcacc aggccgaga ccacaatttc cctggaagga c 51

<210> 3154
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3153 is other entry)

<221> misc_feature
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<223> Accession number cg42942726

<400> 3154
gtcacttcat tgtctcacc aggccgaga ccacaatttc cctggaagga c 51

<210> 3155
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3156 is other entry)

<221> misc_feature
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<223> Accession number cg43008771

<400> 3155
ggggattaga agttagcatt tggtgtagtg attttcaaac cttagtgtgc c 51

<210> 3156
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (3155 is other entry)

<221> misc_feature
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<223> Accession number cg43008771

<400> 3156
ggggattaga agttagcatt tgttgacgtg attttcaaac cttagtgtgc c 51

<210> 3157
<211> 51
<212> DNA
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<220>
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<223> 1 of 2 allelic variants (3158 is other entry)

<221> misc_feature
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<223> Accession number cg43013298

<400> 3157
aggatttcag gaaaaccatg gttataaaaa tgatcaatct tgaaaaagta t 51

<210> 3158
<211> 50
<212> DNA
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<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3157 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43013298

<400> 3158
aggatttcag gaaaaccatg gttataaaat gatcaatctt gaaaaagtat 50

<210> 3159
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<212> DNA
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<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3160 is other entry)

<221> misc_feature
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<223> Accession number cg43013298

<400> 3159
tttcaggaaa accatgggta taaaaatgat caatcttgaa aaagtatgta c 51

<210> 3160
<211> 50
<212> DNA
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<220>
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<223> 2 of 2 allelic variants (3159 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25' and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43013298

<400> 3160
tttcaggaaa accatgggta taaaaatgatc aatcttgaaa aagtatgtac 50

<210> 3161
<211> 51
<212> DNA
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<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3162 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43021539

<400> 3161
cctgagtgtt cagatccagg ctctgcccag agctggatgt aaatztatga c 51

<210> 3162
<211> 50
<212> DNA
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<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3161 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43021539

<400> 3162
cctgagtgtt cagatccagg ctctgccaga gctggatgta aatttatgac 50

<210> 3163
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<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3164 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43021539

<400> 3163
tgagtgttca gatccaggct ctgccagag ctggatgtaa atttatgacc t 51

<210> 3164
<211> 50
<212> DNA
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<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3163 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43021539

<400> 3164
tgagtgttca gatccaggct ctgccagagc tggatgtaaa tttatgacct 50

<210> 3165
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3166 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43028648

<400> 3165
tcttgcttca gtaggcaaac ggacgggtgt cttcatccac ctctaggcc g 51

<210> 3166
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3165 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43028648

<400> 3166
tcttgcttca gtaggcaaac ggacgtgtgt cttcatccac ctctaggcc g 51

<210> 3167
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3168 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43040591

<400> 3167
tccggctttg ctccaaatgc cagcactttc agtcgggggt agagctgaca c 51

<210> 3168
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3167 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43040591

<400> 3168
tccggctttg ctccaaatgc cagcattttc agtcgggggt agagctgaca c 51

<210> 3169
<211> 51
<212> DNA
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<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3170 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43042003

<400> 3169
gtgtaataac tgggcccggtg tcctcacctg aaaactgggg gtcacacggc c 51

<210> 3170
<211> 51
<212> DNA
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<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3169 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43042003

<400> 3170
gtgtaataac tgggcccggtg tcctcgctg aaaactgggg gtcacacggc c 51

<210> 3171
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3172 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43042003

<400> 3171
aagaactctg atgtgataaa caccacagag cagcatcaca ttttcctatc g 51

<210> 3172
<211> 51

<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3171 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43042003

<400> 3172
aagaactctg atgtgataaa caccatagag cagcatcaca ttttcctatc g 51

<210> 3173
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3174 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43045398

<400> 3173
ttgatgtatt cacagagctt ccaaacattt ttttcacagc aacagccgct g 51

<210> 3174
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3173 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43045398

<400> 3174
ttgatgtatt cacagagctt ccaaataattt ttttcacagc aacagccgct g 51

<210> 3175
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)

<223> 1 of 2 allelic variants (3176 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43045398

<400> 3175

tttctccaca gttccacatc ttgagaccaa gttcagcagt ttttactgcc a

51

<210> 3176

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (3175 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43045398

<400> 3176

tttctccaca gttccacatc ttgaggccaa gttcagcagt ttttactgcc a

51

<210> 3177

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (3178 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43047493

<400> 3177

gatggcgact gcgggaaatc gagttttcat gctggggcga aaggaccgtc c

51

<210> 3178

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (3177 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43047493

<400> 3178
gatggcgact gcgggaaatc gagttctcat gctggggcga aaggaccgtc c 51

<210> 3179
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3180 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43051491

<400> 3179
tactgaatca gtgtatgaaa aatatcccaa acagacaaaag cagaacatgg a 51

<210> 3180
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3179 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43051491

<400> 3180
tactgaatca gtgtatgaaa aatatcccaa acagacaaaag cagaacatgg a 51

<210> 3181
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3182 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43054909

<400> 3181
gttttcattg tgataatagg tagcagaatg atgagcatcc ctatcactta c 51

<210> 3182
<211> 51
<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (3181 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43054909

<400> 3182

gttttcattg tgataatagg tagcaaaatg atgagcatcc ctatcactta c

51

<210> 3183

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (3184 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43063075

<400> 3183

tgagcatagc agtcgacttt ttttttatat tttccttcac agtctggcat t

51

<210> 3184

<211> 50

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (3183 is other entry)

<221> misc_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

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<222> (0)...(0)

<223> Accession number cg43063075

<400> 3184

tgagcatagc agtcgacttt tttttatatt ttccttcaca gtctggcatt

50

<210> 3185

<211> 51

<212> DNA

<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (3186 is other entry)

<221> misc_feature
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<223> Accession number cg43063683

<400> 3185
agtgtccacc aaagctgagc accagccatc tgccttagct gtgtgcacag g 51

<210> 3186
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3185 is other entry)

<221> misc_feature
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<223> Accession number cg43063683

<400> 3186
agtgtccacc aaagctgagc accagtcac c tgccttagct gtgtgcacag g 51

<210> 3187
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3188 is other entry)

<221> misc_feature
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<223> Accession number cg43064195

<400> 3187
gcctgtgggc ccagctactc gggagactga ggcaggagaa tcgcttgaac c 51

<210> 3188
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3187 is other entry)

<221> misc_feature

<222> (0)...(0)
<223> Accession number cg43064195

<400> 3188
gcctgtggtc ccagctactc gggaggctga ggcaggagaa tcgcttgaac c 51

<210> 3189
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3190 is other entry)

<221> misc_feature
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<223> Accession number cg43064195

<400> 3189
ggagaatcgc ttgaaccag gaggcagagg ttgcagtga ccaagatcat g 51

<210> 3190
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3189 is other entry)

<221> misc_feature
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<223> Accession number cg43064195

<400> 3190
ggagaatcgc ttgaaccag gaggcggagg ttgcagtga ccaagatcat g 51

<210> 3191
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<220>
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<223> 1 of 2 allelic variants (3192 is other entry)

<221> misc_feature
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<400> 3191
cagaggtgc agtgagccaa gatcatgcca ctgcactcca gcctgggtga c 51

<210> 3192
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (3191 is other entry)

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<400> 3192
cagaggttgc agtgagccaa gatcacgcca ctgcactcca gcctgggtga c 51

<210> 3193
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (3194 is other entry)

<221> misc_feature
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<223> Accession number cg43064233

<400> 3193
caaccagagc cagtggactt cagtatgggt cgctttcatt ggcagaccct c 51

<210> 3194
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (3193 is other entry)

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<223> Accession number cg43064233

<400> 3194
caaccagagc cagtggactt cagtacgggt cgctttcatt ggcagaccct c 51

<210> 3195
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<223> 1 of 2 allelic variants (3196 is other entry)

<221> misc_feature
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<223> Accession number cg43066356

<400> 3195
tggacttgga gcagaagagt ccctccaggg ctgaagattg gacacagaaa a 51

<210> 3196
<211> 50
<212> DNA
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<223> 2 of 2 allelic variants (3195 is other entry)

<221> misc_feature
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<221> misc_feature
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<400> 3196
tggacttgga gcagaagagt ccctcagggc tgaagattgg acacagaaaa 50

<210> 3197
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (3198 is other entry)

<221> misc_feature
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<400> 3197
acaattccca gaaactggaa ttgggatggt gagattttag ttcagccgcc g 51

<210> 3198
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (3197 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43066356

<400> 3198

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51

<210> 3199

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (3200 is other entry)

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<223> Accession number cg43069434

<400> 3199

tgagacctcc agtcccaggg gcggggttca tgcggttcca cagctgttgg c

51

<210> 3200

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (3199 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43069434

<400> 3200

tgagacctcc agtcccaggg gcggggttca tgcggttcca cagctgttgg c

51

<210> 3201

<211> 50

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (3202 is other entry)

<221> misc_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
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<223> Accession number cg43069949

<400> 3201
tcacttgatg acacacacac acacaggtca cggagctgga cgtgcggatg

50

<210> 3202
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (3201 is other entry)

<221> misc_feature
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<223> Accession number cg43069949

<400> 3202
tcacttgatg acacacacac acacacgggc acggagctgg acgtgcggat g

51

<210> 3203
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (3204 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43073473

<400> 3203
ctcacttata attccaaatt catgttgatg tagctcaata tttttcaaata a

51

<210> 3204
<211> 50
<212> DNA
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<223> 2 of 2 allelic variants (3203 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)

<223> Accession number cg43073473

<400> 3204

ctcacttata attccaaatt catgtgtgtt agtcaatat ttttcaaata

50

<210> 3205

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (3206 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43073473

<400> 3205

tatctgcacc atgatgatat gacacgccca tcccccccat ttcacatttt g

51

<210> 3206

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

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<223> 2 of 2 allelic variants (3205 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43073473

<400> 3206

tatctgcacc atgatgatat gacacaccca tcccccccat ttcacatttt g

51

<210> 3207

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (3208 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43073473

<400> 3207

tgatgatatg acacgccccat accccccatt tcacattttg tcagaagtgc a

51

<210> 3208

<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (3207 is other entry)

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<223> Accession number cg43073473

<400> 3208
tgatgatatg acagcccat acccctcatt tcacattttg tcagaagtgc a 51

<210> 3209
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3210 is other entry)

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<222> (0)...(0)
<223> Accession number cg43073924

<400> 3209
taggcacaaa gagaccgagt ggctcgggtg gcttcccagg aggcagttag a 51

<210> 3210
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3209 is other entry)

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<223> Accession number cg43073924

<400> 3210
taggcacaaa gagaccgagt ggctcagggtg gcttcccagg aggcagttag a 51

<210> 3211
<211> 51
<212> DNA
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3212 is other entry)

<221> misc_feature
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<223> Accession number cg43076876

<400> 3211
tctaattggct tcccatgacc acacacagga gtggggaaac cttacttgta c 51

<210> 3212
<211> 50
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (3211 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

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<223> Accession number cg43076876

<400> 3212
tctaattggct tcccatgacc acacaaggag tggggaaacc ttacttgta c 50

<210> 3213
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<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3214 is other entry)

<221> misc_feature
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<223> Accession number cg43076876

<400> 3213
atcgggttttc ttccaaatca gcgacgggag taacattttt attcctatca c 51

<210> 3214
<211> 51
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<213> Homo sapiens

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<223> 2 of 2 allelic variants (3213 is other entry)

<221> misc_feature
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<223> Accession number cg43076876

<400> 3214
atcggttttc ttccaaatca gcgacaggag taacattttt attcctatca c 51

<210> 3215
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3216 is other entry)

<221> misc_feature
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<223> Accession number cg43077574

<400> 3215
gcctcccaga gtgctaggat tacaggtatg agccaccatg cccggcccta g 51

<210> 3216
<211> 51
<212> DNA
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<220>
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<223> 2 of 2 allelic variants (3215 is other entry)

<221> misc_feature
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<223> Accession number cg43077574

<400> 3216
gcctcccaga gtgctaggat tacagatatg agccaccatg cccggcccta g 51

<210> 3217
<211> 50
<212> DNA
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<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3218 is other entry)

<221> misc_feature
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<221> misc_feature

<222> (0)...(0)
<223> Accession number cg43082358

<400> 3217
tatttttaaac ccaattctgt tttttaacag aataaaattc ttctgttctt 50

<210> 3218
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3217 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43082358

<400> 3218
tatttttaaac ccaattctgt ttttttaaca gaataaaatt cttctgttct t 51

<210> 3219
<211> 51
<212> DNA
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<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3220 is other entry)

<221> misc_feature
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<223> Accession number cg43085612

<400> 3219
ctgggatcac aggatccgc ccccatgctc agctaattgtt tgtattttta g 51

<210> 3220
<211> 51
<212> DNA
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<220>
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<223> 2 of 2 allelic variants (3219 is other entry)

<221> misc_feature
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<400> 3220
ctgggatcac aggatccgc cccacgctc agctaattgtt tgtattttta g 51

<210> 3221
<211> 51
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<223> 1 of 2 allelic variants (3222 is other entry)

<221> misc_feature
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<400> 3221
catgctcagc taatgtttgt atttttagta gagatgggggt ttcaccatgt t 51

<210> 3222
<211> 51
<212> DNA
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<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3221 is other entry)

<221> misc_feature
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<223> Accession number cg43085612

<400> 3222
catgctcagc taatgtttgt attttcagta gagatgggggt ttcaccatgt t 51

<210> 3223
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3224 is other entry)

<221> misc_feature
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<223> Accession number cg43085612

<400> 3223
gctcagctaa tgtttgtatt ttttagtagag atgggggtttc accatgttgc t 51

<210> 3224
<211> 51
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3223 is other entry)

<221> misc_feature
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<400> 3224
gctcagctaa tgtttgatt ttttagcagag atgggggttc accatgttgc t 51

<210> 3225
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<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3226 is other entry)

<221> misc_feature
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<223> Accession number cg43090728

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cagaatcgct gggctttaac cacacatgag agtctgggttc cctgtgagac t 51

<210> 3226
<211> 50
<212> DNA
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<220>
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<223> 2 of 2 allelic variants (3225 is other entry)

<221> misc_feature
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<223> Accession number cg43090728

<400> 3226
cagaatcgct gggctttaac cacactgaga gtctgggttc ctgtgagact 50

<210> 3227
<211> 51
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<223> 1 of 2 allelic variants (3228 is other entry)

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<223> Accession number cg43091174

<400> 3227

gggtgtcttca ggctgagttt acttgtagga gtggcaggat tgctcttcaa t

51

<210> 3228

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (3227 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43091174

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gggtgtcttca ggctgagttt acttgcagga gtggcaggat tgctcttcaa t

51

<210> 3229

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (3230 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43094867

<400> 3229

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51

<210> 3230

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (3229 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43094867

<400> 3230
ttctctccag cggcagcgga aaacgagcaa tgggtggatt cgggtccaga t 51

<210> 3231
<211> 51
<212> DNA
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<220>
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<223> 1 of 2 allelic variants (3232 is other entry)

<221> misc_feature
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<223> Accession number cg43094867

<400> 3231
ggggacaaaa accagaggcc ggggaaggcg ccggtgggag gcaaggcacg g 51

<210> 3232
<211> 50
<212> DNA
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<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3231 is other entry)

<221> misc_feature
<222> (25)...(26)
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<221> misc_feature
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<400> 3232
ggggacaaaa accagaggcc ggggaggcgc ccggtgggag caaggcacgg 50

<210> 3233
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3234 is other entry)

<221> misc_feature
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<223> Accession number cg43094867

<400> 3233
ggggaaaact tcaaattatt taaataatga gaggcgaaaa acattgctaa a 51

<210> 3234
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (3233 is other entry)

<221> misc_feature
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<223> Accession number cg43094867

<400> 3234
ggggaaaact tcaaattatt taaattatga gaggcgaaaa acattgctaa a 51

<210> 3235
<211> 51
<212> DNA
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<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3236 is other entry)

<221> misc_feature
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<223> Accession number cg43095751

<400> 3235
caataaaaaa gaatgcactg ccagtcacgc aacatggata attctcaaat g 51

<210> 3236
<211> 51
<212> DNA
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<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3235 is other entry)

<221> misc_feature
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<223> Accession number cg43095751

<400> 3236
caataaaaaa gaatgcactg ccagttcagc aacatggata attctcaaat g 51

<210> 3237
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3238 is other entry)

<221> misc_feature
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<223> Accession number cg43095751

<400> 3237
atgcactgcc agtacagcaa catggataat tctcaaatgc attatgccag t 51

<210> 3238
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3237 is other entry)

<221> misc_feature
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<223> Accession number cg43095751

<400> 3238
atgcactgcc agtacagcaa catgggtaat tctcaaatgc attatgccag t 51

<210> 3239
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3240 is other entry)

<221> misc_feature
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<223> Accession number cg43095751

<400> 3239
gcatttgtca agactcagtg ctatacgctg aaaagggcag gttttactat a 51

<210> 3240
<211> 51
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<220>
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<223> 2 of 2 allelic variants (3239 is other entry)

<221> misc_feature

<222> (0)...(0)
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<400> 3240
gcatttgatca agactcagtgc ctatatgctg aaaagggcag gttttactat a 51

<210> 3241
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3242 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43096831

<400> 3241
tccctatggt gccagggctg gtctcaaact cctggggtca agcgatcctc c 51

<210> 3242
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3241 is other entry)

<221> misc_feature
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<223> Accession number cg43096831

<400> 3242
tccctatggt gccagggctg gtctcgaact cctggggtca agcgatcctc c 51

<210> 3243
<211> 51
<212> DNA
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3244 is other entry)

<221> misc_feature
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<223> Accession number cg43099151

<400> 3243
tcgccgtatg gaggtgaact tctgagaaac ctcttcatag cccattttca t 51

<210> 3244

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<223> 2 of 2 allelic variants (3243 is other entry)

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tgcgcgtatg gaggtgaact tctgaaaaac ctcttcatag cccattttca t

51

<210> 3245

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (3246 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43099552

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<210> 3246

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (3245 is other entry)

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<223> Accession number cg43099552

<400> 3246

atatttggat taccaaataa cacttctgta gatgcactga taccgaagtt t

51

<210> 3247

<211> 51

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<223> Accession number cg43105272

<400> 3247
ggccaacatg gcgaaacccc atctctacta aaaataaaaa ataaaaaata g 51

<210> 3248
<211> 51
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<223> 2 of 2 allelic variants (3247 is other entry)

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<223> Accession number cg43105272

<400> 3248
ggccaacatg gcgaaacccc atctccacta aaaataaaaa ataaaaaata g 51

<210> 3249
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<212> DNA
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<223> Accession number cg43106767

<400> 3249
gaaatagcca ggcgtggtgg ctcacacctg tgatcttagc actttgggag g 51

<210> 3250
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<223> 2 of 2 allelic variants (3249 is other entry)

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<223> Accession number cg43106767

<400> 3250

gaaatagcca ggcgtggtgg ctcacgcctg tgatcttagc actttgggag g

51

<210> 3251

<211> 51

<212> DNA

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<223> 1 of 2 allelic variants (3252 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43107247

<400> 3251

tgcccaggct ggtcttgaac tcctgacctc aagcaatcct cctgcctcgg c

51

<210> 3252

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

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<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43107247

<400> 3252

tgcccaggct ggtcttgaac tcctggcctc aagcaatcct cctgcctcgg c

51

<210> 3253

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

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<223> Accession number cg43107247

<400> 3253

cttgaactcc tgacctcaag caatcctcct gctcggcct cccaaaatgc t

51

<210> 3254

<211> 51
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3253 is other entry)

<221> misc_feature
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<400> 3254
cttgaactcc tgacctcaag caatcttcct gctcggcct cccaaaatgc t 51

<210> 3255
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (3256 is other entry)

<221> misc_feature
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<223> Accession number cg43111395

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<210> 3256
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (3255 is other entry)

<221> misc_feature
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<223> Accession number cg43111395

<400> 3256
agcaccagg gggatggtgt taaactatga gaaaccaccc ccattatcca a 51

<210> 3257
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<212> DNA
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3258 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43111948

<400> 3257
ggcgtggaga catggaacat ggatagggca gccgcctcct tgcccctgat g 51

<210> 3258
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (3257 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43111948

<400> 3258
ggcgtggaga catggaacat ggatagggcag ccgcctcctt gccctgatg 50

<210> 3259
<211> 51
<212> DNA
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<220>
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<223> 1 of 2 allelic variants (3260 is other entry)

<221> misc_feature
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<223> Accession number cg43111993

<400> 3259
aagacggaag cagtcaactgg tccttcccct cgtcccaccc cgcagcacct c 51

<210> 3260
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3259 is other entry)

<221> misc_feature
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<223> Accession number cg43111993

<400> 3260
aagacggaag cagtcaactgg tcctttccct cgtcccaccc cgcagcacct c 51

<210> 3261
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (3262 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43114589

<400> 3261
caacatggtg aaaccccgcc tctactaaaa atacaaaaat cagctgggca t 51

<210> 3262
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (3261 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43114589

<400> 3262
caacatggtg aaaccccgcc tctacaaaaa atacaaaaat cagctgggca t 51

<210> 3263
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3264 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43117303

<400> 3263

tgtgcagccg atggtgaggg actgggcgcc ctgcctgcc cccggggttg t

51

<210> 3264

<211> 50

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (3263 is other entry)

<221> misc_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43117303

<400> 3264

tgtgcagccg atggtgaggg actggcgccc tcgctgccc cccggggttg

50

<210> 3265

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (3266 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43117554

<400> 3265

ggtgctgttt cccgtccttc cctgggcggt gcaggctgtg gagcacgagg a

51

<210> 3266

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (3265 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43117554

<400> 3266

ggtgctgttt cccgtccttc cctggtcggt gcaggctgtg gagcacgagg a

51

<210> 3267
<211> 51
<212> DNA
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3268 is other entry)

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<223> Accession number cg43117554

<400> 3267
ccagaagaat gcagttctga acaaactgaa aactgcaatt ggagcagtgg a 51

<210> 3268
<211> 51
<212> DNA
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3267 is other entry)

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<222> (0)...(0)
<223> Accession number cg43117554

<400> 3268
ccagaagaat gcagttctga acaaattgaa aactgcaatt ggagcagtgg a 51

<210> 3269
<211> 51
<212> DNA
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<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3270 is other entry)

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<222> (0)...(0)
<223> Accession number cg43118191

<400> 3269
ccttcctga aggccatcct gtgcggccag ggccccgcag acccctccac a 51

<210> 3270
<211> 50
<212> DNA
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<221> misc_feature
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<223> 2 of 2 allelic variants (3269 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
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<400> 3270
ccttcctga aggccatcct gtgcgccagg gccccgcaga cccctccaca

50

<210> 3271
<211> 51
<212> DNA
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<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3272 is other entry)

<221> misc_feature
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<223> Accession number cg43120277

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atattgatta ggttttaaag caactgatca cttgctgaca gctcagccac g

51

<210> 3272
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3271 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43120277

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atattgatta ggttttaaag caactcatca cttgctgaca gctcagccac g

51

<210> 3273
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (3274 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43124193

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cattttcaac atacaagtcc ttcacgagtg cgtctgcctt agtgttcttg c

51

<210> 3274

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (3273 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43124193

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cattttcaac atacaagtcc ttcaccagtg cgtctgcctt agtgttcttg c

51

<210> 3275

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (3276 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43126118

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tctcagcctc ccgagtagct gggaccacag gtgccggcca ccacaccgg c

51

<210> 3276

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (3275 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43126118

<400> 3276
tctcagcctc ccgagtagct gggactacag gtgccggcca ccacaccgg c 51

<210> 3277
<211> 51
<212> DNA
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<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3278 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43129484

<400> 3277
tcccagagaa aaaagaatgg gaatcaaatt gacctcagac tatacgtgag a 51

<210> 3278
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3277 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43129484

<400> 3278
tcccagagaa aaaagaatgg gaatcgaatt gacctcagac tatacgtgag a 51

<210> 3279
<211> 51
<212> DNA
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<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3280 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43129603

<400> 3279
tttgggaggc caaggcagga ggatcgcttg agcccaggag tttaagacca g 51

<210> 3280
<211> 51
<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (3279 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43129603

<400> 3280

tttgggaggc caaggcagga ggatcacttg agcccaggag tttaagacca g

51

<210> 3281

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (3282 is other entry)

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<223> Accession number cg43134281

<400> 3281

caaaagacca ccactcagta tttgtgtacc ctgcagccaa caccacctcc t

51

<210> 3282

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (3281 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43134281

<400> 3282

caaaagacca ccactcagta tttgtctacc ctgcagccaa caccacctcc t

51

<210> 3283

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<223> 1 of 2 allelic variants (3284 is other entry)

<221> misc_feature
<222> (0)...(0)
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<400> 3283
ccaccactca gtatttgtgt accctgcagc caacaccacc tcctgggctt c 51

<210> 3284
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (3283 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43134281

<400> 3284
ccaccactca gtatttgtgt acccttcagc caacaccacc tcctgggctt c 51

<210> 3285
<211> 51
<212> DNA
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3286 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43136191

<400> 3285
tacacaagtg atcaatttgt cacaatatga caagttattg ataacaagta t 51

<210> 3286
<211> 51
<212> DNA
<213> Homo sapiens

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<222> (26)...(0)
<223> 2 of 2 allelic variants (3285 is other entry)

<221> misc_feature
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<223> Accession number cg43136191

<400> 3286

tacacaagtg atcaatttgt cacaacatga caagttattg ataacaagta t

51

<210> 3287

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (3288 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43136321

<400> 3287

tggtttgacc aggtgtgacg tttagtagt gcacgagaaa ggctggccac c

51

<210> 3288

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (3287 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43136321

<400> 3288

tggtttgacc aggtgtgacg tttagtagt gcacgagaaa ggctggccac c

51

<210> 3289

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (3290 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43136321

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aggctggcca cccacccaa attctgatta tgcaaatgga ctttccactt g

51

<210> 3290

<211> 51

<212> DNA

<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (3289 is other entry)

<221> misc_feature
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<223> Accession number cg43136321

<400> 3290
aggctggcca cccaccccaa attcttatta tgcaaatgga ctttccactt g 51

<210> 3291
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (3292 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43138399

<400> 3291
atgttttccc attcagcact cattgaaaaa aataattagg aggcaatctt t 51

<210> 3292
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3291 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43138399

<400> 3292
atgttttccc attcagcact cattgaaaaa ataattagga ggcaatcttt 50

<210> 3293
<211> 51
<212> DNA
<213> Homo sapiens

<220>

<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3294 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43139520

<400> 3293
cctgctttgc tattgtccgc ttgcccc ggaagcaggt ctctagctca g 51

<210> 3294
<211> 50
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (3293 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
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<223> Accession number cg43139520

<400> 3294
cctgctttgc tattgtccgc ttgcccc gaagcaggtc tctagctcag 50

<210> 3295
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3296 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43144367

<400> 3295
gaagggaagg tcttaaaaga taaaagggg ggttgctacc ccagtctcag g 51

<210> 3296
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (3295 is other entry)

<221> misc_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43144367

<400> 3296

gaagggaagg tcttaaaaga taaaaggggg gttgctaccc cagtctcagg

50

<210> 3297

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (3298 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43144435

<400> 3297

ataagatggtt atggccagac gcggagctca cgctttaat ctcagcactt t

51

<210> 3298

<211> 50

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (3297 is other entry)

<221> misc_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43144435

<400> 3298

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50

<210> 3299

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature
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<223> 1 of 2 allelic variants (3300 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43144658

<400> 3299
acccccccaa aaaaaaggaa aaaaaatcta gatccaacag tggaaaattc t 51

<210> 3300
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (3299 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43144658

<400> 3300
acccccccaa aaaaaaggaa aaaaatctag atccaacagt ggaaaattct 50

<210> 3301
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3302 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43144658

<400> 3301
ggggagttag cctgggacca atggaggaga agtacgaacc ctgggaaaaa g 51

<210> 3302
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (3301 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43144658

<400> 3302

ggggagttag cctgggacca atggaagaga agtacgaacc ctgggaaaaa g

51

<210> 3303

<211> 51

<212> DNA

<213> Homo sapiens

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<223> Accession number cg43144705

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51

<210> 3304

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51

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<223> 1 of 2 allelic variants (3306 is other entry)

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<223> Accession number cg43144729

<400> 3305
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<210> 3306
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<210> 3307
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acttgaaggc acttcatttt tttttaagat acactcttag gagtttactt 50

<210> 3308
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<223> 2 of 2 allelic variants (3307 is other entry)

<221> misc_feature
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<210> 3309
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50

<210> 3310
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acttgaaggc acttcatttt tttttaaga tacactctta ggagtttact t

51

<210> 3311
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51

<210> 3312

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<221> misc_feature
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caagtgatct ttccacaaca ttaaaaccac attttgctcc tcagacacct c

51

<210> 3314
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<400> 3314
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50

<210> 3315
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<210> 3316
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<210> 3317
<211> 51
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<223> 1 of 2 allelic variants (3318 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43148723

<400> 3317
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<210> 3318
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<223> 2 of 2 allelic variants (3317 is other entry)

<221> misc_feature
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<223> Accession number cg43148723

<400> 3318
aaaaaacgac aattggctgc agaaagctgg ttgggaagg ggtgcctgtt 50

<210> 3319
<211> 51
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<223> 1 of 2 allelic variants (3320 is other entry)

<221> misc_feature
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<400> 3319
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<210> 3320
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<400> 3320
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<210> 3321
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<223> 1 of 2 allelic variants (3322 is other entry)

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51

<210> 3322

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<223> Accession number cg43155030

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51

<210> 3323

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<223> Accession number cg43242324

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51

<210> 3324

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<213> Homo sapiens

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<223> 2 of 2 allelic variants (3323 is other entry)

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<400> 3324
gtgagtgcggtgtgcatctgtatgtgtatgcatgtgggta t 51

<210> 3325
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<210> 3326
<211> 51
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<223> 2 of 2 allelic variants (3325 is other entry)

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<400> 3326
gtgctgtgtgcgtgtgtgtgcgtctatgtgtatgcatgtgggtatgta g 51

<210> 3327
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<223> 1 of 2 allelic variants (3328 is other entry)

<221> misc_feature
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cggtgtgtgcg tgttgtgtgt gtgtgtgcat gcacatttga agtgacctca g

51

<210> 3328

<211> 50

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (3327 is other entry)

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<222> (25)...(26)

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<223> Accession number cg43242324

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cggtgtgtgcg tgttgtgtgt gtgtggcatg cacatttgaa gtgacctcag

50

<210> 3329

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (3330 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43247175

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51

<210> 3330

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (3329 is other entry)

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<223> Accession number cg43247175

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51

<210> 3331
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44

<210> 3332
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<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (3331 is other entry)

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<400> 3332
naaatcatga tccgcccgcc tcggcctctc aaagtgctgg gatt

44

<210> 3333
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<212> DNA
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<400> 3333
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51

<210> 3334
<211> 51
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<223> 2 of 2 allelic variants (3333 is other entry)

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<400> 3334
tgtgaactgg actgaacgag acaagatgtg ctctggggct gcggggtcag c 51

<210> 3335
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<223> 1 of 2 allelic variants (3336 is other entry)

<221> misc_feature
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<223> Accession number cg43250188

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<210> 3336
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<223> 2 of 2 allelic variants (3335 is other entry)

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<400> 3336
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<210> 3337
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<223> 1 of 2 allelic variants (3338 is other entry)

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gagaaaaagg ccctgcatgc cttgtgaagg tttatgaaga ttgggattgt t

51

<210> 3338

<211> 51

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<223> 2 of 2 allelic variants (3337 is other entry)

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51

<210> 3339

<211> 51

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51

<210> 3340

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

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<223> Accession number cg43250188

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51

<210> 3341

<211> 51
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<210> 3342
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tttcaaagta aatgacattc ttgagttata tggcatactg tctgtggatc c 51

<210> 3343
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (3344 is other entry)

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<400> 3343
acattcttga gctatatggc atactgtctg tggatcctgt gctgagtata c 51

<210> 3344
<211> 51
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<223> 2 of 2 allelic variants (3343 is other entry)

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<400> 3344
acattcttga gctatatggc atactctctg tggatcctgt gctgagtata c 51

<210> 3345
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (3346 is other entry)

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<400> 3345
agctatatgg catactgtct gtggatcctg tgctgagtat actgaataat g 51

<210> 3346
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (3345 is other entry)

<221> misc_feature
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<400> 3346
agctatatgg catactgtct gtggaccctg tgctgagtat actgaataat g 51

<210> 3347
<211> 51
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<223> 1 of 2 allelic variants (3348 is other entry)

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<400> 3347
atatggcata ctgtctgtgg atcctgtgct gagtatactg aataatgatg a 51

<210> 3348
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (3347 is other entry)

<221> misc_feature
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<223> Accession number cg43250188

<400> 3348
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<210> 3349
<211> 51
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<223> 1 of 2 allelic variants (3350 is other entry)

<221> misc_feature
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<400> 3349
tactgtctgt ggatcctgtg ctgagtatac tgaataatga tgaaagggat g 51

<210> 3350
<211> 51
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<223> 2 of 2 allelic variants (3349 is other entry)

<221> misc_feature
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tactgtctgt ggatcctgtg ctgagcatac tgaataatga tgaaagggat g 51

<210> 3351
<211> 51

<212> DNA
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<223> 1 of 2 allelic variants (3352 is other entry)

<221> misc_feature
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ctgtgctgag tataactgaat aatgatgaaa gggatgcctc tgcactgctg g 51

<210> 3352
<211> 51
<212> DNA
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<400> 3352
ctgtgctgag tataactgaat aatgaagaaa gggatgcctc tgcactgctg g 51

<210> 3353
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<223> 1 of 2 allelic variants (3354 is other entry)

<221> misc_feature
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<400> 3353
aaagggatgc ctctgcactg ctggatccga tggagtgcac agacacagca g 51

<210> 3354
<211> 51
<212> DNA
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<220>
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<223> 2 of 2 allelic variants (3353 is other entry)

<221> misc_feature

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<223> Accession number cg43250188

<400> 3354

aaagggatgc ctctgcactg ctggacccga tggagtgcac agacacagca g

51

<210> 3355

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (3356 is other entry)

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cctctgcact gctggatccg atggagtgcac cagacacagc agaggagcag a

51

<210> 3356

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<212> DNA

<213> Homo sapiens

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cctctgcact gctggatccg atggaatgca cagacacagc agaggagcag a

51

<210> 3357

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<212> DNA

<213> Homo sapiens

<220>

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<223> 1 of 2 allelic variants (3358 is other entry)

<221> misc_feature

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<223> Accession number cg43250188

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cactgctgga tccgatggag tgcacagaca cagcagagga gcagagagta c 51

<210> 3358
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<220>
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<223> 2 of 2 allelic variants (3357 is other entry)

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cactgctgga tccgatggag tgcacggaca cagcagagga gcagagagta c 51

<210> 3359
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<212> DNA
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<221> misc_feature
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<223> Accession number cg43250188

<400> 3359
tggatccgat ggagtgcaca gacacagcag aggagcagag agtacacagt c 51

<210> 3360
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (3359 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43250188

<400> 3360
tggatccgat ggagtgcaca gacacggcag aggagcagag agtacacagt c 51

<210> 3361
<211> 51
<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (3362 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43250188

<400> 3361

cgatggagtg cacagacaca gcagaggagc agagagtaca cagtcctcct g

51

<210> 3362

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (3361 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43250188

<400> 3362

cgatggagtg cacagacaca gcagaagagc agagagtaca cagtcctcct g

51

<210> 3363

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (3364 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43250188

<400> 3363

cagacacagc agaggagcag agagtacaca gtcctcctgc ttcattagtg c

51

<210> 3364

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (3363 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43250188

<400> 3364
cagacacagc agaggagcag agagtgcaca gtcctcctgc ttcattagtg c 51

<210> 3365
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (3366 is other entry)

<221> misc_feature
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<223> Accession number cg43250708

<400> 3365
agatcttccg attcagtcct gggtcagtcct gagaatttgc atttctaaca t 51

<210> 3366
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (3365 is other entry)

<221> misc_feature
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<223> Accession number cg43250708

<400> 3366
agatcttccg attcagtcct gggtcagtcct gagaatttgc atttctaaca t 51

<210> 3367
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<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (3368 is other entry)

<221> misc_feature
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<223> Accession number cg43252277

<400> 3367

gggagaggag taggccaaaa aaaaaaagtc cttgattcct gaatgtgcct t

51

<210> 3368

<211> 50

<212> DNA

<213> Homo sapiens

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<221> misc_feature

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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43252277

<400> 3368

gggagaggag taggccaaaa aaaaaaagtc ttgattcctg aatgtgcctt

50

<210> 3369

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (0)...(0)

<223> Accession number cg43252277

<400> 3369

ggagaggagt aggccaaaaa aaaaaaagtc ttgattcctg aatgtgcctt a

51

<210> 3370

<211> 50

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (3369 is other entry)

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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43252277

<400> 3370
ggagaggagt aggccaaaaa aaaaaagtct tgattcctga atgtgcctta 50

<210> 3371
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (3372 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43252277

<400> 3371
gagaggagta ggccaaaaaa aaaaaagtct tgattcctga atgtgcctta t 51

<210> 3372
<211> 50
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (3371 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
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<223> Accession number cg43252277

<400> 3372
gagaggagta ggccaaaaaa aaaaagtctt gattcctgaa tgtgccttat 50

<210> 3373
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (3374 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43253001

<400> 3373

ctctgtctcg gggaagccgg ggggtggcaga tccagctgga agtgaactga c

51

<210> 3374

<211> 50

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (3373 is other entry)

<221> misc_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43253001

<400> 3374

ctctgtctcg gggaagccgg ggggtgcagat ccagctggaa gtgaactgac

50

<210> 3375

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (3376 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43253077

<400> 3375

taaattaaaa gcagatttct ttttttaatt ctgcaacttt gtctacaacg t

51

<210> 3376

<211> 50

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (3375 is other entry)

<221> misc_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43253077

<400> 3376
taaattaaaa gcagatttct tttttaattc tgcaactttg tctacaacgt 50

<210> 3377
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3378 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43253093

<400> 3377
ttaccgcatac ttctttgctg actttggttaa cggggtgtcc agagaggagc g 51

<210> 3378
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3377 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43253093

<400> 3378
ttaccgcatac ttctttgctg acttttagtaa cggggtgtcc agagaggagc g 51

<210> 3379
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (3380 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43253436

<400> 3379
agcaagtact ctatgttggc tgttccgcag tgtaatgact ggtaataaaa a 51

<210> 3380
<211> 51

<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3379 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43253436

<400> 3380
agcaagtact ctatgttggc tggtctgcag tgtaatgact ggttaataaa a 51

<210> 3381
<211> 51
<212> DNA
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<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3382 is other entry)

<221> misc_feature
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<223> Accession number cg43253873

<400> 3381
tgtgtgcttt cctctctcca agcacacagc actgggagag tcttgtctcc a 51

<210> 3382
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3381 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43253873

<400> 3382
tgtgtgcttt cctctctcca agcacgcagc actgggagag tcttgtctcc a 51

<210> 3383
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)

<223> 1 of 2 allelic variants (3384 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43257902

<400> 3383

aaggctacta taaaaatatt gcaaaagcaa taaaaacaca atatcgta a

51

<210> 3384

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (3383 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43257902

<400> 3384

aaggctacta taaaaatatt gcaaacgcaa taaaaacaca atatcgta a

51

<210> 3385

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (3386 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43258630

<400> 3385

gtgtcaagag ccaagggcaa aaaaggagga gaagtctgga gtcggcataa t

51

<210> 3386

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (3385 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43258630

<400> 3386
gtgtcaagag ccaagggcaa aaaagaagga gaagtctgga gtcggcataa t 51

<210> 3387
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3388 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43259564

<400> 3387
aaaacattaa attcttaaaa aaaaaaaggc atgccacatg tcacccttta a 51

<210> 3388
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3387 is other entry)

<221> misc_feature
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<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43259564

<400> 3388
aaaacattaa attcttaaaa aaaaaaggca tgccacatgt caccctttaa 50

<210> 3389
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3390 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43259564

<400> 3389
aaacattaa ttcttaaaaa aaaaaaggca tgccacatgt caccctttaa g 51

<210> 3390
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3389 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43259564

<400> 3390
aaacattaaa ttcttaaaaa aaaaaggcat gccacatgtc accctttaag

50

<210> 3391
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (3392 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43259814

<400> 3391
taatgaaaac aaaatcaaga atgatccact ggtactgcag gttacagaga a

51

<210> 3392
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (3391 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43259814

<400> 3392
taatgaaaac aaaatcaaga atgattcact ggtactgcag gttacagaga a

51

<210> 3393

<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3394 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43259814

<400> 3393
aaaatacctt agaaaaatca aacagcacct gcaacacatg cttatataaa g 51

<210> 3394
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3393 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43259814

<400> 3394
aaaatacctt agaaaaatca aacagaacct gcaacacatg cttatataaa g 51

<210> 3395
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3396 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43260502

<400> 3395
tgtgcggtgg gagcgagctg ggcggcgtgc gctccccgag gactggcctg a 51

<210> 3396
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature

<222> (26)...(0)
<223> 2 of 2 allelic variants (3395 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43260502

<400> 3396
tgtgcggtgg gagcgagctg ggcgggtgcg ctccccgagg actggcctga 50

<210> 3397
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3398 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43261866

<400> 3397
atgttgccca ggctggtctc aaacttctgg gctcaagtga tcctctcacc t 51

<210> 3398
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3397 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43261866

<400> 3398
atgttgccca ggctggtctc aaactctctgg gctcaagtga tcctctcacc t 51

<210> 3399
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3400 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43261866

<400> 3399
aaacttctgg gctcaagtga tcctctcacc tcagcctccc atagtgctgg g 51

<210> 3400
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3399 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43261866

<400> 3400
aaacttctgg gctcaagtga tcctcccacc tcagcctccc atagtgctgg g 51

<210> 3401
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3402 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43262113

<400> 3401
ccgcactgag cagcagcagc agcagcagat ggagcgggag gagtgagggg c 51

<210> 3402
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3401 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)
<223> Accession number cg43262113

<400> 3402
ccgcactgag cagcagcagc agcagagatg gagcgggagg agtgaggggc 50

<210> 3403
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3404 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43263775

<400> 3403
tattaagttg ttgtaagcta ctacactatt cttcaggtat ggctgcgggg t 51

<210> 3404
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3403 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43263775

<400> 3404
tattaagttg ttgtaagcta ctacattatt cttcaggtat ggctgcgggg t 51

<210> 3405
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3406 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43263775

<400> 3405
ttccaggttt tgctgcggaa cccctggcc aaggcaaaga tccagcacca t 51

<210> 3406
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3405 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43263775

<400> 3406
ttccagggtt tgctgcggaa cccccaggcc aaggcaaaga tccagcacca t 51

<210> 3407
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3408 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43264142

<400> 3407
ctatttgcgt ggattttttt tttttaagg aaaaatacgt ttggaaaata a 51

<210> 3408
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3407 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43264142

<400> 3408
ctatttgcgt ggattttttt tttttaagga aaaatacgtt tggaaaataa 50

<210> 3409
<211> 50

<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3410 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43266542

<400> 3409
tattgcagac atatTTTTga gatgtaaaaa aaaaaattta aagttaaag 50

<210> 3410
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3409 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43266542

<400> 3410
tattgcagac atatTTTTga gatgtaaaaa aaaaaattt aaagttaaag g 51

<210> 3411
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3412 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43267277

<400> 3411
caagtagctg agaccacagg tgtgcaccac catgcctggc taattttttt a 51

<210> 3412
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3411 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43267277

<400> 3412
caagtagctg agaccacagg tgtgcgccac catgcctggc taattttttt a 51

<210> 3413
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3414 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43267337

<400> 3413
atacacacac acacacacac acacataaag aaaaaaaaga aaattataag a 51

<210> 3414
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3413 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
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<400> 3414
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<210> 3415
<211> 51
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<221> misc_feature
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<223> 1 of 2 allelic variants (3416 is other entry)

<221> misc_feature
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<400> 3415
acacacacac acacacacac ataaagaaaa aaaagaaaat tataagaagt t 51

<210> 3416
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<212> DNA
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<223> 2 of 2 allelic variants (3415 is other entry)

<221> misc_feature
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<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43267337

<400> 3416
acacacacac acacacacac ataaaaaaaa aaagaaaatt ataagaagtt 50

<210> 3417
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (3418 is other entry)

<221> misc_feature
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<223> Accession number cg43267337

<400> 3417
cacacacaca cataaagaaa aaaaagaaaa ttataagaag ttaatatga c 51

<210> 3418
<211> 50
<212> DNA
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<223> 2 of 2 allelic variants (3417 is other entry)

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<223> Nucleotide deleted between bases 25 and 26

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<222> (0)...(0)

<223> Accession number cg43267337

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cacacacaca cataaagaaa aaaaaaaaaat tataagaagt taatattgac

50

<210> 3419

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (3420 is other entry)

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<223> Accession number cg43267337

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agtatttagt cattaacatt ttgctatttc atcaatgtaa ataattaatt t

51

<210> 3420

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (3419 is other entry)

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51

<210> 3421

<211> 51

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<213> Homo sapiens

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<223> 1 of 2 allelic variants (3422 is other entry)

<221> misc_feature
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<223> Accession number cg43267337

<400> 3421
agtacataca tgttttagcta ctaaagaaaa agtaatcaga agcaaattca a 51

<210> 3422
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<223> 2 of 2 allelic variants (3421 is other entry)

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<210> 3423
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<223> 1 of 2 allelic variants (3424 is other entry)

<221> misc_feature
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<223> Accession number cg43268162

<400> 3423
ccccagtgac tcatacttat ttgtctgcaa agttacaaaa gaagatcccc a 51

<210> 3424
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (3423 is other entry)

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<223> Accession number cg43268162

<400> 3424
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<210> 3425
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<223> 1 of 2 allelic variants (3426 is other entry)

<221> misc_feature
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<400> 3425
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<210> 3426
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (3425 is other entry)

<221> misc_feature
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<223> Accession number cg43268348

<400> 3426
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<210> 3427
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<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (3428 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43268348

<400> 3427
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<210> 3428
<211> 51
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<220>
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<223> 2 of 2 allelic variants (3427 is other entry)

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gcctggctca aatatttggt gaatgggtaa atatgctgac ttgctgaag t 51

<210> 3429
<211> 51
<212> DNA
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<220>
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<223> 1 of 2 allelic variants (3430 is other entry)

<221> misc_feature
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<223> Accession number cg43268348

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<210> 3430
<211> 50
<212> DNA
<213> Homo sapiens

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<222> (0)...(0)
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<400> 3430
cacttaatga aacagtaaaa aaaaaatagg ttgaaacac ataatccttc 50

<210> 3431
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<212> DNA
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<223> 1 of 2 allelic variants (3432 is other entry)

<221> misc_feature
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<223> Accession number cg43268348

<400> 3431
acttaatgaa acagtaaaaa aaaaaatagg ttgaaacac ataatccttc g 51

<210> 3432
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<223> 2 of 2 allelic variants (3431 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43268348

<400> 3432
acttaatgaa acagtaaaaa aaaaataggt ttgaaacaca taatccttcg 50

<210> 3433
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (3434 is other entry)

<221> misc_feature
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<400> 3433
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<210> 3434
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<212> DNA
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<221> misc_feature
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<223> Accession number cg43268348

<400> 3434
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<210> 3435
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<223> 1 of 2 allelic variants (3436 is other entry)

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tttgaataat tgacttttga attcataaaa accttcctt attaatcatc c 51

<210> 3436
<211> 51
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<223> 2 of 2 allelic variants (3435 is other entry)

<221> misc_feature
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<400> 3436
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<210> 3437
<211> 51
<212> DNA
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3438 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43268348

<400> 3437

gcaagaatgc ctttttgttt tgttcaactgc tgtgtctaaa ataatgcctg g

51

<210> 3438

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (3437 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43268348

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<210> 3439

<211> 51

<212> DNA

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<223> Accession number cg43268590

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51

<210> 3440

<211> 51

<212> DNA

<213> Homo sapiens

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<223> Accession number cg43268590

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51

<210> 3441

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<223> 1 of 2 allelic variants (3442 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43270809

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cacttgcccc ccaaaccag cctcgcgagc tgtgccctct gagagtgcac a

51

<210> 3442

<211> 51

<212> DNA

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<222> (26)...(0)

<223> 2 of 2 allelic variants (3441 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43270809

<400> 3442

cacttgcccc ccaaaccag cctcgtgagc tgtgccctct gagagtgcac a

51

<210> 3443

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (3444 is other entry)

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51

<210> 3444

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<212> DNA

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<400> 3444
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<210> 3445
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<223> 1 of 2 allelic variants (3446 is other entry)

<221> misc_feature
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<223> Accession number cg43271689

<400> 3445
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<210> 3446
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (3445 is other entry)

<221> misc_feature
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<400> 3446
ctttttcttt ttaacaaaac cttcagtttc acattttagt gtacactgtg g 51

<210> 3447
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<223> 1 of 2 allelic variants (3448 is other entry)

<221> misc_feature
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<223> Accession number cg43271689

<400> 3447
accttcaatt tcacatttta gtgtacactg tggtttccag agaaatatat g 51

<210> 3448
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (3447 is other entry)

<221> misc_feature
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<223> Accession number cg43271689

<400> 3448
accttcaatt tcacatttta gtgtatactg tggtttccag agaaatatat g 51

<210> 3449
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<220>
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<223> 1 of 2 allelic variants (3450 is other entry)

<221> misc_feature
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<223> Accession number cg43271689

<400> 3449
ttttagtgta cactgtgggt tccagagaaa tatatggatc tcctatatatc t 51

<210> 3450
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (3449 is other entry)

<221> misc_feature
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<223> Accession number cg43271689

<400> 3450
tttttagtgta cactgtgggt tccagggaaa tatatggatc tcctatattc t 51

<210> 3451
<211> 51
<212> DNA
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<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3452 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43272452

<400> 3451
cgggtctccag cgggcagggt atccccccc ctaccgggg gaatagcaag c 51

<210> 3452
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3451 is other entry)

<221> misc_feature
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<223> Accession number cg43272452

<400> 3452
cgggtctccag cgggcagggt atcccacccc ctaccgggg gaatagcaag c 51

<210> 3453
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3454 is other entry)

<221> misc_feature
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<223> Accession number cg43273280

<400> 3453
caatcttita aggggcagag gaaatgagga agaaaagaaa aggaattaca g 51

<210> 3454
<211> 51
<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (3453 is other entry)

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<223> Accession number cg43273280

<400> 3454

caatctttta aggggcagag gaaataagga agaaaagaaa aggaattaca g

51

<210> 3455

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (3456 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43273935

<400> 3455

cactgccata ctccagccac tgcttgatca cctccagctg cagagagctc a

51

<210> 3456

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (3455 is other entry)

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<223> Accession number cg43273935

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cactgccata ctccagccac tgcttaatca cctccagctg cagagagctc a

51

<210> 3457

<211> 51

<212> DNA

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<222> (26)...(0)

<223> 1 of 2 allelic variants (3458 is other entry)

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<223> Accession number cg43274254

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gtaaattaca attctttcac acttaaaact ttatgggaaa agtattgcaa a 51

<210> 3458
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (3457 is other entry)

<221> misc_feature
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<223> Accession number cg43274254

<400> 3458
gtaaattaca attctttcac acttataact ttatgggaaa agtattgcaa a 51

<210> 3459
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (3460 is other entry)

<221> misc_feature
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<223> Accession number cg43274931

<400> 3459
tcataagaaa tacaaagcta gttttcggag caggtgtaat tcaggcactg t 51

<210> 3460
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3459 is other entry)

<221> misc_feature
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<223> Accession number cg43274931

<400> 3460

tcataagaaa tacaaagcta gtttttggag caggtgtaat tcaggcactg t

51

<210> 3461

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (3462 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43275466

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51

<210> 3462

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (3461 is other entry)

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<223> Accession number cg43275466

<400> 3462

ctgaaataga acgcacaccc gtactacttt acttcattta gattcttact c

51

<210> 3463

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (3464 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43275466

<400> 3463

ctactctccc atcttaaaaa tgatccgagt agtccttttc cgctcgtcc c

51

<210> 3464

<211> 51

<212> DNA

<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (3463 is other entry)

<221> misc_feature
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<223> Accession number cg43275466

<400> 3464
ctactctccc atcttaaaaa tgatctgagt agtccttttc cgctctgtcc c 51

<210> 3465
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<221> misc_feature
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<223> Accession number cg43275493

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gtatccgccg gtattccagg taacgtgtcg cacaaagtcc tcagtaatga 50

<210> 3466
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3465 is other entry)

<221> misc_feature
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<223> Accession number cg43275493

<400> 3466
gtatccgccg gtattccagg taacgctgtc gcacaaagtc ctacagtaatg a 51

<210> 3467
<211> 51
<212> DNA
<213> Homo sapiens

<220>

<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3468 is other entry)

<221> misc_feature
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<223> Accession number cg43276309

<400> 3467
acagtagaca gaagttgggc aaaaggctga tttgaggaag ttttgggctt c 51

<210> 3468
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (3467 is other entry)

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acagtagaca gaagttgggc aaaagcctga tttgaggaag ttttgggctt c 51

<210> 3469
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<223> 1 of 2 allelic variants (3470 is other entry)

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agctgccatg aggcaagagc tgggcctgga aaaagcccct gggaggcaag a 51

<210> 3470
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<220>
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<223> 2 of 2 allelic variants (3469 is other entry)

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<223> Accession number cg43276309

<400> 3470

agctgccatg aggcgaagagc tgggcttgga aaaagcccct gggaggcaag a

51

<210> 3471

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (3472 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43276309

<400> 3471

gccatgaggc aagagctggg cctggaaaaa gccctggga ggcaagagca g

51

<210> 3472

<211> 50

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (3471 is other entry)

<221> misc_feature

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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43276309

<400> 3472

gccatgaggc aagagctggg cctggaaaag cccctgggag gcaagagcag

50

<210> 3473

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

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<223> 1 of 2 allelic variants (3474 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43276309

<400> 3473
ttctcaagtc aaagctgggc ctgttcatgc caccgggaag cagaaggtgg g 51

<210> 3474
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (3473 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43276309

<400> 3474
ttctcaagtc aaagctgggc ctgttgatgc caccgggaag cagaaggtgg g 51

<210> 3475
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (3476 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43277914

<400> 3475
aatgaggac acacacacac acacacatgc atgcatatgc acacacacag a 51

<210> 3476
<211> 50
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (3475 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43277914

<400> 3476
aatgaggac acacacacac acacaatgca tgcatatgca cacacacaga 50

<210> 3477
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3478 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43279568

<400> 3477
ccactgcact ccatccagcc tgggcaacag agcgagactc catctcaaaa a 51

<210> 3478
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3477 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43279568

<400> 3478
ccactgcact ccatccagcc tgggcgacag agcgagactc catctcaaaa a 51

<210> 3479
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3480 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43280385

<400> 3479
ttcctttaga aattcttatt ggttccttcc ctgcagcgac aaccggctgc c 51

<210> 3480
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (3479 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43280385

<400> 3480
ttcctttaga aattcttatt ggttcgttcc ctgcagcgac aaccggctgc c 51

<210> 3481
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3482 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43280932

<400> 3481
tagtcccagc tactcaggag actgaagcag gaggatcact tgagcccagg a 51

<210> 3482
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3481 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43280932

<400> 3482
tagtcccagc tactcaggag actgaggcag gaggatcact tgagcccagg a 51

<210> 3483
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (3484 is other entry)

<221> misc_feature

<222> (0)...(0)
<223> Accession number cg43281897

<400> 3483
atttcatatg ccaactgagaa gaggtgtcag tatacagaac ataggaagaa g 51

<210> 3484
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3483 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43281897

<400> 3484
atttcatatg ccaactgagaa gaggtatcag tatacagaac ataggaagaa g 51

<210> 3485
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3486 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43281897

<400> 3485
atacagaaca taggaagaag aaaaaagcat gagaacatct gcttagttag a 51

<210> 3486
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3485 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43281897

<400> 3486
atacagaaca taggaagaag aaaaacgcat gagaacatct gcttagttag a 51

<210> 3487
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3488 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43284148

<400> 3487
aacagcaaca attacaaatt tatttcaaca aagccacacc caataggagg c 51

<210> 3488
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (3487 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43284148

<400> 3488
aacagcaaca attacaaatt tattttaaca aagccacacc caataggagg c 51

<210> 3489
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3490 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43284565

<400> 3489
tcgagaccag cctgggcaac atgataaaac ccattctctac taaaagtaca a 51

<210> 3490
<211> 51
<212> DNA
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<220>

<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3489 is other entry)

<221> misc_feature
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<223> Accession number cg43284565

<400> 3490
tcgagaccag cctgggcaac atgatgaaac ccattctctac taaaagtaca a 51

<210> 3491
<211> 51
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<220>
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<223> 1 of 2 allelic variants (3492 is other entry)

<221> misc_feature
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<223> Accession number cg43284565

<400> 3491
catgataaaa cccattctcta ctaaagtac aaaagtagcc aggcgcggtg g 51

<210> 3492
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3491 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43284565

<400> 3492
catgataaaa cccattctcta ctaaagtac aaaagtagcc aggcgcggtg g 51

<210> 3493
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3494 is other entry)

<221> misc_feature
<222> (0)...(0)

<223> Accession number cg43284565

<400> 3493

aaagtagcca ggcgcggtgg cgcacgcctg tggtcctagc tattcgggag c

51

<210> 3494

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (3493 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43284565

<400> 3494

aaagtagcca ggcgcggtgg cgcacacctg tggtcctagc tattcgggag c

51

<210> 3495

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (3496 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43284565

<400> 3495

gccaggcgcg gtggcgcacg cctgtggtcc tagctattcg ggagcctgag g

51

<210> 3496

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (3495 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43284565

<400> 3496

gccaggcgcg gtggcgcacg cctgtagtcc tagctattcg ggagcctgag g

51

<210> 3497

<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (3498 is other entry)

<221> misc_feature
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<223> Accession number cg43284565

<400> 3497
ccaggcgagg tggcgacgc ctgtggctct agctattcgg gagcctgagg c 51

<210> 3498
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3497 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43284565

<400> 3498
ccaggcgagg tggcgacgc ctgtgatcct agctattcgg gagcctgagg c 51

<210> 3499
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3500 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43284565

<400> 3499
tcctagctat tcgggagcct gaggcaggag aatcacatga acccaggagg c 51

<210> 3500
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3499 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43284565

<400> 3500
tcctagctat tcgggagcct gaggcgggag aatcacatga acccaggagg c 51

<210> 3501
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3502 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43284565

<400> 3501
caggagtctg agaccagcct gggcaacatg ataaaaccca tctctactaa a 51

<210> 3502
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3501 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43284565

<400> 3502
caggagtctg agaccagcct gggcagcatg ataaaaccca tctctactaa a 51

<210> 3503
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3504 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43285946

<400> 3503
gggaagaaga ggactggaca tgtttgggcc cctgttcccg gtctttggta a 51

<210> 3504
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
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<223> 2 of 2 allelic variants (3503 is other entry)

<221> misc_feature
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<223> Accession number cg43285946

<400> 3504
gggaagaaga ggactggaca tgtttgggcc cctgttcccg gtctttggta a 51

<210> 3505
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3506 is other entry)

<221> misc_feature
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<223> Accession number cg43285946

<400> 3505
gcttcagatg acgaaaatgc cacatcagat taaatgagaa aaaaaccttt c 51

<210> 3506
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3505 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43285946

<400> 3506

gcttcagatg acgaaaatgc cacatagatt aaatgagaaa aaaacctttc

50

<210> 3507

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (3508 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43286741

<400> 3507

tggttcagggtg agaaaacata atggattttt ttttttctct ctggagctgc c

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<210> 3508

<211> 50

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (3507 is other entry)

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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

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<223> Accession number cg43286741

<400> 3508

tggttcagggtg agaaaacata atggattttt ttttttctct tggagctgcc

50

<210> 3509

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (3510 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43291195

<400> 3509

ttgatgtttg tatggttggg tgggtatttg attcattgtt tgggggttgg a

51

<210> 3510
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> Accession number cg43291195

<400> 3510
ttgatgtttg tatggttggt tgggtgtttg attcattggt tgggggtttgg a

51

<210> 3511
<211> 51
<212> DNA
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3512 is other entry)

<221> misc_feature
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<223> Accession number cg43292021

<400> 3511
tgaaattaac gcgtatgctg ctacagagac cccgcattta aagctgggcc t

51

<210> 3512
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<212> DNA
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<220>
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<223> 2 of 2 allelic variants (3511 is other entry)

<221> misc_feature
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<223> Accession number cg43292021

<400> 3512
tgaaattaac gcgtatgctg ctacaaagac cccgcattta aagctgggcc t

51

<210> 3513
<211> 51
<212> DNA
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<220>

<221> misc_feature
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<223> 1 of 2 allelic variants (3514 is other entry)

<221> misc_feature
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<223> Accession number cg43293043

<400> 3513
ggcccccata ccctcagaga tggagggtga ccaggtaaata acaagggact g 51

<210> 3514
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (3513 is other entry)

<221> misc_feature
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<223> Accession number cg43293043

<400> 3514
ggcccccata ccctcagaga tggagagtga ccaggtaaata acaagggact g 51

<210> 3515
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3516 is other entry)

<221> misc_feature
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<223> Accession number cg43293043

<400> 3515
aaggagcagc agtgggctgg cctgggggtc cgaacatgat ccctgcgga g 51

<210> 3516
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (3515 is other entry)

<221> misc_feature
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<223> Accession number cg43293043

<400> 3516

aaggagcagc agtgggctgg cctggagggtc cgaacatgat cccctgcgga g

51

<210> 3517

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (3518 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43293043

<400> 3517

tgcagggtgc agagggaaac agggcgcggt gagtcacagg gccagagccc c

51

<210> 3518

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (3517 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43293043

<400> 3518

tgcagggtgc agagggaaac agggcacggt gagtcacagg gccagagccc c

51

<210> 3519

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (3520 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43293043

<400> 3519

ggcgcggtga gtcacagggc cagagcccca ggcagtggct gggccaggac a

51

<210> 3520

<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3519 is other entry)

<221> misc_feature
<222> (25)...(26)
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<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43293043

<400> 3520
ggcgcggtga gtcacagggc cagagcccag gcagtggctg ggccaggaca

50

<210> 3521
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3522 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43296511

<400> 3521
ccaaggtcac actgtggaag gaaaacaaat tcataacaat agatgttaac a

51

<210> 3522
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3521 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43296511

<400> 3522
ccaaggtcac actgtggaag gaaaaaaatt cataacaata gatgttaaca

50

<210> 3523
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3524 is other entry)

<221> misc_feature
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<400> 3523
aacaaattca taacaataga tgttaacatt tgtaggcct gaagacattt t 51

<210> 3524
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3523 is other entry)

<221> misc_feature
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<400> 3524
aacaaattca taacaataga tggtatcatt tgtaggcct gaagacattt t 51

<210> 3525
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3526 is other entry)

<221> misc_feature
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<223> Accession number cg43297399

<400> 3525
agggtgaata ttgctaagtc ggattcgcat atgagggtgca gcatcaagtc t 51

<210> 3526
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3525 is other entry)

<221> misc_feature
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<223> Accession number cg43297399

<400> 3526
agggtgaata ttgctaagtc ggattagcat atgaggtgca gcatcaagtc t 51

<210> 3527
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3528 is other entry)

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<222> (0)...(0)
<223> Accession number cg43297399

<400> 3527
tacatttggt tatcatgaga catgcaaact cctccaattt taatgagaac a 51

<210> 3528
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3527 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43297399

<400> 3528
tacatttggt tatcatgaga catgcgaact cctccaattt taatgagaac a 51

<210> 3529
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3530 is other entry)

<221> misc_feature

<222> (0)...(0)
<223> Accession number cg43299091

<400> 3529
ctgagctggc ctgagagggga atgggcagtg tcaccaaagt cagccctgcc c 51

<210> 3530
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (3529 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43299091

<400> 3530
ctgagctggc ctgagagggga atgggtagtg tcaccaaagt cagccctgcc c 51

<210> 3531
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (3532 is other entry)

<221> misc_feature
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<223> Accession number cg43299091

<400> 3531
ctgccctaag agtctgcctc agccctgag gtctggaagg ctgcctgggt c 51

<210> 3532
<211> 50
<212> DNA
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<223> 2 of 2 allelic variants (3531 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
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<223> Accession number cg43299091

<400> 3532
ctgccctaag agtctgcctc agccctgagg tctggaaggc tgcctgggttc 50

<210> 3533
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3534 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43299326

<400> 3533
ctcatgagac ttattcacta tcatgggaac agtatggggg aaactgcccc c 51

<210> 3534
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (3533 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43299326

<400> 3534
ctcatgagac ttattcacta tcatgagaac agtatggggg aaactgcccc c 51

<210> 3535
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3536 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43300082

<400> 3535
ctccagcccc cactgcctct gggactggct ctcgacgcac ctgaaggctg a 51

<210> 3536
<211> 51

<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3535 is other entry)

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<222> (0)...(0)
<223> Accession number cg43300082

<400> 3536
ctccagcccc cactgcctct gggaccggt ctcgacgcac ctgaaggctg a 51

<210> 3537
<211> 51
<212> DNA
<213> Homo sapiens

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<222> (26)...(0)
<223> 1 of 2 allelic variants (3538 is other entry)

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<222> (0)...(0)
<223> Accession number cg43300240

<400> 3537
attgaggcac ctccacagca ggctgctggac aaaaaaagga aaaaaggccc a 51

<210> 3538
<211> 51
<212> DNA
<213> Homo sapiens

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<222> (26)...(0)
<223> 2 of 2 allelic variants (3537 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43300240

<400> 3538
attgaggcac ctccacagca ggctgtggac aaaaaaagga aaaaaggccc a 51

<210> 3539
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)

<223> 1 of 2 allelic variants (3540 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43300347

<400> 3539

aaaacaggac aaaatggctc ttgcttttt tttttaatt aactttcctt t

51

<210> 3540

<211> 50

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

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<223> 2 of 2 allelic variants (3539 is other entry)

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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43300347

<400> 3540

aaaacaggac aaaatggctc ttgcttttt tttttaatta actttccttt

50

<210> 3541

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (3542 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43300765

<400> 3541

tgtaactata cagagcgatt ttttttatac aattattaca acgattaataa a

51

<210> 3542

<211> 50

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (3541 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43300765

<400> 3542
tgtaactata cagagcgatt tttttataca attattacaa cgattaaaaa 50

<210> 3543
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3544 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43301130

<400> 3543
gggggctcga cgtggctgat acccctaata gcctgttta tcacatcccc t 51

<210> 3544
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3543 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43301130

<400> 3544
gggggctcga cgtggctgat accccaatag ccctgtttat cacatcccct 50

<210> 3545
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)

<223> 1 of 2 allelic variants (3546 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43303307

<400> 3545

tctgggacct gtccgtaagg ggaccattgg gggctggcct ggcggtgac t

51

<210> 3546

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

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<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43303307

<400> 3546

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51

<210> 3547

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (3548 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43304430

<400> 3547

ccccagcca gggcctggtg ggaggggttg gtcaccattg cctgccgtgt t

51

<210> 3548

<211> 51

<212> DNA

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<223> 2 of 2 allelic variants (3547 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43304430

<400> 3548
ccccagcca gggcctggtg ggaggagttg gtcaccattg cctgccgtgt t 51

<210> 3549
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3550 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43304430

<400> 3549
gggaggtcag gccaccgccc ccactacagt ctgaatcatc cacgttcccg c 51

<210> 3550
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3549 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43304430

<400> 3550
gggaggtcag gccaccgccc ccactgcagt ctgaatcatc cacgttcccg c 51

<210> 3551
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3552 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43304574

<400> 3551
tgctcacacc tgggcaggcc ccgcggcagc aatggcagct ctctgtaca g 51

<210> 3552
<211> 50
<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (3551 is other entry)

<221> misc_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43304574

<400> 3552

tgctcacacc tgggcaggcc ccgcgcagca atggcagctc tcctgtacag

50

<210> 3553

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (3554 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43304574

<400> 3553

aagtc aaagc taaccgaggc tgtgccttcc gagacccccg ggatggcccc t

51

<210> 3554

<211> 50

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (3553 is other entry)

<221> misc_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43304574

<400> 3554

aagtc aaagc taaccgaggc tgtgcttccg agaccccccg gatggcccct

50

<210> 3555

<211> 48
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3556 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43304574

<400> 3555
acccccggga tggccctgg gaggccaagg agtcggggac tgggtacc

48

<210> 3556
<211> 47
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3555 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43304574

<400> 3556
acccccggga tggccctgg gaggcaagga gtcggggact ggggtacc

47

<210> 3557
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3558 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43304744

<400> 3557
tgcagagaga tctgagcttc gctgtctccc ggtcggacgc tcgcagctgc g

51

<210> 3558
<211> 51
<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (3557 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43304744

<400> 3558

tgcagagaga tctgagcttc gctgtatccc ggctggacgc tcgcagctgc g

51

<210> 3559

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (3560 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43305900

<400> 3559

gaaccttgca catgaaatgt gttggaagaa aagctgagtg ttgggagaga a

51

<210> 3560

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (3559 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43305900

<400> 3560

gaaccttgca catgaaatgt gttgggagaa aagctgagtg ttgggagaga a

51

<210> 3561

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (3562 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43307969

<400> 3561
cctctctcgc tcagcggcca aggtgggcgt ctccaccaca atctcctgga t 51

<210> 3562
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3561 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43307969

<400> 3562
cctctctcgc tcagcggcca aggtgagcgt ctccaccaca atctcctgga t 51

<210> 3563
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3564 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43307969

<400> 3563
cttgccggat cacaaacttg gggagcctgt tcagaaattt ctcagcagtc a 51

<210> 3564
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3563 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43307969

<400> 3564

cttgccggat cacaaacttg gggagtctgt tcagaaattt ctcagcagtc a 51

<210> 3565
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3566 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43311814

<400> 3565
tagtagttaa ttttgccttc tccatgagag cacatcctga ttaactcctt a 51

<210> 3566
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3565 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43311814

<400> 3566
tagtagttaa ttttgccttc tccataagag cacatcctga ttaactcctt a 51

<210> 3567
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3568 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43312162

<400> 3567
gcaccaattt tcaattttgt acataatgca catctcttaa cacttacatt t 51

<210> 3568
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3567 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43312162

<400> 3568
gcaccaattt tcaattttgt acatatgcac atctcttaac acttacattt 50

<210> 3569
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3570 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43312305

<400> 3569
tgtctagtc aggttgatgt taatggaact tgaaggggca gacacaggag a 51

<210> 3570
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3569 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43312305

<400> 3570
tgtctagtc aggttgatgt taatgcaact tgaaggggca gacacaggag a 51

<210> 3571
<211> 51
<212> DNA
<213> Homo sapiens

<220>

<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3572 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43312687

<400> 3571
gccagggaga gaaataattg atttttctct ctgtcaaggt ttctggcagc c 51

<210> 3572
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3571 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43312687

<400> 3572
gccagggaga gaaataattg attttgctct ctgtcaaggt ttctggcagc c 51

<210> 3573
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3574 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43312687

<400> 3573
tctggctctg ccagatggta aaggcgtgct ttagtggtga gacaatatgg g 51

<210> 3574
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3573 is other entry)

<221> misc_feature
<222> (0)...(0)

<223> Accession number cg43312687

<400> 3574

tctggctctg ccagatggta aaggcatgct ttagtgtgta gacaatatgg g

51

<210> 3575

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (3576 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43312687

<400> 3575

ggatttctta gaacacaggc taacaaaaac tacgcttagg ctttgcgtgt t

51

<210> 3576

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (3575 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43312687

<400> 3576

ggatttctta gaacacaggc taaccgaaac tacgcttagg ctttgcgtgt t

51

<210> 3577

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (3578 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43313505

<400> 3577

ttgttcagga gcagatcact tggaagcctc tgagctcttc aaagaattcc a

51

<210> 3578

<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3577 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43313505

<400> 3578
ttgttcagga gcagatcact tggaaacctc tgagctcttc aaagaattcc a 51

<210> 3579
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3580 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43315440

<400> 3579
gctgccagcc cttaccatgc aacaacactg cgctaagtgc atcgaaccac a 51

<210> 3580
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3579 is other entry)

<221> misc_feature
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<223> Accession number cg43315440

<400> 3580
gctgccagcc cttaccatgc aacaatactg cgctaagtgc atcgaaccac a 51

<210> 3581
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature

<222> (26)...(0)
<223> 1 of 2 allelic variants (3582 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43315796

<400> 3581
agctgtaccc atccagctca aaccgaaaaa aaaaaatcat ttgactgtta a 51

<210> 3582
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3581 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43315796

<400> 3582
agctgtaccc atccagctca aaccgaaaaa aaaaatcatt tgactgttaa 50

<210> 3583
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3584 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43316687

<400> 3583
agagcattct aaatgtttca caccctcatt tgattgacaa caggaactcc t 51

<210> 3584
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3583 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43316687

<400> 3584
agagcattct aatgtttca caccgccatt tgattgacaa caggaactcc t 51

<210> 3585
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3586 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43318220

<400> 3585
gcatcgctg tcggatcatc tatcggtcag acgagcacca ccctcccatc c 51

<210> 3586
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3585 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43318220

<400> 3586
gcatcgctg tcggatcatc tatcgtcaga cgagcaccac cctcccatcc 50

<210> 3587
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (3588 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43318445

<400> 3587

tagcattgct agttcaaaga gcttacgcat ttgcactttt gatagacacc g

51

<210> 3588

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (3587 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43318445

<400> 3588

tagcattgct agttcaaaga gcttatgcat ttgcactttt gatagacacc g

51

<210> 3589

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (3590 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43318557

<400> 3589

ggcggatcac ttgaggtcag gagttcgaga ccagcctggc caacatagtg a

51

<210> 3590

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (3589 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43318557

<400> 3590

ggcggatcac ttgaggtcag gagtttgaga ccagcctggc caacatagtg a

51

<210> 3591
<211> 51
<212> DNA
<213> Homo sapiens

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<222> (26)...(0)
<223> 1 of 2 allelic variants (3592 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43318557

<400> 3591
cctgtctcta ctaaaaatac aaaaattag ccagacatgg tggcaggtgc c 51

<210> 3592
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3591 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
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<223> Accession number cg43318557

<400> 3592
cctgtctcta ctaaaaatac aaaaattagc cagacatggt ggcaggtgcc 50

<210> 3593
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3594 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43319575

<400> 3593
cggatgacct gaggtcgggc ctgggcctgt ccctttgtgc atgcggcgctg a 51

<210> 3594
<211> 50

<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3593 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43319575

<400> 3594
cggatgacct gaggtcgggc ctgggctgtc cctttgtgca tgcggcgtga 50

<210> 3595
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3596 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43321121

<400> 3595
gaaaatggct gtggcttagc ttttcagctg atgcagggtg ataagctttc t 51

<210> 3596
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3595 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43321121

<400> 3596
gaaaatggct gtggcttagc ttttctgctg atgcagggtg ataagctttc t 51

<210> 3597
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3598 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43322119

<400> 3597
gcattgactg cagtgagaag gcaggtgcct ccatggctca ctgccccttg g 51

<210> 3598
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3597 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43322119

<400> 3598
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<210> 3599
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3600 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43322827

<400> 3599
aatatttata agttaacact cttgccactt actcatcaga ttatattttt t 51

<210> 3600
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3599 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43322827

<400> 3600
aatatttata agttaacact cttgctactt actcatcaga ttatattttt t 51

<210> 3601
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3602 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43322827

<400> 3601
ttcagcatgg gaaggagcac tgcattgtagg agctaagaaa aagtacacac t 51

<210> 3602
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3601 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43322827

<400> 3602
ttcagcatgg gaaggagcac tgcattatagg agctaagaaa aagtacacac t 51

<210> 3603
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (3604 is other entry)

<221> misc_feature
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<223> Accession number cg43323576

<400> 3603
ttattgaggc tgtgttttga agcatgccat tgatagggtg aacataacat t 51

<210> 3604
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (3603 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43323576

<400> 3604
ttattgaggc tgtgttttga agcataccat tgataggttg aacataacat t 51

<210> 3605
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3606 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43323676

<400> 3605
tcttttagatg gaaaaggcgt tgggtgtggtg tggattgtag cttcccgaaa c 51

<210> 3606
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (3605 is other entry)

<221> misc_feature
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<223> Accession number cg43323676

<400> 3606
tcttttagatg gaaaaggcgt tgggtgcggtg tggattgtag cttcccgaaa c 51

<210> 3607
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3608 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43323860

<400> 3607
ggccaacatg gtaaaaccct gtctctacta aaaaatacaa aaattagctg g 51

<210> 3608
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3607 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43323860

<400> 3608
ggccaacatg gtaaaaccct gtctccacta aaaaatacaa aaattagctg g 51

<210> 3609
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3610 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43324124

<400> 3609
acaaatccat ggcaatagaa agattaatgc tattctctga tgatcttaaa g 51

<210> 3610
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3609 is other entry)

<221> misc_feature

<222> (0)...(0)
<223> Accession number cg43324124

<400> 3610
acaaatccat ggcaatagaa agatttatgc tattctctga tgatcttaaa g 51

<210> 3611
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (3612 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43325035

<400> 3611
gaatttcctt gctagaaggc tttttcctc aaagattcct tttaggctta c 51

<210> 3612
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<221> misc_feature
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<221> misc_feature
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<223> Accession number cg43325035

<400> 3612
gaatttcctt gctagaaggc tttttcctca aagattcctt ttaggcttac 50

<210> 3613
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<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3614 is other entry)

<221> misc_feature
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<223> Accession number cg43325035

<400> 3613
ccttttaggc ttactttgat gttcaggatc tccaattata aatgtagtct c 51

<210> 3614
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3613 is other entry)

<221> misc_feature
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<223> Accession number cg43325035

<400> 3614
ccttttaggc ttactttgat gttcaagatc tccaattata aatgtagtct c 51

<210> 3615
<211> 51
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<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3616 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43325862

<400> 3615
ccatctgggc atcggggatc tcaccgctga agcggtcact tagtgccttc a 51

<210> 3616
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3615 is other entry)

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<222> (0)...(0)
<223> Accession number cg43325862

<400> 3616
ccatctgggc atcggggatc tcaccactga agcggtcact tagtgccttc a 51

<210> 3617
<211> 50

<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3618 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43326835

<400> 3617
gagggtcatca actcaccaag aaaagagggg cttatttgct acccagcagc

50

<210> 3618
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3617 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43326835

<400> 3618
gagggtcatca actcaccaag aaaagaaggg gcttatttgc taccagcag c

51

<210> 3619
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3620 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43327292

<400> 3619
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51

<210> 3620
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<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3619 is other entry)

<221> misc_feature
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<223> Accession number cg43327292

<400> 3620
ctgagtagct gggactacag gcacatacca ccacacctgg ctaatttttg t 51

<210> 3621
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3622 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43327899

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atcacctcaa ttggactgga tgttaacaaa acagatgaag ttaaaaatga a 51

<210> 3622
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (3621 is other entry)

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<222> (0)...(0)
<223> Accession number cg43327899

<400> 3622
atcacctcaa ttggactgga tgtagcaaaa acagatgaag ttaaaaatga a 51

<210> 3623
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3624 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43328701

<400> 3623
taaaacagaa ccaagtgatg aaggagtag gttggcctgt ggtgcactgt g 51

<210> 3624
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3623 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43328701

<400> 3624
taaaacagaa ccaagtgatg aaggcgtag gttggcctgt ggtgcactgt g 51

<210> 3625
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (3626 is other entry)

<221> misc_feature
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<223> Accession number cg43330024

<400> 3625
acacattacc cacatctcag tcaaagaaa agggtagcct ggcccagccc c 51

<210> 3626
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3625 is other entry)

<221> misc_feature
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<223> Accession number cg43330024

<400> 3626
acacattacc cacatctcag tcaaagaaa agggtagcct ggcccagccc c 51

<210> 3627
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3628 is other entry)

<221> misc_feature
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<223> Accession number cg43330024

<400> 3627
aaaggtccca cgcgtgcacc cacagtccgt ggcaccttcc tctggtgcac c

51

<210> 3628
<211> 51
<212> DNA
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<220>
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<223> 2 of 2 allelic variants (3627 is other entry)

<221> misc_feature
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<400> 3628
aaaggtccca cgcgtgcacc cacagcccgt ggcaccttcc tctggtgcac c

51

<210> 3629
<211> 51
<212> DNA
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<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3630 is other entry)

<221> misc_feature
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<223> Accession number cg43330024

<400> 3629
tccgggcctt ggaagtttct tcctactctg acgcaggctg ggaattctag a

51

<210> 3630
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3629 is other entry)

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<223> Accession number cg43330024

<400> 3630
tccgggcctt ggaagtttct tcctattctg acgcaggctg ggaattctag a 51

<210> 3631
<211> 51
<212> DNA
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<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3632 is other entry)

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<222> (0)...(0)
<223> Accession number cg43330373

<400> 3631
gcgccactcg tccgggtccc gggttctccgc cgccaacgcc tcgcaggggg a 51

<210> 3632
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3631 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43330373

<400> 3632
gcgccactcg tccgggtccc gggtcccccgc cgccaacgcc tcgcaggggg a 51

<210> 3633
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3634 is other entry)

<221> misc_feature

<222> (0)...(0)
<223> Accession number cg43330373

<400> 3633
gccactcgtc cgggtcccgg ttctccgccg ccaacgcctc gcagggggat a 51

<210> 3634
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3633 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43330373

<400> 3634
gccactcgtc cgggtcccgg ttctctgccg ccaacgcctc gcagggggat a 51

<210> 3635
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3636 is other entry)

<221> misc_feature
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<223> Accession number cg43331856

<400> 3635
gaaaagagaa acctggaaat gctccagaca ttccagaacc agattgcggc c 51

<210> 3636
<211> 51
<212> DNA
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<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3635 is other entry)

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gaaaagagaa acctggaaat gctccggaca ttccagaacc agattgcggc c 51

<210> 3637
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<212> DNA
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<220>
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<223> 1 of 2 allelic variants (3638 is other entry)

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<400> 3637
gtgaaggaaa atccttaata gattacattt tggttgttca agaaagtctg t 51

<210> 3638
<211> 51
<212> DNA
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<400> 3638
gtgaaggaaa atccttaata gattatattt tggttgttca agaaagtctg t 51

<210> 3639
<211> 51
<212> DNA
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<220>
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<223> 1 of 2 allelic variants (3640 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43333186

<400> 3639
gagcagcctt cctctgaaaa tgcttagttt tggatcctcc ttaacaagt a 51

<210> 3640
<211> 51
<212> DNA
<213> Homo sapiens

<220>

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<400> 3640
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<210> 3641
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<223> 1 of 2 allelic variants (3642 is other entry)

<221> misc_feature
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<210> 3642
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<223> 2 of 2 allelic variants (3641 is other entry)

<221> misc_feature
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<210> 3643
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<223> 1 of 2 allelic variants (3644 is other entry)

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<223> Accession number cg43333186

<400> 3643

ggcgcttctc caaagctaga ctggaacata cacaaccag tcgacagaag t

51

<210> 3644

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<223> 2 of 2 allelic variants (3643 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43333186

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51

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<223> 1 of 2 allelic variants (3646 is other entry)

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<222> (0)...(0)

<223> Accession number cg43333186

<400> 3645

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51

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<212> DNA

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<223> 2 of 2 allelic variants (3645 is other entry)

<221> misc_feature

<222> (0)...(0)

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ccagtcgaca gaagtcattg ttgcatggag gggctcggtt ccttatgatt g

51

<210> 3647

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51

<210> 3648
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<223> 2 of 2 allelic variants (3647 is other entry)

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51

<210> 3649
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<223> 1 of 2 allelic variants (3650 is other entry)

<221> misc_feature
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51

<210> 3650
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<212> DNA
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<210> 3651
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (3652 is other entry)

<221> misc_feature
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<223> Accession number cg43333186

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<210> 3652
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (3651 is other entry)

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<400> 3652
ttaaggatac atctgctgc tcttcagtga tgtatgtcct tggttttcct t 51

<210> 3653
<211> 51
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<223> 1 of 2 allelic variants (3654 is other entry)

<221> misc_feature
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<210> 3654
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (3653 is other entry)

<221> misc_feature
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cacagtcttc caggtccata agctttacct gagatttaga caagcctgga g 51

<210> 3655
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (3656 is other entry)

<221> misc_feature
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<223> Accession number cg43335897

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<210> 3656
<211> 51
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<223> 2 of 2 allelic variants (3655 is other entry)

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ttgatgggga ttgcattgaa tctgttgatt gcttttggtg aaatggccat t 51

<210> 3657
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<223> 1 of 2 allelic variants (3658 is other entry)

<221> misc_feature
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<223> Accession number cg43335897

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<210> 3658
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<223> 2 of 2 allelic variants (3657 is other entry)

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<223> Accession number cg43335897

<400> 3658
tggggattgc attgaatctg tagatcgctt ttggtaaaat ggccattttt a 51

<210> 3659
<211> 51
<212> DNA
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<220>
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<223> 1 of 2 allelic variants (3660 is other entry)

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<223> Accession number cg43335897

<400> 3659
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<210> 3660
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (3659 is other entry)

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<223> Accession number cg43335897

<400> 3660

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51

<210> 3661

<211> 51

<212> DNA

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<223> 1 of 2 allelic variants (3662 is other entry)

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51

<210> 3662

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (3661 is other entry)

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<223> Accession number cg43335897

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51

<210> 3663

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (3664 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43335897

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<210> 3664
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<223> 2 of 2 allelic variants (3663 is other entry)

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<210> 3665
<211> 51
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<223> 1 of 2 allelic variants (3666 is other entry)

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<223> Accession number cg43335897

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<210> 3666
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<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (3665 is other entry)

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<223> Accession number cg43335897

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ttttgttatt ccaaataaat ttgcagattg ctctgtctaa ctctttgaag a 51

<210> 3667
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<212> DNA

<213> Homo sapiens

<220>

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<223> 1 of 2 allelic variants (3668 is other entry)

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<222> (0)...(0)

<223> Accession number cg43335897

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51

<210> 3668

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (3667 is other entry)

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<223> Accession number cg43335897

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aaataaattt gcaaattgct ctgtccaact ctttgaagaa ttgaattgga a

51

<210> 3669

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (3670 is other entry)

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<223> Accession number cg43335897

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51

<210> 3670

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (3669 is other entry)

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<223> Accession number cg43335897

<400> 3670
aatttgcaaa ttgctctgtc taactttttg aagaattgaa ttggaatttt g 51

<210> 3671
<211> 51
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<223> 1 of 2 allelic variants (3672 is other entry)

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<400> 3671
ctaactcttt gaagaattga attggaattt tgatggggat tgcattgaat c 51

<210> 3672
<211> 51
<212> DNA
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<400> 3672
ctaactcttt gaagaattga attggtattt tgatggggat tgcattgaat c 51

<210> 3673
<211> 51
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<213> Homo sapiens

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<223> 1 of 2 allelic variants (3674 is other entry)

<221> misc_feature
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<400> 3673

tttgaagaat tgaattggaa ttttgatggg gattgcattg aatctgtaga t

51

<210> 3674

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (3673 is other entry)

<221> misc_feature

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<223> Accession number cg43335897

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51

<210> 3675

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (3676 is other entry)

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51

<210> 3676

<211> 51

<212> DNA

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<223> 2 of 2 allelic variants (3675 is other entry)

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51

<210> 3677

<211> 51

<212> DNA

<213> Homo sapiens

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<223> Accession number cg43336005

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<210> 3678
<211> 50
<212> DNA
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<221> misc_feature
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<400> 3678
cagggggcct gagcgggaca ggctggccac agcccatgtc cttggccttc 50

<210> 3679
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<212> DNA
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<223> 1 of 2 allelic variants (3680 is other entry)

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<400> 3679
agggggcctg agcgggacag gcctggccac agcccatgtc cttggccttc c 51

<210> 3680
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<223> 2 of 2 allelic variants (3679 is other entry)

<221> misc_feature
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<400> 3680
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<210> 3681
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<212> DNA
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3682 is other entry)

<221> misc_feature
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<223> Accession number cg43336714

<400> 3681
gcctcagatg gctccccaag gtcattcata tctcggtttg agtcatatc t 51

<210> 3682
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (3681 is other entry)

<221> misc_feature
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gcctcagatg gctccccaag gtcattcata tctcggtttg agtcatatc t 51

<210> 3683
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<223> 1 of 2 allelic variants (3684 is other entry)

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<223> Accession number cg43336760

<400> 3683

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51

<210> 3684

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<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (3683 is other entry)

<221> misc_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43336760

<400> 3684

tggtgacagt caggcctggg aggagccaca aactggagca cagagacatg

50

<210> 3685

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

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<222> (0)...(0)

<223> Accession number cg43336794

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51

<210> 3686

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (3685 is other entry)

<221> misc_feature
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<223> Accession number cg43336794

<400> 3686
ctataaacat ctcttttatat ccagacgttt tccaaatcac aaggactcaa a 51

<210> 3687
<211> 51
<212> DNA
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<220>
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<223> 1 of 2 allelic variants (3688 is other entry)

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<222> (0)...(0)
<223> Accession number cg43336815

<400> 3687
ttactaaacc tgaaatccgt cgtatatctg tttttacact tgtaatcttg a 51

<210> 3688
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (3687 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43336815

<400> 3688
ttactaaacc tgaaatccgt cgtattctgt ttttacactt gtaatcttga 50

<210> 3689
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3690 is other entry)

<221> misc_feature
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<223> Accession number cg43336925

<400> 3689

tttggaac aaactgtttc ttgttacta gatagaatct gtattgtagt a

51

<210> 3690

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (3689 is other entry)

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<222> (0)...(0)

<223> Accession number cg43336925

<400> 3690

tttggaac aaactgtttc ttgttacta gatagaatct gtattgtagt a

51

<210> 3691

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<212> DNA

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<223> 1 of 2 allelic variants (3692 is other entry)

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<400> 3691

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51

<210> 3692

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<212> DNA

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<223> 2 of 2 allelic variants (3691 is other entry)

<221> misc_feature

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<223> Accession number cg43336925

<400> 3692

tattactcaa taatatatgt atggttacag gttcctggag ttgttttatt t

51

<210> 3693

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<223> 1 of 2 allelic variants (3694 is other entry)

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<223> Accession number cg43337702

<400> 3693
aatctttttg tagagacaag gtctcaccat gttgccagg ctggtcttga a

51

<210> 3694
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<212> DNA
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<223> Accession number cg43337702

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aatctttttg tagagacaag gtctcccat gttgccagg ctggtcttga a

51

<210> 3695
<211> 51
<212> DNA
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<221> misc_feature
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<223> Accession number cg43338533

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aatgcagatc cttaaatttt cacacaaatg agataattat agtacatgta g

51

<210> 3696
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<223> 2 of 2 allelic variants (3695 is other entry)

<221> misc_feature
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<223> Accession number cg43338533

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aatgcagatc cttaaatttt cacacgaatg agataattat agtacatgta g 51

<210> 3697
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<223> Accession number cg43916985

<400> 3698
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<210> 3699
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ctccatcttc tatcttttgt cctcgcacat tgtctgtctt gatccttatg c 51

<210> 3700
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ctccatcttc tatcttttgt cctcaacat tgtctgtctt gatccttatg c 51

<210> 3701
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<210> 3702
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<210> 3703
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<223> 1 of 2 allelic variants (3704 is other entry)

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<210> 3704
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (3703 is other entry)

<221> misc_feature
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<223> Accession number cg43917418

<400> 3704
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<210> 3705
<211> 51
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<400> 3705
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<210> 3706
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<212> DNA
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<223> 2 of 2 allelic variants (3705 is other entry)

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<223> Accession number cg43917418

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51

<210> 3707

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (3708 is other entry)

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<210> 3708

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<212> DNA

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<223> Accession number cg43917418

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<210> 3709

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<223> 1 of 2 allelic variants (3710 is other entry)

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<223> Accession number cg43917418

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<210> 3710
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<210> 3711
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<400> 3711
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<210> 3712
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<400> 3712
tgatagcttc ttcaactagg tgctcttctc ttttcgggtt cctactggta g 51

<210> 3713
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<223> 1 of 2 allelic variants (3714 is other entry)

<221> misc_feature

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<223> Accession number cg43917443

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acacaacagt gctttttttt ttttttttaa tccccccaca aagcttttcc a

51

<210> 3714

<211> 50

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (3713 is other entry)

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acacaacagt gctttttttt tttttttaat cccccacaa agcttttcca

50

<210> 3715

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<212> DNA

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<223> 1 of 2 allelic variants (3716 is other entry)

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<223> Accession number cg43917544

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51

<210> 3716

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<210> 3717
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<223> Accession number cg43917746

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<210> 3718
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<210> 3719
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<221> misc_feature
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<223> Accession number cg43917764

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<210> 3720
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<400> 3720
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<210> 3721
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<221> misc_feature
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<223> Accession number cg43918187

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<210> 3722
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<223> 2 of 2 allelic variants (3721 is other entry)

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<400> 3722
tgcttggtgct cctcttggtt ggctaaagta ggcacacac tggggagcgt g 51

<210> 3723
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<223> 1 of 2 allelic variants (3724 is other entry)

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<223> Accession number cg43918199

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<210> 3724
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<223> Accession number cg43918199

<400> 3724
taatgtacac ttccttaaaa atctactttt gccacttata tacattcaat a 51

<210> 3725
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<223> Accession number cg43918326

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<210> 3727

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<223> 1 of 2 allelic variants (3728 is other entry)

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<210> 3728

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<223> Accession number cg43918370

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51

<210> 3729

<211> 51

<212> DNA

<213> Homo sapiens

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<223> Accession number cg43918591

<400> 3729
cccgatggac tagggccaag gcctggttga cagacggccc gtggggcccg g 51

<210> 3730
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (3729 is other entry)

<221> misc_feature
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<223> Accession number cg43918591

<400> 3730
cccgatggac tagggccaag gcctgattga cagacggccc gtggggcccg g 51

<210> 3731
<211> 51
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<223> 1 of 2 allelic variants (3732 is other entry)

<221> misc_feature
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<223> Accession number cg43918620

<400> 3731
agttcagtcg tctctgtctt ggagggcact gtgggcccc tcaggttgaa g 51

<210> 3732
<211> 50
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<210> 3733
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<223> 1 of 2 allelic variants (3734 is other entry)

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<210> 3734
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<223> 2 of 2 allelic variants (3733 is other entry)

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<400> 3734
cttcatgtaa acagttctag atggaggacc cagatggcac tcctcccggg g 51

<210> 3735
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<223> 1 of 2 allelic variants (3736 is other entry)

<221> misc_feature
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<223> Accession number cg43918725

<400> 3735

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51

<210> 3736

<211> 51

<212> DNA

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<223> 2 of 2 allelic variants (3735 is other entry)

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<223> Accession number cg43918725

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51

<210> 3737

<211> 51

<212> DNA

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<223> 1 of 2 allelic variants (3738 is other entry)

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<223> Accession number cg43918725

<400> 3737

ctaggtctag ttagtatctc agtggcgagg ctaccaaag ccttcgcagt g

51

<210> 3738

<211> 51

<212> DNA

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<222> (26)...(0)

<223> 2 of 2 allelic variants (3737 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43918725

<400> 3738

ctaggtctag ttagtatctc agtggcgagg ctaccaaag ccttcgcagt g

51

<210> 3739

<211> 51
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3740 is other entry)

<221> misc_feature
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<223> Accession number cg43919050

<400> 3739
ttctttcaca tagtttccta cctgctgccca gttaccccgg cctccggagc t 51

<210> 3740
<211> 50
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (3739 is other entry)

<221> misc_feature
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<400> 3740
ttctttcaca tagtttccta cctgcgccag ttaccccggc ctccggagct 50

<210> 3741
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3742 is other entry)

<221> misc_feature
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<223> Accession number cg43919189

<400> 3741
tgcagtcctc cagttgccca gcagcagtg gacgctcagt ggcacacagt g 51

<210> 3742
<211> 51
<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (3741 is other entry)

<221> misc_feature

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tgcagtcctc cagttgcccc gcagcgggtgg gacgctcagt ggacacacagt g

51

<210> 3743

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (3744 is other entry)

<221> misc_feature

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<223> Accession number cg43919189

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ccagttgccc agcagcagtg ggacgctcag tggcacacag tgggtctctg t

51

<210> 3744

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (3743 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43919189

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51

<210> 3745

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (3746 is other entry)

<221> misc_feature
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<223> Accession number cg43919529

<400> 3745
tcagcctcct gagtagctgg gattataggg gcacaccacc acaccggct a 51

<210> 3746
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3745 is other entry)

<221> misc_feature
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<223> Accession number cg43919529

<400> 3746
tcagcctcct gagtagctgg gattacaggg gcacaccacc acaccggct a 51

<210> 3747
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3748 is other entry)

<221> misc_feature
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cccggctaatt ttttttgttat ttttttttta gtagagacag ggtttcgcca t 51

<210> 3748
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<220>
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<222> (0)...(0)
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<400> 3748
cccggttaatt tttttgtat ttttttttag tagagacagg gtttcgcat 50

<210> 3749
<211> 51
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<400> 3749
ccggctaatt tttttgtatt ttttttttag tagagacagg gtttcgcat g 51

<210> 3750
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<210> 3751
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<223> 1 of 2 allelic variants (3752 is other entry)

<221> misc_feature
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<223> Accession number cg43919529

<400> 3751
cggttaattt ttttgatatt ttttttagt agagacaggg ttcgccatg t 51

<210> 3752
<211> 50
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (3751 is other entry)

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<221> misc_feature
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<223> Accession number cg43919529

<400> 3752
cggttaattt ttttgatatt ttttttagta gagacagggg ttcgccatgt 50

<210> 3753
<211> 51
<212> DNA
<213> Homo sapiens

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<221> misc_feature
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<223> Accession number cg43919529

<400> 3753
tttgatattt ttttttagta gagacagggg ttcgccatgt tggccaggct g 51

<210> 3754
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (3753 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43919529

<400> 3754

tttgtatattt ttttttagta gagacggggt ttcgccatgt tggccaggct g

51

<210> 3755
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (3756 is other entry)

<221> misc_feature
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<223> Accession number cg43919529

<400> 3755
tttttttagt agagacaggg ttcgccatg ttggccaggc tggctctgaa c

51

<210> 3756
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (3755 is other entry)

<221> misc_feature
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<223> Accession number cg43919529

<400> 3756
tttttttagt agagacaggg ttcgctcatg ttggccaggc tggctctgaa c

51

<210> 3757
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (3758 is other entry)

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<223> Accession number cg43919529

<400> 3757
ttcgcctatgt tggccaggct ggtcttgaac tcctgacctc aggtgatcca c

51

<210> 3758
<211> 51
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<213> Homo sapiens

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<221> misc_feature
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<223> Accession number cg43919529

<400> 3758
ttcgccatgt tggccaggct ggtctcgac tctgacctc agtgatcca c 51

<210> 3759
<211> 51
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<223> 1 of 2 allelic variants (3760 is other entry)

<221> misc_feature
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<223> Accession number cg43919655

<400> 3759
cttttgccgc tttgttccac cattgctttg attaaaaatct ggatcttttt c 51

<210> 3760
<211> 51
<212> DNA
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<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3759 is other entry)

<221> misc_feature
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<223> Accession number cg43919655

<400> 3760
cttttgccgc tttgttccac cattgatcttg attaaaaatct ggatcttttt c 51

<210> 3761
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (3762 is other entry)

<221> misc_feature
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<223> Accession number cg43919705

<400> 3761
ataaaactgaa ggacagggat ggtttctttc tttcttcttt ttttctttcc a

51

<210> 3762
<211> 51
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<213> Homo sapiens

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<223> 2 of 2 allelic variants (3761 is other entry)

<221> misc_feature
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<223> Accession number cg43919705

<400> 3762
ataaaactgaa ggacagggat ggtttatttc tttcttcttt ttttctttcc a

51

<210> 3763
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (3764 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43919707

<400> 3763
ctcttctgat tagtaagaaa aaaaaaatga tagggcctgg agaattcaag g

51

<210> 3764
<211> 50
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (3763 is other entry)

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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)

<223> Accession number cg43919707

<400> 3764

ctcttctgat tagtaagaaa aaaaaatgat agggcctgga gaattcaagg

50

<210> 3765

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (3766 is other entry)

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<222> (0)...(0)

<223> Accession number cg43919707

<400> 3765

tcttctgatt agtaagaaaa aaaaaatgat agggcctgga gaattcaagg a

51

<210> 3766

<211> 50

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (3765 is other entry)

<221> misc_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43919707

<400> 3766

tcttctgatt agtaagaaaa aaaaaatgata gggcctggag aattcaagga

50

<210> 3767

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (3768 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43919798

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ggcgccagggtgtccccaatcctggagccccactggcttcgagggtggggg g 51

<210> 3768
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<212> DNA
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<223> 2 of 2 allelic variants (3767 is other entry)

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<223> Accession number cg43919798

<400> 3768
ggcgccagggtgtccccaatcctggaacccccactggcttcgagggtggggg g 51

<210> 3769
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3770 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43919798

<400> 3769
accctgaaggggagggagga aaatggataa atgagagagg gaggggaacag t 51

<210> 3770
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3769 is other entry)

<221> misc_feature
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<223> Accession number cg43919798

<400> 3770
accctgaaggggagggagga aaatgaataa atgagagagg gaggggaacag t 51

<210> 3771
<211> 51
<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (3772 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43919880

<400> 3771

actctggcaa atataaatac atgcagagaa gtttctgaca gtttaaattt g

51

<210> 3772

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (3771 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43919880

<400> 3772

actctggcaa atataaatac atgcacagaa gtttctgaca gtttaaattt g

51

<210> 3773

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (3774 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43919880

<400> 3773

ttaaaaatac acaacagtg aactacggtg aacatgttat gggtttgtcc c

51

<210> 3774

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (3773 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43919880

<400> 3774
ttaaaaatac acatacgtga aactatggtg aacatgttat gggtttgtcc c 51

<210> 3775
<211> 51
<212> DNA
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<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3776 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43920332

<400> 3775
agtgactatc atcttctgaa tttcaagacc catatatcc gacagtttca g 51

<210> 3776
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3775 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43920332

<400> 3776
agtgactatc atcttctgaa tttcaggacc catatatcc gacagtttca g 51

<210> 3777
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3778 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43920449

<400> 3777

aagtactttca tttcaacaca gaagaaatga acaggtgagg gatgcctctc a

51

<210> 3778

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (3777 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43920449

<400> 3778

aagtactttca tttcaacaca gaagagatga acaggtgagg gatgcctctc a

51

<210> 3779

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (3780 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43920465

<400> 3779

aatattttgt tccagaaaca tacagcctta tcagctaatt cataaaaagag c

51

<210> 3780

<211> 51

<212> DNA

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<222> (26)...(0)

<223> 2 of 2 allelic variants (3779 is other entry)

<221> misc_feature

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<223> Accession number cg43920465

<400> 3780

aatattttgt tccagaaaca tacagtctta tcagctaatt cataaaaagag c

51

<210> 3781

<211> 51

<212> DNA

<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (3782 is other entry)

<221> misc_feature
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<223> Accession number cg43920465

<400> 3781
ttatcagcta attcataaaa gagctatddd acaaaggtag atctggataa t 51

<210> 3782
<211> 50
<212> DNA
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<223> 2 of 2 allelic variants (3781 is other entry)

<221> misc_feature
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<221> misc_feature
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<223> Accession number cg43920465

<400> 3782
ttatcagcta attcataaaa gagctdddta caaaggtaga tctggataat 50

<210> 3783
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<212> DNA
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<223> 1 of 2 allelic variants (3784 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43920465

<400> 3783
cataaaagag ctatdddta aaggtagatc tggataatta gaacaataaa g 51

<210> 3784
<211> 51
<212> DNA
<213> Homo sapiens

<220>

<221> misc_feature
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<223> 2 of 2 allelic variants (3783 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43920465

<400> 3784
cataaaagag ctattttaca aaggtgcatc tggataatta gaacaataaa'g 51

<210> 3785
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3786 is other entry)

<221> misc_feature
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<223> Accession number cg43920465

<400> 3785
acaaagggtac atctggataa ttagaacaat aaagtctttt aggcatttca a 51

<210> 3786
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3785 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43920465

<400> 3786
acaaagggtac atctggataa ttagagcaat aaagtctttt aggcatttca a 51

<210> 3787
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3788 is other entry)

<221> misc_feature
<222> (0)...(0)

<223> Accession number cg43920465

<400> 3787

agtaaaaata catgattatt aataaagttt ttttaaagat agttccagat a

51

<210> 3788

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (3787 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43920465

<400> 3788

agtaaaaata catgattatt aataaggttt ttttaaagat agttccagat a

51

<210> 3789

<211> 50

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (3790 is other entry)

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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43920465

<400> 3789

aaaatacatg attattaata aagttttttt aaagatagtt ccagatattt

50

<210> 3790

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (3789 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43920465

<400> 3790
aaaatacatg attattaata aagttctttt taaagatagt tccagatatt t 51

<210> 3791
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3792 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43920465

<400> 3791
agttttttta aagatagttc cagatatattt ttaaaagcaa tttctgttaa a 51

<210> 3792
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3791 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43920465

<400> 3792
agttttttta aagatagttc cagatttttt ttaaaagcaa tttctgttaa a 51

<210> 3793
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3794 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43920465

<400> 3793
aacctgcagt cacctccagg acatgcggct ctaactttta tctgagtgt t 51

<210> 3794
<211> 51
<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (3793 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43920465

<400> 3794

aacctgcagt cacctccagg acatgaggct ctaactttta tctgagtgc t

51

<210> 3795

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (3796 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43920465

<400> 3795

cctttaagct tatattaat tggaaatctt attttctatt ttcccagacc c

51

<210> 3796

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (3795 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43920465

<400> 3796

cctttaagct tatattaat tggaaatctt attttctatt ttcccagacc c

51

<210> 3797

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (3798 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43920465

<400> 3797
ttcccagacc ccagaaaaca gaaagttttt agatgaccaa tattttgttc c 51

<210> 3798
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3797 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43920465

<400> 3798
ttcccagacc ccagaaaaca gaaagtttta gatgaccaat attttgttcc 50

<210> 3799
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (3800 is other entry)

<221> misc_feature
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<223> Accession number cg43920465

<400> 3799
cagaccccg aaaacagaaa gtttttagat gaccaatatt ttgttccaga a 51

<210> 3800
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (3799 is other entry)

<221> misc_feature

<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
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<223> Accession number cg43920465

<400> 3800
cagaccccag aaaacagaaa gtttttagatg accaatatatt tgttccagaa 50

<210> 3801
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3802 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43920498

<400> 3801
agagccaggc catctacctg gagtcaaagg acaaccagaa actgagctgc g 51

<210> 3802
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3801 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43920498

<400> 3802
agagccaggc catctacctg gagtctaagg acaaccagaa actgagctgc g 51

<210> 3803
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3804 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43920498

<400> 3803
gcaccaagat gaggatctac ctgggccagc ttcagcgcg gctcttcgtg a 51

<210> 3804
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3803 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43920498

<400> 3804
gcaccaagat gaggatctac ctgggtcagc ttcagcgcg gctcttcgtg a 51

<210> 3805
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3806 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43920546

<400> 3805
catcacaatg aaatcctaga aaaaacaaaa aacaaaaaac cctcaaagga a 51

<210> 3806
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3805 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43920546

<400> 3806

catcacaaatg aaatcctaga aaaaaaaaaa acaaaaaaac ctcaaaggaa

50

<210> 3807

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (3808 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43920546

<400> 3807

atgaaatcct agaaaaaaca aaaaacaaaa aaccctcaa ggaaaaaaca g

51

<210> 3808

<211> 50

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (3807 is other entry)

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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43920546

<400> 3808

atgaaatcct agaaaaaaca aaaaaaaaaa accctcaaag gaaaaaacag

50

<210> 3809

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (3810 is other entry)

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<222> (0)...(0)

<223> Accession number cg43920616

<400> 3809

ggtgttccag ccctaaggct catatgacat taacagacaa gacacttttc a

51

<210> 3810
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3809 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43920616

<400> 3810
gggtgttcag ccctaaggct catataacat taacagacaa gacacttttc a 51

<210> 3811
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3812 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43920738

<400> 3811
actgcagccg gtcagggatc tccccagca acagctccac cacgatgaga a 51

<210> 3812
<211> 50
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (3811 is other entry)

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<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43920738

<400> 3812
actgcagccg gtcagggatc tccccagcaa cagctccacc acgatgagaa 50

<210> 3813
<211> 50

<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (3814 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43920883

<400> 3813
taaatttcac ccatttttta aaaaagagct aaaagttact caatagcaca

50

<210> 3814
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (3813 is other entry)

<221> misc_feature
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<223> Accession number cg43920883

<400> 3814
taaatttcac ccatttttta aaaaaagagc taaaagttac tcaatagcac a

51

<210> 3815
<211> 51
<212> DNA
<213> Homo sapiens

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<222> (26)...(0)
<223> 1 of 2 allelic variants (3816 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43920919

<400> 3815
ggtttaaatt cccatatgca actattccca tatgtactat gtacaagtga t

51

<210> 3816
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (3815 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43920919

<400> 3816
ggtttaaatt cccatatgca actatcccca tatgtactat gtacaagtga t 51

<210> 3817
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (3818 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43920959

<400> 3817
gcaatgagct atgatcatgc cactgcactc cagcctgggc cacagagtga g 51

<210> 3818
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3817 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43920959

<400> 3818
gcaatgagct atgatcatgc cactgtactc cagcctgggc cacagagtga g 51

<210> 3819
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3820 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43921044

<400> 3819
agcttccaaa ccagcgccat ttcaaggaca tcgacacagc agccaagttc 50

<210> 3820
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3819 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43921044

<400> 3820
agcttccaaa ccagcgccat ttcaagggac atcgacacag cagccaagtt c 51

<210> 3821
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3822 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43921050

<400> 3821
acttaaagat gaaacagtta agccaatttt tttttttgaa gaatgtagat c 51

<210> 3822
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3821 is other entry)

<221> misc_feature
<222> (0)...(0)

<223> Accession number cg43921050

<400> 3822

acttaaagat gaaacagtta agccattttt tttttttgaa gaatgtagat c

51

<210> 3823

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (3824 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43921103

<400> 3823

tgtttattcc atgatcagta cagaccaa at gcatattcac cgtatgaaag t

51

<210> 3824

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (3823 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43921103

<400> 3824

tgtttattcc atgatcagta cagacaaa at gcatattcac cgtatgaaag t

51

<210> 3825

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (3826 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43921103

<400> 3825

agtttgagcca aactgagggc accagcgtagc tgggtgtagag tgggttctca t

51

<210> 3826

<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3825 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43921103

<400> 3826
agtttgccca acactgaggc accaggtcgt ggtgtagagt gggttctcat 50

<210> 3827
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3828 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43921103

<400> 3827
gggagtctct gccttagtct gtggcgcccc cagggcccggt tcccacctc a 51

<210> 3828
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3827 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43921103

<400> 3828
gggagtctct gccttagtct gtggcccccc agggcccggt tcccacctca 50

<210> 3829
<211> 51
<212> DNA
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<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3830 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43921332

<400> 3829
taaagtgctg tttagattta gtagagtccc atatttactt actgctacct a 51

<210> 3830
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3829 is other entry)

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<222> (0)...(0)
<223> Accession number cg43921332

<400> 3830
taaagtgctg tttagattta gtagattccc atatttactt actgctacct a 51

<210> 3831
<211> 48
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3832 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43921332

<400> 3831
cctgagtatt aactagtgga cgtaggaaaa aaaaattccc tacctagg 48

<210> 3832
<211> 48
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3831 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43921332

<400> 3832
cctgagtatt aactagtga cgtagaaaaa aaaaattccc tacctagg 48

<210> 3833
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3834 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43921594

<400> 3833
cccgcgccc tctcgctctc gcagcaacaa gggaagagcc ggaggaaaga g 51

<210> 3834
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3833 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43921594

<400> 3834
cccgcgccc tctcgctctc gcagcgacaa gggaagagcc ggaggaaaga g 51

<210> 3835
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3836 is other entry)

<221> misc_feature

<222> (0)...(0)
<223> Accession number cg43921594

<400> 3835
ccgccctctc gctctcgcag caacaaggga agagccggag gaaagaggcg t 51

<210> 3836
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3835 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43921594

<400> 3836
ccgccctctc gctctcgcag caacagggga agagccggag gaaagaggcg t 51

<210> 3837
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3838 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43921594

<400> 3837
cgctctcgca gcaacaaggg aagagccgga ggaaagaggc gtccacgccg c 51

<210> 3838
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3837 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43921594

<400> 3838
cgctctcgca gcaacaaggg aagagacgga ggaaagaggc gtccacgccg c 51

<210> 3839
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3840 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43921596

<400> 3839
tggggtcagc tcgttactca actccagttg acatttggag tataggcacc a 51

<210> 3840
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3839 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43921596

<400> 3840
tggggtcagc tcgttactca actccggttg acatttggag tataggcacc a 51

<210> 3841
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3842 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43921645

<400> 3841
cccaagaact gttgccagag atggaggaaa ggggaagagg cctggaagga c 51

<210> 3842
<211> 51
<212> DNA
<213> Homo sapiens

<220>

<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3841 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43921645

<400> 3842
cccaagaact gttgccagag atggaagaaa ggggaagagg cctggaagga c 51

<210> 3843
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3844 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43921651

<400> 3843
aaggaaatta cactatatgt tcaaaaaatg taataatgct ttagaaaaat g 51

<210> 3844
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3843 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43921651

<400> 3844
aaggaaatta cactatatgt tcaaagaatg taataatgct ttagaaaaat g 51

<210> 3845
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3846 is other entry)

<221> misc_feature
<222> (0)...(0)

<223> Accession number cg43921722

<400> 3845

ttccctccct tggcaaagag acatgatgca cacatgactg gaagggactc a

51

<210> 3846

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (3845 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43921722

<400> 3846

ttccctccct tggcaaagag acatggtgca cacatgactg gaagggactc a

51

<210> 3847

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (3848 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43922038

<400> 3847

tcatacacac aatgctacca atggactaaa accagaattc cctgctctgt a

51

<210> 3848

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (3847 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43922038

<400> 3848

tcatacacac aatgctacca atggattaaa accagaattc cctgctctgt a

51

<210> 3849

<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3850 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43922038

<400> 3849
tccccttgta agggttttaa aaaaaacccc aagggtattt aaagcaaaca g 51

<210> 3850
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3849 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43922038

<400> 3850
tccccttgta agggttttaa aaaaacccca aggggtattta aagcaaacag 50

<210> 3851
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3852 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43922038

<400> 3851
aaaaccccaa ggggtatttaa agcaaacagc agaaaccaga agcttctgac c 51

<210> 3852
<211> 50
<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (3851 is other entry)

<221> misc_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43922038

<400> 3852

aaaaccccaa gggatatttaa agcaacagca gaaaccagaa gcttctgacc

50

<210> 3853

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (3854 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43922074

<400> 3853

gggtggaagg gcactcggga gtggccgctg ccaacagcaa cagactgccc a

51

<210> 3854

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (3853 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43922074

<400> 3854

gggtggaagg gcactcggga gtggctgctg ccaacagcaa cagactgccc a

51

<210> 3855

<211> 51

<212> DNA

<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3856 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43922313

<400> 3855
tggttttagaa gatggcttga gctcaacaga ttgtccatgg aaatgcagaa a 51

<210> 3856
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3855 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43922313

<400> 3856
tggttttagaa gatggcttga gctcagcaga ttgtccatgg aaatgcagaa a 51

<210> 3857
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3858 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43922333

<400> 3857
ggagcagtc agtttcacgg gaggaaggca gagctccttg gcgatatctg t 51

<210> 3858
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3857 is other entry)

<221> misc_feature

<222> (0)...(0)
<223> Accession number cg43922333

<400> 3858
ggagcagtg agtttcacgg gaggaggga gagctccttg gcgatatctg t 51

<210> 3859
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3860 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43922353

<400> 3859
aatggcaagt aaaacaaagt aaggcttttt tttctcctt tccccctttt t 51

<210> 3860
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3859 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43922353

<400> 3860
aatggcaagt aaaacaaagt aaggcttttt tttctcctt tccccctttt 50

<210> 3861
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3862 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43922353

<400> 3861
cccaatgtat ttactggaaa aaaaaagaaa aaaatgcctt tactaatttc t 51

<210> 3862
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3861 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43922353

<400> 3862
cccaatgtat ttactggaaa aaaaagaaaa aaatgccttt actaatttct 50

<210> 3863
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3864 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43922409

<400> 3863
aaacaaaaaa caaaaacccc ccaatgaaca aaacaaaaac cctcaaaaca a 51

<210> 3864
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3863 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43922409

<400> 3864

aaacaaaaaa caaaaacccc ccaataaaca aaaacaaaac cctcaaaaca a

51

<210> 3865

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (3866 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43923026

<400> 3865

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51

<210> 3866

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<222> (0)...(0)

<223> Accession number cg43923026

<400> 3866

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51

<210> 3867

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (3868 is other entry)

<221> misc_feature

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<223> Accession number cg43923299

<400> 3867

ctgggtggac ctaaggttcc ttcccgcccc attctggcga cacttggagc c

51

<210> 3868

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (3867 is other entry)

<221> misc_feature
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<223> Accession number cg43923299

<400> 3868
ctgggtggac ctaaggttcc ttcccacccc attctggcga cacttggagc c 51

<210> 3869
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (3870 is other entry)

<221> misc_feature
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<223> Accession number cg43923357

<400> 3869
cccaccaca gtaaaaagac aaatttctaaa aattaaaaaa aagcgcataa t 51

<210> 3870
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (3869 is other entry)

<221> misc_feature
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<223> Accession number cg43923357

<400> 3870
cccaccaca gtaaaaagac aaatttttaaa aattaaaaaa aagcgcataa t 51

<210> 3871
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (3872 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43923357

<400> 3871
ccctcccca ttttgctttt taaacttttt tttttttaag ttttgatttt t 51

<210> 3872
<211> 50
<212> DNA
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<400> 3872
ccctcccca ttttgctttt taaacttttt ttttttaagt ttttgatttt 50

<210> 3873
<211> 51
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<223> Accession number cg43923357

<400> 3873
tttgcttttt aaactttttt ttttttaagt ttttgatttt tttttaatcc t 51

<210> 3874
<211> 50
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<223> Accession number cg43923357

<400> 3874

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50

<210> 3875

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (3876 is other entry)

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<223> Accession number cg43923357

<400> 3875

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51

<210> 3876

<211> 50

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (3875 is other entry)

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<223> Nucleotide deleted between bases 25 and 26

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<223> Accession number cg43923357

<400> 3876

tttttttaag ttttgatttt tttttaatcc tgaaaagtag acagtaaaac

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<210> 3877

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<213> Homo sapiens

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<223> 1 of 2 allelic variants (3878 is other entry)

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<223> Accession number cg43923648

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gaaaggccaa agaaacaaaa aaaaaacctt ttcattaagc atttcatctt c 51

<210> 3878
<211> 50
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (3877 is other entry)

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<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43923648

<400> 3878
gaaaggccaa agaaacaaaa aaaaaccttt tcattaagca tttcatcttc 50

<210> 3879
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<213> Homo sapiens

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<223> 1 of 2 allelic variants (3880 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43923681

<400> 3879
ccaaatgcag accagtgcac ctctgtgtag ttcccgacta gtcacctggt a 51

<210> 3880
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<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (3879 is other entry)

<221> misc_feature
<222> (0)...(0)

<223> Accession number cg43923681

<400> 3880

ccaaatgcag accagtgcac ctctgcgtag ttcccgacta gtcacctggt a 51

<210> 3881

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (3882 is other entry)

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<222> (0)...(0)

<223> Accession number cg43923691

<400> 3881

agtaaaagaa gctagctaca tgatatatac ttgggttaac catatattgt g 51

<210> 3882

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (3881 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43923691

<400> 3882

agtaaaagaa gctagctaca tgatacatatc ttgggttaac catatattgt g 51

<210> 3883

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (3884 is other entry)

<221> misc_feature

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<223> Accession number cg43923691

<400> 3883

acagtttgat gttaaagtat ttgacagttt tctcaaaagc caacagtttt g 51

<210> 3884

<211> 51
<212> DNA
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3883 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43923691

<400> 3884
acagtttgat gttaaagtat ttgaccgttt tctcaaaagc caacagtttt g

51

<210> 3885
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (3886 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43923801

<400> 3885
gttcatagac tccttctttt ggagggtttt ctaatttgca ccatggtacc a

51

<210> 3886
<211> 51
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<223> 2 of 2 allelic variants (3885 is other entry)

<221> misc_feature
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<223> Accession number cg43923801

<400> 3886
gttcatagac tccttctttt ggagggtttt ctaatttgca ccatggtacc a

51

<210> 3887
<211> 51
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<222> (26)...(0)
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<221> misc_feature
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<223> Accession number cg43923884

<400> 3887
gccattagg gcgttgaagg cgtgctgggg ctgctgctgc tggtggtgat g 51

<210> 3888
<211> 51
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<223> 2 of 2 allelic variants (3887 is other entry)

<221> misc_feature
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<223> Accession number cg43923884

<400> 3888
gccattagg gcgttgaagg cgtgcagggg ctgctgctgc tggtggtgat g 51

<210> 3889
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (3890 is other entry)

<221> misc_feature
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<223> Accession number cg43923910

<400> 3889
gtttttagc atctcaaac catctgcact gaagcttctc ttcgagagtc t 51

<210> 3890
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (3889 is other entry)

<221> misc_feature
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<223> Accession number cg43923910

<400> 3890
gttttgtagc atctcaaadc catctacact gaagcttctc ttcgagagtc t 51

<210> 3891
<211> 51
<212> DNA
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3892 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43924053

<400> 3891
ctttcggagc ccaactgtgga catggtgggg gccagcctgt gctgctaaac a 51

<210> 3892
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3891 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43924053

<400> 3892
ctttcggagc ccaactgtgga catggggggg gccagcctgt gctgctaaac a 51

<210> 3893
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3894 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43924063

<400> 3893
tgaaaattag tgactgggta aggtgtgcca ctgtacatat catcattttc t 51

<210> 3894
<211> 51

<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3893 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43924063

<400> 3894
tgaaaattag tgactgggta aggtgcgcca ctgtacatat catcattttc t

51

<210> 3895
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3896 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43924180

<400> 3895
catactgctg ctgcagcagc ggggtgcgaca cgcgctccac tgcgggggaa g

51

<210> 3896
<211> 50
<212> DNA
<213> Homo sapiens

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<223> Accession number cg43924180

<400> 3896
catactgctg ctgcagcagc ggggtggacac gcgctccacc tgcgggggaag

50

<210> 3897
<211> 51
<212> DNA
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<221> misc_feature
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<223> Accession number cg43924188

<400> 3897
aatcacattt taatactttt ttttttggga ctctctcaac tgttgtttgc t 51

<210> 3898
<211> 50
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (3897 is other entry)

<221> misc_feature
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<221> misc_feature
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<223> Accession number cg43924188

<400> 3898
aatcacattt taatactttt ttttttggac tctctcaact gttgtttgc 50

<210> 3899
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (3900 is other entry)

<221> misc_feature
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<223> Accession number cg43924212

<400> 3899
ttaattttga atattaacaa tagcaaaaga aaaacaaact caaaaatgac c 51

<210> 3900
<211> 51
<212> DNA
<213> Homo sapiens

<220>

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<223> 2 of 2 allelic variants (3899 is other entry)

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<223> Accession number cg43924212

<400> 3900
ttaattttga atattaacaa tagcagaaga aaaacaaact caaaaatgac c 51

<210> 3901
<211> 51
<212> DNA
<213> Homo sapiens

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<222> (26)...(0)
<223> 1 of 2 allelic variants (3902 is other entry)

<221> misc_feature
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<223> Accession number cg43924289

<400> 3901
ttacatcttt atttaaattt tttttaaca ttttatgttt acaggcttcc t 51

<210> 3902
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<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3901 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
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<223> Accession number cg43924289

<400> 3902
ttacatcttt atttaaattt tttttaacat cttatgttta caggcttcc t 50

<210> 3903
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (3904 is other entry)

<221> misc_feature

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<223> Accession number cg43924289

<400> 3903

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51

<210> 3904

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (3903 is other entry)

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<223> Accession number cg43924289

<400> 3904

caagacaaca tttattaact gttaggacac ttgctttatg tttgtgtgta c

51

<210> 3905

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (3906 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43924289

<400> 3905

taaaggtgct gcagttaaaa aaaaaacaac cttttctttc aatatggcat g

51

<210> 3906

<211> 50

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (3905 is other entry)

<221> misc_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43924289

<400> 3906
taaaggtgct gcagttaaaa aaaaacaacc ttttctttca atatggcatg 50

<210> 3907
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3908 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43924384

<400> 3907
gactcaatct cgtcacggca gtaacggttg caggtatttt cgtcatgtag g 51

<210> 3908
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3907 is other entry)

<221> misc_feature
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<223> Accession number cg43924384

<400> 3908
gactcaatct cgtcacggca gtaacagttg caggtatttt cgtcatgtag g 51

<210> 3909
<211> 51
<212> DNA
<213> Homo sapiens

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<222> (26)...(0)
<223> 1 of 2 allelic variants (3910 is other entry)

<221> misc_feature
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<223> Accession number cg43924384

<400> 3909
cttcttacac tccacacatt ctttcttaaa ggtgcaggca tctgggcagg t 51

<210> 3910
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3909 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43924384

<400> 3910
cttcttacac tccacacatt ctttcctaaa ggtgcaggca tctgggcagg t 51

<210> 3911
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (3912 is other entry)

<221> misc_feature
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<223> Accession number cg43924384

<400> 3911
cacttgccgc ggccgctgca cagcagccca ttgctggaca tgcaggtgtc a 51

<210> 3912
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (3911 is other entry)

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<223> Accession number cg43924384

<400> 3912
cacttgccgc ggccgctgca cagcaaccca ttgctggaca tgcaggtgtc a 51

<210> 3913
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<212> DNA
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<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3914 is other entry)

<221> misc_feature
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<223> Accession number cg43924511

<400> 3913
gaccgttggt gttggcatct tctggaaaaa gaagcaaagg aatgggttacc c 51

<210> 3914
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (3913 is other entry)

<221> misc_feature
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<223> Accession number cg43924511

<400> 3914
gaccgttggt gttggcatct tctggcaaaa gaagcaaagg aatgggttacc c 51

<210> 3915
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3916 is other entry)

<221> misc_feature
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<223> Accession number cg43924511

<400> 3915
tgtcatgtgg ctacctgtaa cttgaagggtg gctacaaaga tgactgtgga c 51

<210> 3916
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3915 is other entry)

<221> misc_feature

<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
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<223> Accession number cg43924511

<400> 3916
tgtcatgtgg ctacctgtaa cttgaggtgg ctacaaagat gactgtggac 50

<210> 3917
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3918 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43924620

<400> 3917
aactaggaaa aaagggttttt gttgggttttt ttttttttaa atcatagtag 50

<210> 3918
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3917 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43924620

<400> 3918
aactaggaaa aaagggttttt gttgggttttt ttttttttta aatcatagta g 51

<210> 3919
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3920 is other entry)

<221> misc_feature
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<223> Accession number cg43924620

<400> 3919
aaagggttttt gttgggttttt ttttttttaa atcatagtag tactagagtc a 51

<210> 3920
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<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (3919 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
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<223> Accession number cg43924620

<400> 3920
aaagggttttt gttgggttttt tttttttaaa tcatagtagt actagagtca 50

<210> 3921
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<212> DNA
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T A B L E 1

Seq ID	CuraGen sequence ID	Base pos. of SNP	Polymorphic sequence	Base before	Base after	Amino acid before	Amino acid after	Type of change	Protein classifica tion of CuraGen gene	Name of protein identified following a BLASTX analysis of the CuraGen sequence	Similarity (pValue) following a BLASTX analysis
1-2	cg42918213	1280	GCTACTCAGGAG GCTGAGGCAGG AG A/G ATCGCTT GAACCCAGGAG GCGGAGG	A	G			SILENT- NONCODI NG	amyloid	Human Gene Similar to SWISSNEW- ID:P10997 ISLET AMYLOID POLYPEPTIDE PRECURSOR (DIABETES-ASSOCIATED PEPTIDE) (DAP) (AMYLIN) (INSULINOMA AMYLOID PEPTIDE) - HOMO SAPIENS (HUMAN), 89 aa. pcis:SWISSPROT- ID:P10997 ISLET AMYLOID POLYPEPTIDE PRECURSOR (DIABETES-ASSOCIATED PEPTIDE) (DAP) (AMYLIN) (INSULINOMA AMYLOID PEPTIDE) - HOMO SAPIENS (HUMAN), 89 aa.	2.8E-42
3-4	cg42918213	1293	CTGAGGCAGGA GAATCGCTTGAA CC C/T AGGAGG CGGAGGTTGCA GTGAGCCG	C	T			SILENT- NONCODI NG	amyloid	Human Gene Similar to SWISSNEW- ID:P10997 ISLET AMYLOID POLYPEPTIDE PRECURSOR (DIABETES-ASSOCIATED PEPTIDE) (DAP) (AMYLIN) (INSULINOMA AMYLOID PEPTIDE) - HOMO SAPIENS (HUMAN), 89 aa. pcis:SWISSPROT- ID:P10997 ISLET AMYLOID POLYPEPTIDE PRECURSOR (DIABETES-ASSOCIATED PEPTIDE) (DAP) (AMYLIN) (INSULINOMA AMYLOID PEPTIDE) - HOMO SAPIENS (HUMAN), 89 aa.	2.80E-42

5-6	cg42918213	1301	GGAGAATCGCTT GAACCCAGGAG GC[G/A]GAGGTT GCAGTGAGCCG AGATTGCA	G	A			SILENT- NONCODI NG	amyloid	Human Gene Similar to SWISSNEW- ID:P10997 ISLET AMYLOID POLYPEPTIDE PRECURSOR (DIABETES-ASSOCIATED PEPTIDE) (DAP) (AMYLIN) (INSULINOMA AMYLOID PEPTIDE) - HOMO SAPIENS (HUMAN), 89 aa. pcis:SWISSPROT- ID:P10997 ISLET AMYLOID POLYPEPTIDE PRECURSOR (DIABETES-ASSOCIATED PEPTIDE) (DAP) (AMYLIN) (INSULINOMA AMYLOID PEPTIDE) - HOMO SAPIENS (HUMAN), 89 aa.	2.80E-42
7-8	cg42918213	1326	GGAGGTTGCAGT GAGCCGAGATTG C[A/G]CCACTGC ACTCCAGCCTGG GCGACA	A	G			SILENT- NONCODI NG	amyloid	Human Gene Similar to SWISSNEW- ID:P10997 ISLET AMYLOID POLYPEPTIDE PRECURSOR (DIABETES-ASSOCIATED PEPTIDE) (DAP) (AMYLIN) (INSULINOMA AMYLOID PEPTIDE) - HOMO SAPIENS (HUMAN), 89 aa. pcis:SWISSPROT- ID:P10997 ISLET AMYLOID POLYPEPTIDE PRECURSOR (DIABETES-ASSOCIATED PEPTIDE) (DAP) (AMYLIN) (INSULINOMA AMYLOID PEPTIDE) - HOMO SAPIENS (HUMAN), 89 aa.	2.80E-42

9-10	cg42918213	1355	CTGCACTCCAGC CTGGGCGACAG AGT/CJGAGACTC TGCTCAAAAAA AAGAAA	T	C			SILENT- NONCODI NG	amyloid	Human Gene Similar to SWISSNEW- ID:P10997 ISLET AMYLOID POLYPEPTIDE PRECURSOR (DIABETES-ASSOCIATED PEPTIDE) (DAP) (AMYLIN) (INSULINOMA AMYLOID PEPTIDE) - HOMO SAPIENS (HUMAN), 89 aa. pcis:SWISSPROT- ID:P10997 ISLET AMYLOID POLYPEPTIDE PRECURSOR (DIABETES-ASSOCIATED PEPTIDE) (DAP) (AMYLIN) (INSULINOMA AMYLOID PEPTIDE) - HOMO SAPIENS (HUMAN), 89 aa.	2.80E-42
11-12	cg42918213	1356	TGCACTCCAGCC TGGGCGACAGA GT[G/A]GACTCT GTCTCAAAAAA AGAAAA	G	A			SILENT- NONCODI NG	amyloid	Human Gene Similar to SWISSNEW- ID:P10997 ISLET AMYLOID POLYPEPTIDE PRECURSOR (DIABETES-ASSOCIATED PEPTIDE) (DAP) (AMYLIN) (INSULINOMA AMYLOID PEPTIDE) - HOMO SAPIENS (HUMAN), 89 aa. pcis:SWISSPROT- ID:P10997 ISLET AMYLOID POLYPEPTIDE PRECURSOR (DIABETES-ASSOCIATED PEPTIDE) (DAP) (AMYLIN) (INSULINOMA AMYLOID PEPTIDE) - HOMO SAPIENS (HUMAN), 89 aa.	2.80E-42
13-14	cg44029012	502	GGAACGGCCAC ATCCTCGGGCAG AG[C/gap]CAAGA GTCACCGTCTTT CGTGGGCC	C	-			SILENT- NONCODI NG	angiopoi etin	Human Gene Similar to SPTREMBL- ID:O08538 ANGIOPOIETIN-1 - MUS MUSCULUS (MOUSE), 498 aa.	2.50E-44
15-16	cg43093113	1265	GAGCGCCGAAAT TTCCCTGCCCAT T[A/G]TCAGAGC GGTGGTAACAAG GATGAA	A	G			SILENT- NONCODI NG	angiopoi etin	Human Gene Similar to SPTREMBL- ID:O08538 ANGIOPOIETIN-1 - MUS MUSCULUS (MOUSE), 498 aa.	5.60E-44

17-18	cg43987690	286	AAGAGAAAGACT TAGGGGAAAAA A[G/gap]ACCAGA GAGCATCCCAAG GACAGAC	G	-			SILENT- NONCODI NG	collagen	Human Gene Similar to SWISSNEW- ID:P29400 COLLAGEN ALPHA 5(IV) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1685 aa. pcds:SWISSPROT- ID:P29400 COLLAGEN ALPHA 5(IV) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1685 aa.	3.00E-35
19-20	cg29479549	78	GCGTAAGATCGA TTGTGGATCAGC ATT/CJCGATGCTG GTCCCCCGGAC GTGTGT	T	C			SILENT- NONCODI NG	dehydrog enase	Human Gene Similar to SWISSPROT- ID:P30234 ALANINE DEHYDROGENASE (EC 1.4.1.1) (40 KD ANTIGEN) - MYCOBACTERIUM TUBERCULOSIS, 373 aa.	2.00E-39
21-22	cg29479549	94	GGATCAGCATCG ATGCTGGTCCCC C[C/gap]GACGTT GTGTGGCGG GTGTGTGT	C	-			SILENT- NONCODI NG	dehydrog enase	Human Gene Similar to SWISSPROT- ID:P30234 ALANINE DEHYDROGENASE (EC 1.4.1.1) (40 KD ANTIGEN) - MYCOBACTERIUM TUBERCULOSIS, 373 aa.	2.00E-39
23-24	cg43299481	185	CAGAGCTGGGA GCGGGTCCCG AAG[G/gap]CGGG TCAGTCCCGGTC AGGGTGGGC	G	-			SILENT- NONCODI NG	dehydrog enase	Human Gene Similar to SPTREMBL- ID:Q44020 4-HYDROXYBUTYRATE DEHYDROGENASE (GBD), ORF 2 AND 4-10 GENES, COMPLETE CDS, AND ORF3 AND 11, 3' END - ALCALIGENES EUTROPHUS, 173 aa.	9.30E-33
25-26	cg43299481	807	CACCTTCACAGC CACCCCTTTCCG C[A/G]TCTCCTTC CATGTCGGGATC TTCTT	A	G			SILENT- NONCODI NG	dehydrog enase	Human Gene Similar to SPTREMBL- ID:Q44020 4-HYDROXYBUTYRATE DEHYDROGENASE (GBD), ORF 2 AND 4-10 GENES, COMPLETE CDS, AND ORF3 AND 11, 3' END - ALCALIGENES EUTROPHUS, 173 aa.	9.30E-33
27-28	cg43941958	1453	GGAATGCCACA TTCCATAGCGCA G[C/T]TTCGACTG CACACTGCTATG AATTC	C	T			SILENT- NONCODI NG	dehydrog enase	Human Gene Similar to SPTREMBL- ID:Q21233 SIMILAR TO NADH DEHYDROGENASE - CAENORHABDITIS ELEGANS, 436 aa.	3.30E-31
29-30	cg27363108	285	GTGCAATGCAGT TCACACATACCT GIG/AJAATTATG CAGATGTTTCTAG TATAG	G	A			SILENT- NONCODI NG	dna_rna_ bind	Human Gene Similar to SPTREMBL- ID:Q15933 DNA-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 94 aa (fragment).	2.00E-32

31-32	cg44921820	5304	TGGGTAAAGG GATTCTGGGAGT TG[A/G]GAGCTCT GCCAGGGTGAG ATGTTTC	A	G				SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to SPTREMBL- ID:P97484 CELL-SURFACE GLYCOPROTEIN P91 - MUS MUSCULUS (MOUSE), 841 aa.	2.2E-47
33-34	cg43988115	475	ATGCTAGATGT GGTGCTGTGGT GC[T/A]GTGCATT TATCTAAAATATT TTAAA	T	A				SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to TREMBLNEW- ID:G260066 MACROPHAGE MANNOSSE RECEPTOR, MRC1=GROUP I HEPATIC GLYCOPROTEIN RECEPTOR HOMOLOG (CARBOHYDRATE- RECOGNITION DOMAINS 1-8) - HOMO SAPIENS, 88 aa.	8.3E-45
35-36	cg27783345	790	TCATGAGACATG CACAGCCCGCAT C[C/A]CATGCTCC GGCGGGGATC GGGAGC	C	A				SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to SWISSPROT- ID:P21997 SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185) - VOLVOX CARTERI, 485 aa.	7.6E-38
37-38	cg27783345	815	CCATGCTCCGG GCGGGGATCGG GAG[C/gap]GTCC GCTCACCGACGT GGGGCGCCG	C	.				SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to SWISSPROT- ID:P21997 SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185) - VOLVOX CARTERI, 485 aa.	7.6E-38
39-40	cg43256113	1305	CCTCAGCTTCCT GAGTAGCTGGG ACT[C/J]ACAGGTA TATACCACTGCA CCCAGC	T	C				SILENT- NONCODI NG	homeobo x	Human Gene Similar to SWISSPROT- ID:P53564 CCAAT DISPLACEMENT PROTEIN (CDP) (HOMEBOX PROTEIN CUX) - MUS MUSCULUS (MOUSE), 1332 aa.	5.3E-37
41-42	cg43256113	1311	CTTCCTGAGTAG CTGGGACTACAG GT[C/J]ATATACCA CTGCACCCAGCT GTAAG	T	C				SILENT- NONCODI NG	homeobo x	Human Gene Similar to SWISSPROT- ID:P53564 CCAAT DISPLACEMENT PROTEIN (CDP) (HOMEBOX PROTEIN CUX) - MUS MUSCULUS (MOUSE), 1332 aa.	5.3E-37

43-44	cg44023415	66	GGACCGGAGAT GGCGCCGCCAG CGG[C/G]GCGGG CGGCGGCGGCG GCCTCGGAC	C	G			SILENT- NONCODI NG	kinase	Human Gene Similar to TREMBLNEW- ID:G2760825 PROTEIN KINASE C- BINDING PROTEIN BETA 15 - RATTUS NORVEGICUS (RAT), 498 aa.	4.10E-32
45-46	cg44023415	68	ACCGGAGATGG CGCCGCCAGCG GCG[C/G]GCGCG GCGGCGGCGGC CTCGGACTT	C	G			SILENT- NONCODI NG	kinase	Human Gene Similar to TREMBLNEW- ID:G2760825 PROTEIN KINASE C- BINDING PROTEIN BETA 15 - RATTUS NORVEGICUS (RAT), 498 aa.	4.10E-32
47-48	cg44929662	4534	AGCACTTTGGGA GGCCGAGGCAG GC[G/A]GATCAC CGGAGGTCAGG AGATCGAG	G	A			SILENT- NONCODI NG	nuclease	Human Gene Similar to SWISSNEW- ID:P11369 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - MUS MUSCULUS (MOUSE), 1300 aa.lpcis:SWISSPROT-ID:P11369 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - MUS MUSCULUS (MOUSE), 1300 aa.	1.20E-36
49-50	cg44929662	4557	GCGGATCACCG GAGGTCAGGAG ATC[G/A]AGACCA TCCTGGCCAACA TGGTGAA	G	A			SILENT- NONCODI NG	nuclease	Human Gene Similar to SWISSNEW- ID:P11369 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - MUS MUSCULUS (MOUSE), 1300 aa.lpcis:SWISSPROT-ID:P11369 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - MUS MUSCULUS (MOUSE), 1300 aa.	1.20E-36

51-52	cg29691725	171	GGGCATGGGCC GGCCCTCTGTG GCG[T/G]CCCGG AACTTTTCGCAA TCGGCCCC	T	G			SILENT- NONCODI NG	nuclease	Human Gene Similar to TREMBLNEW- ID:E1264534 ENDONUCLEASE III - MYCOBACTERIUM TUBERCULOSIS, 226 aa.	1.90E-34
53-54	cg29691725	307	AGGCGGCCATC ACCGCGCCGAA AAC[G/C]TTCATC CCCCTCATCGAC GCGGCTC	G	C			SILENT- NONCODI NG	nuclease	Human Gene Similar to TREMBLNEW- ID:E1264534 ENDONUCLEASE III - MYCOBACTERIUM TUBERCULOSIS, 226 aa.	1.90E-34
55-56	cg43985676	2515	AATAAAGTATC ATGAAAAAACCT A[T/gap]TTTTTTT TCCACTGTCCTT CCACTA	T	-			SILENT- NONCODI NG	oncogen e	Human Gene Similar to SWISSPROT- ID:P55258 RAS-RELATED PROTEIN RAB-8 (ONCOGENE C-MEL) - MUS MUSCULUS (MOUSE), 206 aa.	2.30E-39
57-58	cg44010970	342	TCCTGGTCCCGA AGATGGGGGGG GG[G/gap]GCGAG AGTGAGATCTTC ACAGTTTC	G	-			SILENT- NONCODI NG	oncogen e	Human Gene Similar to SWISSNEW- ID:Q00653 NUCLEAR FACTOR NF- KAPPA-B P100 SUBUNIT (H2TF1) (ONCOGENE LYT-10) (LYT10) [CONTAINS: NUCLEAR FACTOR NF- KAPPA-B P52 SUBUNIT] - HOMO SAPIENS (HUMAN), 898 aa. pds:SWISSPROT-ID:Q00653 NUCLEAR FACTOR NF-KAPPA-B P100 SUBUNIT (CONTAINS: NUCLEAR FACTOR NF- KAPPA-B P52 SUBUNIT) (H2TF1) (ONCOGENE LYT-10) (LYT10) - HOMO SAPIENS (HUMAN), 898 aa.	5.70E-34

59-60	cg44010970	343	CCTGGTCCCGAA GATGGGGGGG GG[G/gap]GCAGA GTGAGATCTTCA CAGTTTCC				SILENT- NONCODING	oncogene	Human Gene Similar to SWISSNEW- ID:Q00653 NUCLEAR FACTOR NF- KAPPA-B P100 SUBUNIT (H2TF1) (ONCOGENE LYT-10) (LYT10) [CONTAINS: NUCLEAR FACTOR NF- KAPPA-B P52 SUBUNIT] - HOMO SAPIENS (HUMAN), 898 aa.lpcds:SWISSPROT-ID:Q00653 NUCLEAR FACTOR NF-KAPPA-B P100 SUBUNIT (CONTAINS: NUCLEAR FACTOR NF- KAPPA-B P52 SUBUNIT) (H2TF1) (ONCOGENE LYT-10) (LYT10) - HOMO SAPIENS (HUMAN), 898 aa.	5.70E-34
61-62	cg44010970	344	CTGGTCCCGAAG ATGGGGGGGG GG[G/gap]CAGAG TGAGATCTTCAC AGTTTCCA				SILENT- NONCODING	oncogene	Human Gene Similar to SWISSNEW- ID:Q00653 NUCLEAR FACTOR NF- KAPPA-B P100 SUBUNIT (H2TF1) (ONCOGENE LYT-10) (LYT10) [CONTAINS: NUCLEAR FACTOR NF- KAPPA-B P52 SUBUNIT] - HOMO SAPIENS (HUMAN), 898 aa.lpcds:SWISSPROT-ID:Q00653 NUCLEAR FACTOR NF-KAPPA-B P100 SUBUNIT (CONTAINS: NUCLEAR FACTOR NF- KAPPA-B P52 SUBUNIT) (H2TF1) (ONCOGENE LYT-10) (LYT10) - HOMO SAPIENS (HUMAN), 898 aa.	5.70E-34
63-64	cg42718385	268	TATTTGTAGAG ATGGGGTTTTGC C[G/T]GTATATCC AGGCTGGTTTG AACTC	T			SILENT- NONCODING	phosphorylase	Human Gene Similar to SWISSPROT- ID:P19971 THYMIDINE PHOSPHORYLASE PRECURSOR (EC 2.4.2.4) (TDRPASE) (PLATELET- DERIVED ENDOTHELIAL CELL GROWTH FACTOR) (PD-ECGF) (GLIOSTATIN) - HOMO SAPIENS (HUMAN), 482 aa.	5.30E-32

65-66	cg43263821	476	AAACAGCACTCC TCTTCTAAAAAG ATT/CJACACAGGC CGCCTTTCTCGG CAGTG	T	C				SILENT- NONCODI NG	protease	Human Gene Similar to SWISSNEW- ID:P31795 POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE (EC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4)] - RADIATION MURINE LEUKEMIA VIRUS (STRAIN KAPLAN), 581 aa (fragment). pcls:SWISSPROT- ID:P31795 POL POLYPROTEIN (PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE (EC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4)) - RADIATION MURINE LEUKEMIA VIRUS (STRAIN KAPLAN), 581 aa (fragment).	2.5E-34
67-68	cg41644093	1754	AAGACCAGCCTG GGCAACATGGG GA[AG/JACCCCAT CTCTACAAAAAT ACAAAA	A	G				SILENT- NONCODI NG	tm7	Human Gene Similar to SWISSPROT- ID:O00254 PROTEINASE ACTIVATED RECEPTOR 3 PRECURSOR (PAR-3) (THROMBIN RECEPTOR 2) - HOMO SAPIENS (HUMAN), 374 aa.	1.5E-47
69-70	cg43284479	2048	CAGTCGCATTTA AAAAAATCAACA A[C/GJAATGATGA TAATGAAAAAAT CTGAA	C	G				SILENT- NONCODI NG	tm7	Human Gene Similar to SWISSPROT- ID:P49683 PROBABLE G PROTEIN- COUPLED RECEPTOR GPR10 - HOMO SAPIENS (HUMAN), 369 aa.	5.30E-37
71-72	cg43284479	2778	GGAATGAAGAGA GAAAGCAGCTCC C[C/TJAACITTCAA AACCATTTTGGT ACCTG	C	T				SILENT- NONCODI NG	tm7	Human Gene Similar to SWISSPROT- ID:P49683 PROBABLE G PROTEIN- COUPLED RECEPTOR GPR10 - HOMO SAPIENS (HUMAN), 369 aa.	5.30E-37
73-74	cg43971784	446	GCACAGCTAGGT AAAGGGGGAAAA A[A/gap]TCAGAT CTCAAGACAGAC TCITTTGA	A	-				SILENT- NONCODI NG	Infrecept or	Human Gene Similar to SPTREMBL- ID:O00463 TNF RECEPTOR ASSOCIATED FACTOR 5 - HOMO SAPIENS (HUMAN), 538 aa (fragment).	1.50E-44

75-76	cg43971784	585	ACCGGCACCAA GGCATGCTGCGC CTA/GJCCCAAGA AGGAGACAGG CCCTGGG	A	G				SILENT- NONCODI NG	Infrecept or	Human Gene Similar to SPTREMBL- ID:O00463 TNF RECEPTOR ASSOCIATED FACTOR 5 - HOMO SAPIENS (HUMAN), 538 aa (fragment).	1.50E-44
77-78	cg42719787	645	TCAGGCTCCCTA GAATTACCCCAA A/GJGTCAACAC TATCTCAGTGCC AGCCC	G	T				SILENT- NONCODI NG	transferase	Human Gene Similar to SWISSPROT- ID:P04905 GLUTATHIONE S- TRANSFERASE YB1 (EC 2.5.1.18) (CHAIN 3) (CLASS-MU) - RATTUS NORVEGICUS (RAT), 217 aa.	2.40E-36
79-80	cg44938005	669	CCCCAGAGGGA GGCCATCTCAGT CTG/CJTCCACTG TGGTTTCAGCTG GTGCAT	G	C				SILENT- NONCODI NG	tubulin	Human Gene Similar to SWISSPROT- ID:P09653 TUBULIN BETA-5 CHAIN (CLASS-V) - GALLUS GALLUS (CHICKEN), 446 aa.	3.40E-44
81-82	cg43983675	4048	AGCCTCATTATT AAAAGTGAAGGC A/T/gapJTTTTTTT TTCTGCTGCCTT TCCCAA	T	-				SILENT- NONCODI NG	ubiquitin	Human Gene Similar to SPTREMBL- ID:P78355 E6-ASSOCIATED PROTEIN E6-AP/UBIQUITIN-PROTEIN LIGASE - HOMO SAPIENS (HUMAN), 852 aa.	2.9E-47
83-84	cg43983675	4057	ATTAAAACTGAA GGCATTTTTTTTT T/gapJCTGCTGC CTTCCCAAAGT GGTTAG	T	-				SILENT- NONCODI NG	ubiquitin	Human Gene Similar to SPTREMBL- ID:P78355 E6-ASSOCIATED PROTEIN E6-AP/UBIQUITIN-PROTEIN LIGASE - HOMO SAPIENS (HUMAN), 852 aa.	2.9E-47
85-86	cg43983675	4137	TTTATTGTGCTT TTTAAGCCATTI C/TJCCCAAATGG GACTAGCATGCT TGTT	C	T				SILENT- NONCODI NG	ubiquitin	Human Gene Similar to SPTREMBL- ID:P78355 E6-ASSOCIATED PROTEIN E6-AP/UBIQUITIN-PROTEIN LIGASE - HOMO SAPIENS (HUMAN), 852 aa.	2.9E-47
87-88	cg43330621	885	CCAGGGAATACT GAGAGCACTAAC TJA/GJTGCACTAA CCTAGATTTTCA TTTCG	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O65386 F12F1.20 PROTEIN - ARABIDOPSIS THALIANA (MOUSE- EAR CRESS), 255 aa.	3.2E-49

89-90	cg44021993	1234	CCATGAAGCTAA TGATGCAGCAG A[A/G]CTGGTAAA ACAGCCTCCGGA TGTC	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O16216 F17A9.2 PROTEIN - CAENORHABDITIS ELEGANS, 254 aa.	8.9E-48
91-92	cg44021993	1335	ATTCTTGCCCT GTGGAAGATCA G[C/A]CTGTGAGT TTTTCTTTGATTT AAAT	C	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O16216 F17A9.2 PROTEIN - CAENORHABDITIS ELEGANS, 254 aa.	8.9E-48
93-94	cg44012362	449	GCAAGACACATG AAAAAAAAAAAA A[A/gap]ACTCAA GTCCCAACTGAA TCTTTAC	A	-				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O70323 FLIGHTLESS-I ASSOCIATED PROTEIN 1 (LRR DOMAIN) (FLI-LRR ASSOCIATED PROTEIN-1) - MUS MUSCULUS (MOUSE), 628 aa.	4.2E-47
95-96	cg44012362	450	CAAGACACATGA AAAAAAAAAAAA A[A/gap]CTCAAG TCCCAACTGAAT CTTTACT	A	-				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O70323 FLIGHTLESS-I ASSOCIATED PROTEIN 1 (LRR DOMAIN) (FLI-LRR ASSOCIATED PROTEIN-1) - MUS MUSCULUS (MOUSE), 628 aa.	4.2E-47
97-98	cg43309765	166	CCTCAGACTTTC ACAGATGCGGG CG[G/gap]CATCG CCAGCTGGTTCA CCTGCTGC	G	-				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O01927 C13C4.5 - CAENORHABDITIS ELEGANS, 531 aa.	2.3E-46
99-100	cg43309765	173	CTTTCACAGATG CGGGCGGCATC GC[C/gap]AGCTG GTTACACCTGCTG CTCAGCCC	C	-				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O01927 C13C4.5 - CAENORHABDITIS ELEGANS, 531 aa.	2.3E-46
101- 102	cg43294390	860	TTCTTGCTTTCTT TTTTTTTTTTTTT /gap]CAATAAACA AAGTTTTCTCGC TTCT	T	-				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O45407 F26H11.3B - CAENORHABDITIS ELEGANS, 510 aa.	1.6E-45

103-104	cg39570730	39	CGATGAAGAGGA CGATGGCCCGTG GC[C]gap]GGGGC CTGCTGCGCTG GGACAGCTT	C	-			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O45074 F53H1.3 PROTEIN - CAENORHABDITIS ELEGANS, 417 aa.	1.5E-44
105-106	cg44011255	455	ATCATGGCAGCT GCGTTGTTCAAA A[G/A]GAAGTTTC ATTGAGCTTCAT CTTG	G	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD42876 NY-REN-45 ANTIGEN - HOMO SAPIENS (HUMAN), 815 aa.	3.1E-43
107-108	cg43926454	427	GGATGGGAGGA GGGATAGCAGG GGA[G/A]GCCCC CTGAACGGTCAA ATCTGGGT	G	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P51116 FRAGILE X MENTAL RETARDATION SYNDROME RELATED PROTEIN 2 - Homo sapiens (Human), 673 aa.	1.2E-41
109-110	cg4393127	556	CTGTAAACTTGC CCTTGACTGGGG A[G/A]ATACCATC TCCTTAAAAATA CTCIT	G	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q20445 F46B6.3 - CAENORHABDITIS ELEGANS, 491 aa.	3.7E-39
111-112	cg4393127	680	CTTCATGCACCA GTGCAGCGTGAA C[A/T]GGGGCTTT ATTGATGGGGCT TGGA	A	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q20445 F46B6.3 - CAENORHABDITIS ELEGANS, 491 aa.	3.7E-39
113-114	cg43054187	279	GTTGGAGACTCA GCATTGGGGTTC G[ga]G]CCCTGC CCGTAGCACAGC CAAGCCC	-	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P07902 GALACTOSE-1- PHOSPHATE URIDYLTRANSFERASE (EC 2.7.7.10) - Homo sapiens (Human), 379 aa.	4.4E-39
115-116	cg44911042	1288	TCCCTTAGGTC CCTCCCAACA C[G/A]TGGGAATT ATGGGAGTACAA TTCAA	G	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB51754 DJ153G14.2 (PUTATIVE NOVEL PROTEIN SIMILAR TO WORM F55A11.1 AND T04F3.4) - HOMO SAPIENS (HUMAN), 89 aa (fragment).	1.6E-38

117-118	cg39722830	792	AATGGCCGGCC ATTATCAGTTCTT C(C)gapJTGCGGT TCGGGTTTTGGC AGTAACA	C	-				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14120 DBP-5 NUCLEAR PROTEIN - HOMO SAPIENS (HUMAN), 1179 aa.	2.9E-37
119-120	cg39570416	299	CCTGCGGAGCTA AAACAGATTCT G(A)GJGGACTTAT CCTCCAGTCCT CAGCT	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75150 KIAA0661 PROTEIN - HOMO SAPIENS (HUMAN), 1001 aa.	8.4E-36
121-122	cg43281110	942	CGTTGTGACCTT GTCTCAAAAAA A(gap)AJCTAAAAA ATAAAGCAGTTG CATCTT	-	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39194 !!! ALU SUBFAMILY SQ WARNING ENTRY !!!! - Homo sapiens (Human), 593 aa.	3.6E-35
123-124	cg43933032	1186	GTATTATTGCAC AGATCTGAAGAT C(gap)AJAAAAA AGCTCAAGGAAA TACAGAT	-	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P34661 HYPOTHETICAL 9.8 KD PROTEIN ZK652.3 IN CHROMOSOME III - Caenorhabditis elegans, 94 aa.	4E-35
125-126	cg43965698	942	CCCAAAGCTTCC AGAGTGTGGCT G(A)GJTCAGGGA GTGTACAGTCAG TCTGG	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q20487 SIMILAR TO RAT TRG GENE PRODUCT. NCBI GI: 1109880 - CAENORHABDITIS ELEGANS, 2018 aa.	7.2E-35
127-128	cg42719279	183	AAGCCTTTACAT TCCCACTGGCAG A(A)GJAATGAGTA CCCAAGTGCC CCAAG	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB44431 XENOBIOTIC/MEDIUM- CHAIN FATTY ACID:COA LIGASE FORM XL-III PRECURSOR - BOS TAURUS (BOVINE), 576 aa.	3.2E-34
129-130	cg43142151	973	ACTCAAAGGCCA AACCTTCTTGCC C(A)GJAGGTGAA AGTGGTCAGGCT TCGATT	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:O95847 MITOCHONDRIAL UNCOUPLING PROTEIN 4 (UCP 4) - Homo sapiens (Human), 323 aa.	3.5E-34

131-132	cg42538578	369	TTCAGGAACTGG GGAGAGGCTGG CT[C/T]CTTTGGA GGCTGAGCTGA CAGAGGC	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q09753 BETA-DEFENSIN 1 PRECURSOR (HBD-1) (DEFENSIN, BETA 1) - Homo sapiens (Human), 68 aa	7.4E-34
133-134	cg42481111	341	GCAAGACTCCAC CTCAAAAAA A[A/gap]CCACAA AAAAACACAAAA GGATTCT	A	-				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39195 !!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!! - Homo sapiens (Human), 591 aa.	9.8E-34
135-136	cg39710199	632	CAAACTCGACTC AGCGGTGAGCT CT[A/G]GCACAGT TCCATGAGTTGC GACCCCT	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB50754 PUTATIVE INTEGRAL MEMBRANE TRANSPORT PROTEIN - STREPTOMYCES COELICOLOR, 269 aa.	1.20E-33
137-138	cg38821538	378	AAAAAATAATAAT AATAATAATAAT gap[A]TTTTTTAA AAAGAGGTGTTT TTGAG	-	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39195 !!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!! - Homo sapiens (Human), 591 aa.	3.50E-33
139-140	cg38821538	378	AAAAAATAATAAT AATAATAATAAT gap[A]TTTTTTAA AAAGAGGTGTTT TTGAG	-	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39195 !!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!! - Homo sapiens (Human), 591 aa.	3.50E-33
141-142	cg38821538	384	TAATAATAATAAT AATAATTTTTTTTg ap/TJAAAAAGAG GTGTTTTTGAGG TCTTA	-	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39195 !!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!! - Homo sapiens (Human), 591 aa.	3.50E-33
143-144	cg40038435	643	TGATCCTGCAGA GGAGCCAAAAA A[A/gap]TCTTAG GTATAGAACTAA TACAATT	A	-				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39195 !!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!! - Homo sapiens (Human), 591 aa.	2.40E-32
145-146	cg43963046	374	GGCCCTGTGGTT AGCATCCCCCAG A[C/gap]CCATAT CAGCCACTAGCA TTTTAA	C	-				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P49675 STEROIDGENIC ACUTE REGULATORY PROTEIN PRECURSOR Homo sapiens (Human), 285 aa.	4.70E-32

147-148	cg43963046	376	CCCTGTGGTTAG CATCCCCCACAC C(C/gap)ATATCA GCCACTAGCATT TTAAAGA	C	-				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P49675 STEROIDOGENIC ACUTE REGULATORY PROTEIN PRECURSOR Homo sapiens (Human), 285 aa.	4.70E-32
149-150	cg43979733	185	AAATGTATGAT CAAGTCCCAGAA A(A/gap)CTTTGC CTTCCCAAGGAA TGTGTTT	A	-				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD28083 WS BETA- TRANSDUCIN REPEATS PROTEIN - HOMO SAPIENS (HUMAN), 426 aa.	9.70E-32
151-152	cg43979733	583	CCAAAATCACA TTCCTCTCTCT C(T/gap)CCTCTC CTCTCTACCACT CTCCTCA	T	-				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD28083 WS BETA- TRANSDUCIN REPEATS PROTEIN - HOMO SAPIENS (HUMAN), 426 aa.	9.70E-32
153-154	cg43979733	777	CAGTAAGAAAC CAGGAGACTCCT T(C/A)TGAAAGGC TTCCACCTGGGA GGAAA	C	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD28083 WS BETA- TRANSDUCIN REPEATS PROTEIN - HOMO SAPIENS (HUMAN), 426 aa.	9.70E-32
155-156	cg42286566	235	CTGGGATTACAG GCATGAGCCACC G(T/G)GCCTGGC CAGAAAATTGTA AACACA	T	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39194 !!! ALU SUBFAMILY SQ WARNING ENTRY !!!! - Homo sapiens (Human), 593 aa.	1.40E-31
157-158	cg42286566	239	GATTACAGGCAT GAGCCACCGTG CC(T/C)GGCCAG AAATTGTAAAC ACACACA	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39194 !!! ALU SUBFAMILY SQ WARNING ENTRY !!!! - Homo sapiens (Human), 593 aa.	1.40E-31
159-160	cg42286566	260	TGCCTGGCCAGA AAATTGTAAACA C(A/G)CACAACT CTCAAGTGGCCT AATTC	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39194 !!! ALU SUBFAMILY SQ WARNING ENTRY !!!! - Homo sapiens (Human), 593 aa.	1.40E-31

161-162	cg42286566	312	CTCTCACCAAAAC CAATCACAATAC A[G/A]ATAAAAGA GAATAACTTGTG TTTAT	G	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39194 !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!! - Homo sapiens (Human), 593 aa.	1.40E-31
163-164	cg42286566	330	CAATACAGATAAA AAGAGAACTTGT T[G/A]TGTTCATT TTTGTACAAACA AAAAA	G	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39194 !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!! - Homo sapiens (Human), 593 aa.	1.40E-31
165-166	cg42286566	332	ATACAGATAAAA GAGATAAAGAG T[G/A]TTCATTTT TGTACAAACAAA AAAGA	G	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39194 !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!! - Homo sapiens (Human), 593 aa.	1.40E-31
167-168	cg42286566	335	CAGATAAAGAG AATAACTTGTGT T[G/A]ATTTTGT ACAAACAAAAA GATAT	C	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39194 !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!! - Homo sapiens (Human), 593 aa.	1.40E-31
169-170	cg42286566	357	TTTATTTTGTAC AAACAAAAAAGA[gap/C]TATAAATT GTGAATGATGCA TGATT	-	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39194 !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!! - Homo sapiens (Human), 593 aa.	1.40E-31
171-172	cg42468290	614	CAAAACCAACAA CCCAACAAAAA A[A/gap]TCCCTC ACTTTGTTTTCT GTTTAT	A	-			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39194 !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!! - Homo sapiens (Human), 593 aa.	2.00E-31
173-174	cg44010179	347	TCCCATAGGTAG CAGTGCCTGTGG G[C/gap]AGGTGG AAGGTGCCCGTC CCCTAG	C	-			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39194 !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!! - Homo sapiens (Human), 593 aa.	2.50E-31
175-176	cg42927851	883	CCTAGGAGGAA GACAAAGCTTGAA GG[A/G]CGACCC TTAATAAGAGC TTCTAGG	A	G			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39194 !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!! - Homo sapiens (Human), 593 aa.	4.20E-31

177-178	cg43998776	1064	TGATGGGGAGTT TTAGAGGAGCAA T(A/C)AAAAACTT CCTTCITTTGTGC TTGTG	A	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:004091 ENDOMEMBRANE PROTEIN EMP70 PRECURSOR ISOLOG- ARABIDOPSIS THALIANA (MOUSE- EAR CRESS), 589 aa.	4.30E-31
179-180	cg43923142	462	CCCACTCGCGTT CTGAGCCCCGA GA(G/C)CGTCCC GCACGCTCAGTT TGGCTGA	G	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P52276 PROBABLE ASPARAGINYL-TRNA SYNTHETASE (EC 6.1.1.22) (ASPARAGINE-TRNA LIGASE) (ASNRS) - Synechocystis sp. (strain PCC 6803), 513 aa.	6.60E-31
181-182	cg10053419	82	GGGGGAGGTAG GCAGTACCCCC CC(T/gap)GCTCC TGTGGGAAATA GGGGCTTA	T	-			SILENT- NONCODI NG			
183-184	cg10333107	179	TGCCCCCTGAGGT CAAGCAGACCCA C(A/C)CCGTCGA CCCGTTGTCGT CGTAAC	A	C			SILENT- NONCODI NG			
185-186	cg10353763	348	TGGCAGGCTTTG TCAGTGTTCAG C(G/A)GGTAAGA AATCTTGACTAG TAGGAA	G	A			SILENT- NONCODI NG			
187-188	cg10854402	94	TTGTGATCTCAA CAACAACATTGA A(A/T)ACAGCAGG AGCACCAGGAC CGATCT	A	T			SILENT- NONCODI NG			
189-190	cg11763542	273	AGGCTGAGGCA GGAGAAATCGCTT GA(G/A)CCTGGG AGGCAGAGGTT GCAGTGAG	G	A			SILENT- NONCODI NG			

191- 192	cg11763542	291	CGCTTGAGCCTG GGAGGCAGAGG TT[G/T]CAGTGAG CCAAGATCATGC CACTGC	G	T				SILENT- NONCODI NG		
193- 194	cg11794373	227	CCGGAATACCTT ATACITTTTCCC C[C/T]TTTTTTT GGGGAAGGAA TGIGTG	C	T				SILENT- NONCODI NG		
195- 196	cg11801777	365	ACCCTATCAACC CATTAAATGGA T[T/A]TTAATGAA TTGATAATAGGG GCTCA	T	A				SILENT- NONCODI NG		
197- 198	cg11801777	413	TCAATCAGCTGA TAAACCCCTAA A[A/G]AAGTTGCG GAAACCCAATTG TTACA	A	G				SILENT- NONCODI NG		
199- 200	cg12991942	97	AGAGTTTATTC CTTTGAGGGCCA C[A/T]GAAGAAAG TAGTCTAGCTCT CTTCA	A	T				SILENT- NONCODI NG		
201- 202	cg13084930	113	TGTTGTGCGTG TGGTCAAGATGC T[G/A]ACTCACGA TCACAGTGGGCT CTTCG	G	A				SILENT- NONCODI NG		
203- 204	cg13086160	106	ACTAAGCACAGG CTCAGCCCCGGT C[G/A]CCATGCG CCCAGGCTCGG TTATCAG	G	A				SILENT- NONCODI NG		
205- 206	cg13502101	34	GCGGGGTTAAC GGGTCAGGAGA CAA[G/A]AAGGT GGTGGTAGTTGG GTCGIAGA	G	A				SILENT- NONCODI NG		

207- 208	cg14203037	126	AGTAACAGAAAT ATAACAAAATTG G[C/A]ATAAACAT TTGGGTATCTGT TAACC	C	A				SILENT- NONCODI NG		
209- 210	cg14203037	132	AGAAATATAACA AAATTGGCATAA A[C/A]ATTTGGGT ATCTGTTAACCA AGAGT	C	A				SILENT- NONCODI NG		
211- 212	cg14203037	151	CATAAACATTG GGTATCTGTTAA C[C/A]AAGAGTGT GAAGATAAGGTA GTTC	C	A				SILENT- NONCODI NG		
213- 214	cg14369904	195	GCGGAACCTCG CGCTTCGCCCG GGG[G/gap]ACAA TCCGAAAGTCCGC GCTATGGAA	G	-				SILENT- NONCODI NG		
215- 216	cg14395282	118	CACCCCTGATGC CGGCCTGGCTG GG[A/G]ATGGGC CCGTCCTGCACC TCGAGCT	A	G				SILENT- NONCODI NG		
217- 218	cg14395282	157	CACCTCGAGCTA GGGCAAGAAGA GG[gap/A]CAGAG CTGGAGGAGTTC CTGTGCCC	-	A				SILENT- NONCODI NG		
219- 220	cg14396111	46	TCAGATATGGAA CTACATGAGATC T[G/gap]TAGCGA ACTGCGGAGGAT CAGACAC	G	-				SILENT- NONCODI NG		

221- 222	cg16311688	129	GTTCTCGGGTGC CGTCGCTGTGC GCT/CJTCGCTGT CGTGACGCTCAC TGGGCG	T	C				SILENT- NONCODI NG		
223- 224	cg16311688	183	GCGTCCAGTCCC ACAGTTCGACCA C/AJTCGGCG GCTCCGTGCCC GCGACCA	A	T				SILENT- NONCODI NG		
225- 226	cg16311688	278	TGTCATTGCGG GTGAGTTTCGG G/CJGCGCGAA GCCGGGGGTTT CACTAGG	C	T				SILENT- NONCODI NG		
227- 228	cg16311688	300	GGCGCGCGGAA GCCGGGGGTTT CAC/T/GJAGGCG TGGGAGCCCGA CACCGAGCG	T	G				SILENT- NONCODI NG		
229- 230	cg16392609	219	TGCTCATTGATC CCTACGACAAGG TT/CJGTCATGGC TCATGACAGGGT GGTCG	T	C				SILENT- NONCODI NG		
231- 232	cg16392609	231	CCTACGACAAGG TTGTCATGGCTC A/T/AJGACAGGGT GGTCGCGGTTT CCACTG	T	A				SILENT- NONCODI NG		
233- 234	cg16392609	237	ACAAGGTTGTCA TGGCTCATGACA G/G/AJGTGGTCG CGGTTCCCACTG AGGGTG	G	A				SILENT- NONCODI NG		

235- 236	cg16697187	68	ATGTGTTTCATTG CCATCGGGTCGA TTC/TCTGCTCAT CACTGGATTCTG TGACG	C	T				SILENT- NONCODI NG			
237- 238	cg16843354	84	AAAAGACTAGTA ACGGCGAAGCC GATCTGAGACA GTTATCTGCCAC GTTGCTG	C	T				SILENT- NONCODI NG			
239- 240	cg16845019	322	CCTCTCTGATAT TTGGGTGGGA AGG/TGGGGTT GGGGTCTCTT TCTTCAA	G	T				SILENT- NONCODI NG			
241- 242	cg17201640	64	CCAGTTCATAT GATCCAAATTTCT A/GA/AAAAACAAA TGCTGAAGTTCA TTGCA	G	A				SILENT- NONCODI NG			
243- 244	cg17872027	153	TGACTTCAAGTG ATCCTCCTGCCT C/GA/GCCTCTCA AAGTCTGGGAT TACAG	G	A				SILENT- NONCODI NG			
245- 246	cg17872027	159	CAAGTGATCCTC CTGCCTCGGCCT CT/C/CAAAAGTGC TGGGATTACAGA TATGA	T	C				SILENT- NONCODI NG			
247- 248	cg17964567	141	GCCCTGTCCACA CTCAGCTCCCAC A/GT/CCTCACCC TGTCACACACAG CACAC	G	T				SILENT- NONCODI NG			
249- 250	cg17964567	176	GTCACACACAGAC ACACACAGCTTA GT/C/GACACAG ATTCTGGAAGCT T	T	C				SILENT- NONCODI NG			

251- 252	cg17964567	88	GCTGAGGCCIG AGCCCATCAAG AC[G/A]AGAACTG ACTGAGCACACC TGGGCA	G	A				SILENT- NONCODI NG		
253- 254	cg19426737	329	CGTTCAGCTCTG CCAATGGGAAGC C[G/A]GAGGCGC CTCCTTCAGCGA GAAGGT	G	A				SILENT- NONCODI NG		
255- 256	cg19540358	15	NGGAGAGACGA CAA[G/C]GGTGA AGGAAAGAATG ACTGATGG	G	C				SILENT- NONCODI NG		
257- 258	cg19636928	64	CTATCAGAGGCG TCCATCACTCCA T[C/T]GTAAGGAG GCAGCTGGTGG CGAGTC	C	T				SILENT- NONCODI NG		
259- 260	cg19650073	166	AGCTTTGGCAGA GGACCCCTCTGCA C[G/A]CTTCCTCT CCTCTAGCCAGA GCTTC	G	A				SILENT- NONCODI NG		
261- 262	cg19847826	131	ACGCCGACCGG ATCGTCGATCCC AT[T/C]ACTCGGG ATCTGCTGGAAT CCCTGG	T	C				SILENT- NONCODI NG		
263- 264	cg19847826	14	ACGCGTCCGCTC C[G/C]GATTTCGT TGACGAGCTGC GCTCAG	G	C				SILENT- NONCODI NG		
265- 266	cg19847826	158	CTCGGGATCTGCT TGGAAATCCCTGG T[T/C]CGCGAAG CCGGCGAGGCT GCGGTGA	T	C				SILENT- NONCODI NG		

267- 268	cg19847826	166	CTGCTGGAATCC CTGGTTGCGAA GIC/TJCGGCGAG GCTGCGGTGATC TTGGGT	C	T				SILENT- NONCODI NG			
269- 270	cg19847826	77	TCACCCATCTGC CCCGACGACCC AGT/CJAAACGTC CCCGGCTGTTCC TCATTG	T	C				SILENT- NONCODI NG			
271- 272	cg19848544	168	ACCGCGACGCG ATTCTGGCCTTC CC/C/TJGTTGAGA CGGTGTATACCG CCGACC	C	T				SILENT- NONCODI NG			
273- 274	cg19848544	181	TCTGGCCTTCCC CGTTGAGACGGT GT/CJATACCGCC GACCGCCCGGT GCAGCG	T	C				SILENT- NONCODI NG			
275- 276	cg19848544	208	TACCGCCGACC GCCCGGTGCAG CG/C/TJTGCC GAAATCGTTGCC GAGTACGA	C	T				SILENT- NONCODI NG			
277- 278	cg19848544	255	ACGAACCGGTTG AAGTCATCATGG G/A/GJC/TCCGG TCGCCCTTAACG GGACTG	A	G				SILENT- NONCODI NG			
279- 280	cg19848544	264	TTGAAGTCATCA TGGGACTTCCGG TIC/TJGCCCTTAA CGGGACTGAGC AGTTGG	C	T				SILENT- NONCODI NG			
281- 282	cg19848544	96	CGGACACGTGTC TGTGCGGTGTGA G/G/AJCTTGCCAT CGACTGGGGAA AGGCAC	G	A				SILENT- NONCODI NG			

283- 284	cg19869623	142	CAGAGTCTGTGA GCGGCCAGGAG GC[C/gap]ACCTG CTCGACTGGCCC GTCCTCTC	C	-				SILENT- NONCODI NG			
285- 286	cg19891431	59	CTTCAGGAGGCC AAGAGGGAGG AT[A/G]GACTAAG GTGAGTTCAAGA CCAGCC	A	G				SILENT- NONCODI NG			
287- 288	cg19891431	99	CAAGACCAGCCT AGGCAATACAGT G[A/G]GACCCCTG CCTCTATAAAA AAAATT	A	G				SILENT- NONCODI NG			
289- 290	cg19906230	122	CAGACTGACAAG CAAGGGATTTT T[C/T]CACTCACC GTCAGTGGGATG GTTCT	C	T				SILENT- NONCODI NG			
291- 292	cg19906230	196	ACACGATTATTT CACAAAAAGAAA C[T/C]TTCTGTGG GACGTGCCTGG GCGACT	T	C				SILENT- NONCODI NG			
293- 294	cg19906230	256	GCCAGCAAAACT GAGAACCTTGT C[G/T]CAAATCCG TACCCTCTCCCA AGGCA	G	T				SILENT- NONCODI NG			
295- 296	cg19906230	263	AAACTGAGAACC TTGTTGCAAAAT C[C/T]GTACCCCTC TCCCAAGGCAGC CTCAG	C	T				SILENT- NONCODI NG			

297- 298	cg20177119	237	CTCAGAACCTGG AGATCAGGTTTT G A G CCGGTGA GCCAGCCCGGG ACCTTCC	A	G				SILENT- NONCODI NG			
299- 300	cg20177119	541	CAGCCGACGTC GCGGCTGACGA CGT[C/gap]CCCC CCAAATCCGTTG GGCGATACC	C	-				SILENT- NONCODI NG			
301- 302	cg20177119	547	ACGTCGGGCT GACGACGTCCC CCC[C/gap]AAAT CCGTTGGCGGAT ACCCGCCTC	C	-				SILENT- NONCODI NG			
303- 304	cg20177119	565	TCCCCCCCCAAAT CCGTTGGCGGAT A C T CCGCCTC GAACCAACCCG GGATTGA	C	T				SILENT- NONCODI NG			
305- 306	cg20177119	580	TTGGGCGATACC CGCCTCGAACCA A C T CCGGGATT GACCCCGGGAG ATCCAA	C	T				SILENT- NONCODI NG			
307- 308	cg20283978	37	AGGAAACACCAG ATTGCCCAGGA A G T ACAGTGG GATGGCTTTGAT ATCTCT	G	T				SILENT- NONCODI NG			
309- 310	cg20287156	76	CGCGGCCCAA TCTGCCGGACGT GA C T GCCGGG ATGTCGCTGGGA CTTATGT	C	T				SILENT- NONCODI NG			

311-312	cg20287300	330	TTGCCGGCCGAT TTCGACTTTATC A[G/A]TCTCTTCC ACGGAGTCGAC GAGAGA	G	A			SILENT- NONCODI NG		
313-314	cg20289946	143	TCCAGGCTGTGA GCGTGCAAGAAC A[G/C]CACGGCG GCGAAAGAGAAC CCGGTA	G	C			SILENT- NONCODI NG		
315-316	cg20289946	153	GAGCGTGCAAG AACAGCACGGC GGC[G/C]AAAGA GAACCCGGTAC GCGGTGCGG	G	C			SILENT- NONCODI NG		
317-318	cg20375502	333	GGATCTGTGGCC ACCTCCTCAAGG G[T/G]TGCCACA CGCACCCAGGTC CTGACTG	T	G			SILENT- NONCODI NG		
319-320	cg20375502	366	CGCACCCAGGTC CTGACTGGGAGT CC[G/A]GCCCCC AGGCTGTGG ATGGCTGG	G	A			SILENT- NONCODI NG		
321-322	cg20436198	144	AAGTTTCTCTCG AGAAGCCTGCG CA[G/gap]CATCT CCGAGAGGGCG CCTGGAGCG	G	-			SILENT- NONCODI NG		
323-324	cg20436198	44	GGGCCCCGGTGG GGTCTGCGGG GAC[G/gap]CGGG CGAGGACGGCG CGGACGAGGC	G	-			SILENT- NONCODI NG		

325- 326	cg20436638	62	CTACCAGGCCG CCGCCCTTCGCC GGA[T/A]CCCGT CCCGACCTTGAG TTGGTTCA	T	A				SILENT- NONCODI NG		
327- 328	cg20436638	70	CCGCCGCCCTTC GCCGGATCCCG TCC[C/A]GACCTT GAGTTGGTTCAG CTGAATT	C	A				SILENT- NONCODI NG		
329- 330	cg20440553	137	TGAGGGTCCCCT CTTCTTCCTCTC C[G/A]TGAGCTG AAATGTTTCCCT TTTCTT	G	A				SILENT- NONCODI NG		
331- 332	cg20442259	288	CGGCCACTCCC CATCGCCTATGA GG[C/gap]GACCA TCATCACCTTCA CCGAACAA	C	-				SILENT- NONCODI NG		
333- 334	cg20452710	68	GGGAGAGAGAG CGGGAGGGGACA CTG[G/A]CCTGG AGAGAGGCGGG AGGGACGCT	G	A				SILENT- NONCODI NG		
335- 336	cg20457127	224	CGAGGAAATGAC CTCCTTCGCGGT A[G/gap]CCGACC AGCGATCCACCG ACGAGAC	G	-				SILENT- NONCODI NG		
337- 338	cg20549295	332	TTAGAGGGGACAA GGAAGAAGCCA GG[A/G]AGCCGC CCCAGGCCCAT GCCATTG	A	G				SILENT- NONCODI NG		

339-340	cg20562029	338	TTGGTCTTTTGA GATGGTTTTTCAG A/C/T/T/T/T/TGCAT TATGGCAACCAA CTGAC	C	T				SILENT- NONCODI NG		
341-342	cg20562607	157	TGAGCTTGTTCA CACCTCTGGCA G/G/A/AAGTTTCAG AAGGGAACACAG AACCA	G	A				SILENT- NONCODI NG		
343-344	cg44921008	213	AAACCCAAAGTGT GGCAAAGGAACT C/A/G/T/TGCTCTC GAAATGCATATA TGTTG	A	G				SILENT- NONCODI NG		
345-346	cg44921017	576	ACATCTGTTTAG CCACAGAAAAGCA T/T/C/JGGGCCATA CTCACTGCAGAA GATAA	T	C				SILENT- NONCODI NG		
347-348	cg44921017	622	GATAAGACTTCC TCAGAATCTTATT [C/T/G/T/TAGTGC ACTCAATTTTACT TCA	C	T				SILENT- NONCODI NG		
349-350	cg44921180	1381	GGATGCGGACAT CGACAAGGCCTT G/C/A/JAGGATCT GCTGGGGCACC TTGAAGC	C	A				SILENT- NONCODI NG		
351-352	cg44921180	1411	TCTGCTGGGGCA CCTTGAAGCGGA C/A/G/JTAGGAGC AGAGCTGAAGCA TTTCAC	A	G				SILENT- NONCODI NG		
353-354	cg44921180	1426	TGAAGCGGACAT AGGAGCAGAGC TG/A/C/JAGCATTT CACTCATCTCTT CTGGGG	A	C				SILENT- NONCODI NG		

355-356	cg44921180	1432	GGACATAGGAG CAGAGCTGAAGC ATTTCJCACTCA TCTCTCTGGGG TAGACG	T	C				SILENT- NONCODI NG		
357-358	cg44921180	1447	GCTGAAGCATT CACTCATCTCTT CTTCJGGGGTAG ACGGGATCAAG GGAATCT	T	C				SILENT- NONCODI NG		
359-360	cg44921180	1453	GCATTTCACTCA TCTCTTCTGGGG TIA/GJGACGGGA TCAAGGGGAATCT TCTCCA	A	G				SILENT- NONCODI NG		
361-362	cg44921180	1465	TCTCTTCTGGGG TAGACGGGATCA AIG/AJGGAATCTT CTCCACGGCGG CAGAGC	G	A				SILENT- NONCODI NG		
363-364	cg44921180	558	TCCTCCCTGGTC TTGCAGCCCAATG G/G/AJCTGCAGT CATACATGGGTC TCTATG	G	A				SILENT- NONCODI NG		
365-366	cg44921801	1693	GCCTGGGCAAC AAGAGTGAAACT CCIA/GJTCCTCAA AAAAAATAA AAAGA	A	G				SILENT- NONCODI NG		
367-368	cg44921847	561	AATAATATGTTAA CATAAACATAAC[A/GJACACACATA TTATTTTCTACC CCT	A	G				SILENT- NONCODI NG		
369-370	cg44921882	77	AAACCTTGAAC CTTCTAGACAGA TIA/CJCCGAGTG GCAATCTGGGT TGTTG	A	C				SILENT- NONCODI NG		

371-372	cg44921882	96	ACAGATACCGAG TGGCAATCTGGG T[AG]TGTTTGGC AATAGCGGAGCA GCACA	A	G				SILENT- NONCODI NG		
373-374	cg44921986	284	CCTGAATGGGGT GGTAGATTTTTT T[gap]CTTAAAAA AATTTTTTGTTT TTTT	T	-				SILENT- NONCODI NG		
375-376	cg44921986	301	ATTTTTTCTTA AAAAATTTTTT[T[gap]GTTTTTTTT AATACTCAGAGG AGAG	T	-				SILENT- NONCODI NG		
377-378	cg44921986	303	TTTTTCTTAA AAAATTTTTTG[T[gap]TTTTTTTAA TACTCAGAGGAG AGGG	T	-				SILENT- NONCODI NG		
379-380	cg44921986	310	CTTAAAAAATTT TTTTGTTTTTTT[[gap]AATACTCAG AGGAGAGGGAC ATAGG	T	-				SILENT- NONCODI NG		
381-382	cg44922032	560	ACGTGGAGACCA TCCTGGGCCTCA CIA/GGGAGCGA CCATGGGAAGC CTCATCT	A	G				SILENT- NONCODI NG		
383-384	cg44922119	354	CAGCCCAGGCC CAGTATGATACC CC[G/A]AAAGCT GGGAAGCCAGG TCTACCTG	G	A				SILENT- NONCODI NG		

385-386	cg44922119	522	AAGCATCGTTTT AAAGCACATGGC C[gap]/TTTTTTTT TTTAATTATTAGT GGTAG	-	T				SILENT- NONCODI NG			
387-388	cg44922119	532	TTTAAAGCACAT GGCCTTTTTTTTT [T/gap]AATTATTA GTGGTAGTAATA TATAG	T	-				SILENT- NONCODI NG			
389-390	cg44922119	621	ATGTGGTGACTG AGGTACAGGAAA CTT/C/ACTAATCT TGCCATCTTGCT TTAAG	T	C				SILENT- NONCODI NG			
391-392	cg44922173	525	TGGCTATAAATT CTCAATTATGAT A[C/T]GAACATTT ATTTACAAATTC TACA	C	T				SILENT- NONCODI NG			
393-394	cg44923068	551	ATAAAACCGGC ACAGCCCGTCTG G[C/G]ATGTTTGA TTATGACTTTGA GATTG	C	G				SILENT- NONCODI NG			
395-396	cg44923491	1249	GTAAGCAGAGGT ACCAAAGAAAGT A[C/T]TGGGAGG TGCAGACTTTGT TAAAG	C	T				SILENT- NONCODI NG			
397-398	cg44923661	536	ATCACTTAGGAC CATCAAAAAAT G[T/C]GTACCTTT CTCCAAACGACA ACTGA	T	C				SILENT- NONCODI NG			
399-400	cg44923666	290	ATTGGTAGCATG GGTTCACCTGGC T[A/G]CAACTGAG CAAAATAGATGC AACTT	A	G				SILENT- NONCODI NG			

401- 402	cg44923675	364	AAGATTTGAAGC AATTGGTGGAGT CIAVGACAGAATG GGAGGTTAGAGA AAGAT	A	G				SILENT- NONCODI NG		
403- 404	cg44923675	484	GAGATTAAGTAC AAAGTGAGGAAG ATTCJGGAAGATG GTTGAATAGTGC TGAAT	T	C				SILENT- NONCODI NG		
405- 406	cg44923758	90	ACTTAAATAACG CCATGTTTAATA CTTAJGACAATTA TTTGCTAACCTT AAGAC	T	A				SILENT- NONCODI NG		
407- 408	cg44923987	1672	CCACTCTTTTGA GACCATTATGAT AIC/TJATGACCA GAGTACAGGCAA AAGGC	C	T				SILENT- NONCODI NG		
409- 410	cg44924189	252	AGGATGCACTGA GTCAGAGCTAAG GIG/AJAGGGTGG ACAAGCGCTGAA CTCTGC	G	A				SILENT- NONCODI NG		
411- 412	cg44924398	464	CTGAGGAGCCA GGAGACAGGGG ACC[G/C]GCCAA GGGTCACCGGC AATCACATC	G	C				SILENT- NONCODI NG		
413- 414	cg44924398	477	AGACAGGGGAC CGGCCAAGGGT CACIC/GJGGCAA TCACATCCTTAA AGCTGCCG	C	G				SILENT- NONCODI NG		

415-416	cg44924398	688	GACAGGGGACA TTCTCTCTCTC AC[G/A]GGTGAG GACAGTTATCCC ACCAGGT	G	A				SILENT- NONCODI NG		
417-418	cg44924574	524	AAGACGAAGTGA TCCAGCCCCAGC TTC/TGGAGAGCT CTCAGGAGAGAA GCCTC	C	T				SILENT- NONCODI NG		
419-420	cg44924623	154	GTGCTGAGATTA CAGGCATGAACC A/C/T/TGCCCTTG GACAAGGCAGG GTTTTA	C	T				SILENT- NONCODI NG		
421-422	cg44924630	210	GCCTTTGGGTGA AGGGTGATTTCT A/C/T/TAGACACA TCTGTGCTTCAG TCATA	C	T				SILENT- NONCODI NG		
423-424	cg44924824	342	GGGAGGCTGG AGAGTCTGGTG GA/T/C/ACCCCTCT CAATAGCCCAT CCAAGG	T	C				SILENT- NONCODI NG		
425-426	cg44924824	369	CCCTCTCAATAG CCCATTCCAAGG T/C/T/ACTTATGA AGCTCATAAGGA ATACC	C	T				SILENT- NONCODI NG		
427-428	cg44924824	381	CCCATTCCAAGG TCACCTATGAAG C/T/A/CATAAGGA ATACCTAGCCAA AATGT	T	A				SILENT- NONCODI NG		
429-430	cg44924824	396	CTTATGAAGCTC ATAAGGAATACC T/A/G/GCCAAAT GTATGAGGAATA TCAAA	A	G				SILENT- NONCODI NG		

431-432	cg44924824	483	GGAATGTGAGCA CCATCTCTGGTC TT/CITCATCACA GACAAACAGGAG CAAAAG	T	C				SILENT- NONCODI NG			
433-434	cg44924961	118	AACCTCCTGGCCT CAAGCTATCCTC C/C/TJGSCCTCAG CCTCCCAAAGTG CTGAGA	C	T				SILENT- NONCODI NG			
435-436	cg44925079	213	CTGGGCTCCCG CTTCATGGCCTC T/G/AJACACCTCCA CACTCCCAACCA CTGAC	G	A				SILENT- NONCODI NG			
437-438	cg44925235	363	TCGTGTTAACT GATGTGGCAGTA A/A/TJCCAAGGGA CTAAGCACATGA TTATT	A	T				SILENT- NONCODI NG			
439-440	cg44925358	3047	CGGAACTCGCTA TATGCACGTGTG T/G/AJTGTCGTA TGTAAGAAAGTG TGCAC	G	A				SILENT- NONCODI NG			
441-442	cg44925402	258	ACAGAAGATGCT AGGTTGCACGC T/G/AJATGAGATC CTGGCTAACACT GCTGC	G	A				SILENT- NONCODI NG			
443-444	cg44925402	517	TTCAGACTTCG AGTTAGACAGAA A/C/TJCCAGGGG GCTGCGGCTCT GGTGGTT	C	T				SILENT- NONCODI NG			
445-446	cg44925406	1476	AAAGAGCCAAGG CGCTGGACCAAGT C/C/TJGACAAACGA TATGTCGCCCGT GTACC	C	T				SILENT- NONCODI NG			

447-448	cg44925534	1216	CTTCTATAACTTTA CTTGCCCACTGCC [T/gap]TTTTTTTT TGATAGAATCTT GCTCT	T	-				SILENT- NONCODI NG			
449-450	cg44925534	1230	TTGCCACTGCCT TTTTTTTTTGATA G/AJAATCTTGCT CTGCGCCAG GGGG	G	A				SILENT- NONCODI NG			
451-452	cg44925849	702	GAATGCCACTTG GATGACAGTTCT C/C/TCTAAGACC CCCTTTTCAGCA TGGT	C	T				SILENT- NONCODI NG			
453-454	cg44925849	877	GCTGGTGCTCTC CTTGGGATACT C/T/C/CACCCCTT GGTTCCTCAGAT GAAAG	T	C				SILENT- NONCODI NG			
455-456	cg44926335	328	CACACACACACA CACACACACACA C(gap/A)CCCTTAC ACGAATGGTAAT GAAATGA	-	A				SILENT- NONCODI NG			
457-458	cg44927187	608	GGCTGGGGGGC TAAGAAGGAGAT CTT/C/JGAGAAAG GATGGACCTGAG CTAAAGA	T	C				SILENT- NONCODI NG			
459-460	cg44927553	417	ACTACAGGCATG CACCACCACACC C/A/G/GCTAATTT TTGTATTTTAGT AGAG	A	G				SILENT- NONCODI NG			

461- 462	cg44927553	437	CACCCAGCTAAT TTTTGTATTTTA GATAGAGACGG GGTTTCATCATG TTGG	G	A			SILENT- NONCODI NG		
463- 464	cg44927553	438	ACCCAGCTAATT TTTGTATTTTAG T/gap/AGAGACG GGGTTTCATCAT GTTGGC	T	-			SILENT- NONCODI NG		
465- 466	cg44927553	468	ACGGGGTTTCAT CATGTTGGCCAG GIC/TJGGTCTCA AACTCCTGACCT CATGA	C	T			SILENT- NONCODI NG		
467- 468	cg44928037	1155	AAAAAGAAAAAG AAAAAGCAAAAA G/A/gap/AAAAAA AAAGGATTGGGT GGGGGGA	A	-			SILENT- NONCODI NG		
469- 470	cg44928037	1164	AAGAAAAAGCAAA AAAGAAAAAA A/A/gap/IGGATTG GGTGGGGGAA GGAGGTGG	A	-			SILENT- NONCODI NG		
471- 472	cg44928037	1450	TAGATTTCAAAG ATGAACCTGGCT CT/C/CCATCACT GAGCCAGACATT CATTG	T	C			SILENT- NONCODI NG		
473- 474	cg44928115	749	CATGGTGACTCA AGCCTGTAATCC C/A/GGCACCTTG GGAGGCCGAGG CGGGCG	A	G			SILENT- NONCODI NG		

475-476	cg44928274	259	TGCAGTGCACAC GTGGTATGCATG TTC/TTCGGCATTG ATCAAGTCCATC TGGGC	C	T				SILENT- NONCODI NG		
477-478	cg44928274	282	GTCCGGCATTGA TCAAGTCCATCT G[G/A]GCTATGG CCATAAGCCCAAC ACCACT	G	A				SILENT- NONCODI NG		
479-480	cg44928274	349	GCAGAGTAAGTC CAAAATCCATGC A[G/A]CAGCGAG CCTGAGTGAGAT CGCCAT	G	A				SILENT- NONCODI NG		
481-482	cg44928274	426	AGACCTCGAAGC TGGCCAAACATGG GT[C]AGCAAGG GGAAGATCATCA GCGGCA	T	C				SILENT- NONCODI NG		
483-484	cg44928274	461	AAGATCATCAGC GGCAGCAGCGG CA[G/gap]CCTGC TGCTTCAGGTT CTCAGGAA	G	-				SILENT- NONCODI NG		
485-486	cg44928329	512	TTAAGAAAGTGA AAAAACAACAAC G[gap/A]AAAAAA AACCCCAAAATCA TGGAGAA	-	A				SILENT- NONCODI NG		
487-488	cg44928356	218	CCCCAACGTGTA CAAGAAATCCAG G[A/G]GGAAAGG CCGTCAAGGTAA AAATG	A	G				SILENT- NONCODI NG		

489-490	cg44928356	221	CAACGTGTACAA GAAATCCAGGAG G/A/GAAGGCCG TCAAGGTAAAA ATGGAA	A	G			SILENT- NONCODI NG			
491-492	cg44928356	253	GTCAGGTAAAA AATGGAATTC C/T/GJCTGTCCA ACGCTGATTGAG TCTGT	T	G			SILENT- NONCODI NG			
493-494	cg44928356	266	ATGGAATTCCT TCTGTTCCAACG C/T/CJGATTGAGT CTGTTGCTTAA AAGAG	T	C			SILENT- NONCODI NG			
495-496	cg44928356	269	GAAATCCCTCT GTCCAACGCTG AT/CJTGAGTCTG TTGCTTAAAG AGCTT	T	C			SILENT- NONCODI NG			
497-498	cg44928356	281	GTCCAACGCTG ATTGAGTCTGTT G/T/CJCTTAAAG AGCTTTAAAGG CCCC	T	C			SILENT- NONCODI NG			
499-500	cg44928356	290	CTGATTGAGTCT GTGTCTTAAA G/A/GJGCTTAAA GGGCCCCCTT CTTTT	A	G			SILENT- NONCODI NG			
501-502	cg44928356	323	AGGGCCCCCTT CTTTCCAGCAC T/A/CJCCACTGCC CATTCCAGTCTT GGGTG	A	C			SILENT- NONCODI NG			
503-504	cg44928665	549	CAAGCCAAACT TGCAACCAAAAA A/A/gapJGGTCAT GGTCACTGTTCG GTGGTCT	A	-			SILENT- NONCODI NG			

505-506	cg44928771	1046	AGCTGGCCAGG CACTTAATTTGG GGJ/GJAGAGA AGGATTTTGAGG TAAACTA	A	G			SILENT- NONCODI NG			
507-508	cg44929331	115	GATGACAGCAAC TATAAAGGAGAG AJ/GJGTTTTCGT TGAAGTACACTG GAAAT	A	G			SILENT- NONCODI NG			
509-510	cg44930314	297	TGGCGGTGTCG GTGGTGACGCA CCC[T/C]GGGG CTGCCGGGGCC ATGAGGTGG	T	C			SILENT- NONCODI NG			
511-512	cg44930892	284	GTGTACATATTC CTTGCAATTTTT [T/gap]AGTTGTT GTCTTAAAAAA AAAAAA	T	.			SILENT- NONCODI NG			
513-514	cg44931317	429	AAAAGTTTAGTA GAGACATGGAAG A[C/T]GTAAAGGG GACCCCAAGCAA GCCTC	C	T			SILENT- NONCODI NG			
515-516	cg44931528	263	TCTACCAGCTGC TCATAGTCCTCA T[C/G]ATAGGTAA CATAGGGAATCT GGAAG	C	G			SILENT- NONCODI NG			
517-518	cg44932156	302	GCGCGGCAGCC CCACAGTCCCG GGG[G/C]GCCTC GTCACAGGCTGT AGGCCGTG	G	C			SILENT- NONCODI NG			

519-520	cg44932430	130	ATGTCACATTAA AAGTGCATCATC G[A/G]CACTCAAT AGAGATTAGGTT TTACC	A	G			SILENT- NONCODI NG			
521-522	cg44932430	191	ATTCTTGGCAGA TGCTGCAGATAA C[G/A]TGGAGAG CATACGAAAGGC ACATGT	G	A			SILENT- NONCODI NG			
523-524	cg44932430	209	AGATAACGTGGA GAGCATACGAAA G[G/A]CACATGTT TGAACCAATAGT GACAT	G	A			SILENT- NONCODI NG			
525-526	cg44932430	212	TAACTGTGGAGAG CATACGAAAGGC A[C/T]ATGTTTGA ACCAATAGTGAC ATACA	C	T			SILENT- NONCODI NG			
527-528	cg44932430	219	GAGAGCATACGA AAGGCACATGTT T[G/T]AACCAATA GTGACATACAGG TGCTA	G	T			SILENT- NONCODI NG			
529-530	cg44932430	228	CGAAAGGCACAT GTTTGAACCAAT A[G/C]TGACATAC AGGTGCTAAGTT CTGCA	G	C			SILENT- NONCODI NG			
531-532	cg44932430	238	ATGTTGAACCA ATAGTGACATAC A[G/A]GTGCTAAG TTCTGCAGTAGG GGAAG	G	A			SILENT- NONCODI NG			
533-534	cg44932430	239	TGTTTGAACCAA TAGTGACATACA G[G/A]TGCTAAGT TCTGCAGTAGGG GAAGG	G	A			SILENT- NONCODI NG			

535-536	cg44932430	254	TGACATACAGGT GCTAAGTTCTGC AIG/TTAGGGGA AGGCAGAGAG CCATGGA	G	T				SILENT- NONCODI NG			
537-538	cg44932430	326	AGCCTCAGAAAA AAGTTCCCGTTG A/A/TJTTGCTGTT TTAGCTGAGACT TGIGG	A	T				SILENT- NONCODI NG			
539-540	cg44932430	381	GGTAGTAGTTGG AGATCCCAGACA G/G/CJAGGTGAC CGAGTTAGCCAG GGAAAA	G	C				SILENT- NONCODI NG			
541-542	cg44932430	438	TCCTGGCACCCA TGGCAGAGTTGA G/T/CJGATCCAGT CTTTCTGTCTCC TCTGG	T	C				SILENT- NONCODI NG			
543-544	cg44932430	501	CAGATCTGGGAA GTCCAGTTGGG G/G/AJAGGGGGC TGACAATGATCA TGACCT	G	A				SILENT- NONCODI NG			
545-546	cg44932719	246	TAGGCCTTGTTT CTCTCCAGGGA A/A/GJAAAAGCCA AATCCTTATCAA GGAAA	A	G				SILENT- NONCODI NG			
547-548	cg44938377	307	TCAAAATGTCAA AAGACTCAGAGC C/G/AJGGGGGA CCAGTGCAGTGA CTGCGG	G	A				SILENT- NONCODI NG			
549-550	cg44938377	322	ACTCAGAGCCG GGGGGCACCCAG TGC/AJGTGACT GCGGATTCATGG GAAATGA	A	G				SILENT- NONCODI NG			

551-552	cg44938828	651	CACCTCCTGGTG AGTAAATGTGTA A[A/G]CGCGTGA AGGTCAGGGA TGTGTTT	A	G				SILENT- NONCODI NG		
553-554	cg44938869	494	TAATTTGGTGA ATAAAATGATG C[A/gap]AAAAA AAAAAATCAGG GTTGTTT	A	-				SILENT- NONCODI NG		
555-556	cg44938869	506	ATAAAATGATG CAAAAAA A[A/gap]ATCAGG GTTGTTTGACAC CTTTTTT	A	-				SILENT- NONCODI NG		
557-558	cg44938869	507	TAAAAATGATGC AAAAA A[A/gap]TCAGGG TTGTTTGACACC TTTTTC	A	-				SILENT- NONCODI NG		
559-560	cg44938869	566	AAACCTTCACCA AAAGGGGATAAA A[G/A]TTTAAAG GCAAAATGAGTA AACAA	G	A				SILENT- NONCODI NG		
561-562	cg44939935	351	ACAGTGTGGCCT CACAGGTATGGC A[G/A]CGGAAGC AGCTCCGGTGG AAGAAAT	G	A				SILENT- NONCODI NG		
563-564	cg44939935	442	CCCACAAAGTGC ACACAGGTCCCC A[G/A]CACCGC CTCCTGGTGTG GGATGG	G	A				SILENT- NONCODI NG		
565-566	cg44939948	19	NTGCAGCGGAG GAGAGAG[G/T]G GGGCCACCGT GGGGCGGTCGC AC	G	T				SILENT- NONCODI NG		

567- 568	cg44963511	295	TGTCCTTTAGG CTGAGGCAGTG CC[C/gap]ATAGC TGCAGTGCCTCG AGTTCCG	C	-				SILENT- NONCODI NG		
569- 570	cg44963787	210	TGGTAAGGGAT TTTTGTATAAGTC [A/gap]ATTAGTTG TTGAATCATTTTC TCAT	A	-				SILENT- NONCODI NG		
571- 572	cg44963787	327	CAGGATTCCTATG AATTAATTTTAA [G/C]TAGCTTAGT ATCATTCAATAG TATT	G	C				SILENT- NONCODI NG		
573- 574	cg44963787	382	AATACCAGGTTA CTTATACTACCT A[T/C]TCATGTAT GACATTTGTGT AGTAT	T	C				SILENT- NONCODI NG		
575- 576	cg44963787	442	TCATCAAGGGG CTATGAGCTAGA C[C/gap]TGCAGA TTAACACGCAGA TGTGGCC	C	-				SILENT- NONCODI NG		
577- 578	cg44963787	478	CACGCAGATGTG GCCTTAAAAAA A[A/gap]TCAGTTA ATCTGGGATCCA GAGAAG	A	-				SILENT- NONCODI NG		
579- 580	cg44964193	479	CCTTAGCCTTCC ATAATGGAGAAG TTC/TGGGCAGG GGATGTCTGCAT GCAATA	C	T				SILENT- NONCODI NG		
581- 582	cg44964193	505	GGCAGGGGAT GTCTGCATGCAA TA[G/A]ACAACTG AATTAGAAAGAG CAGAAA	G	A				SILENT- NONCODI NG		

583-584	cg44964193	540	TTAGAAAGAGCA GAAATGTAAACC AIG/AICAGTGCTT CCCTATCTTGGG CCTGG	G	A				SILENT- NONCODI NG		
585-586	cg44965051	271	TGTCCCAACATT TACTGGCTTTGG GT/CJCCAGTGG CACAGATGCAGC ATCAGA	T	C				SILENT- NONCODI NG		
587-588	cg44965051	292	TGGGTCCAGTG GCACAGATGCAG CAT/GJCAGAACCC CTCCCTCCCATC CTCAAG	T	G				SILENT- NONCODI NG		
589-590	cg44965597	2840	CCTGACCTTAAC CTATATACTGAT G/G/AJAAGTTTAT TTGTGGAGAAATG GGATA	G	A				SILENT- NONCODI NG		
591-592	cg44965597	2686	GGATACAAAGGGA CAGGTTATGCCA T/A/GJGTTAGTGA TGTAACCATACT TGAAA	A	G				SILENT- NONCODI NG		
593-594	cg44965597	2748	CCCCAGGGACC AGTGCCCAGTTA GC/G/AJGAACTA GTGGCACCTTACC CGAGCCT	G	A				SILENT- NONCODI NG		
595-596	cg5621185	20	TCCTAGGATTGC TAGCGCA[G/gap] CAAACGCCATTG TTTGAGAGCTTG T	G	.				SILENT- NONCODI NG		
597-598	cg5738781	60	AATAGAAAAGGTA TGAGTCTCAGGA CIG/TTGGTTCTCT GCAAAGCAGGCCA TCGGC	G	T				SILENT- NONCODI NG		

599- 600	cg6370826	80	GTTCTCTCTCTTT GTCCTTTTTTTTTT /gap]CTTTAGAGA CGGGGCTAGCT ATGT	T	-				SILENT- NONCODI NG		
601- 602	cg6586279	81	GCGGGAATGTG ACTGAGGGCA GGG[C/gap]CCAG CGGCTCCCTGCA GCCATCAGG	C	-				SILENT- NONCODI NG		
603- 604	cg8754307	327	TTGTATGCTAGG GCTTTCAAGGG C[C/gap]TTCGA GTGGCTGTTGAT TGTAGCA	C	-				SILENT- NONCODI NG		
605- 606	cg9886159	488	AAACATGGTAT ATCTCGATTAT C[AT]CATAAAGA TCCACATGAATT AGACG	A	T				SILENT- NONCODI NG		
607- 608	cg9886159	495	ATAAGATCCAC ATGAATTAGACG T[AT]AAACTAGG TGGTATCATTGA AATCT	A	T				SILENT- NONCODI NG		
609- 610	cg20595730	184	AAATTGAACAGA GAGCCAAATAAA C[AC]TGAGAAAC TTTATTTCTCAA AGAC	A	C				SILENT- NONCODI NG		
611- 612	cg20611295	144	AGCAAGGTGGA CCTGGTGCCTG GGC[A/gap]CACC ATGCCATGCTCT GGAGCCCTG	A	-				SILENT- NONCODI NG		
613- 614	cg20614578	320	ATTCTCTGGTT GGAGCGTGATG GC[G/A]TCATCTA TGGTTGGGGCA CACTGGA	G	A				SILENT- NONCODI NG		

615- 616	cg20614578	332	GGAGCGTGATG GCGTCATCTATG GTTC/JGGGCA CACTGGACGACA AGAACTC	T	C				SILENT- NONCODI NG			
617- 618	cg20615101	201	ATTATTAATTTGT AATCATTTTAACT A/GGCCCTTTCTT CCACTGTAAAA GGGT	A	G				SILENT- NONCODI NG			
619- 620	cg20622181	35	CCATCTTGATGA AGAGCGGACGT AC(C/A)GCCAAC ACCACGGCGAC AGCCAGGA	C	A				SILENT- NONCODI NG			
621- 622	cg20627797	177	CTTCGTTAAAA CTGTCAGTGTGG G/GTJGATACCAT CGGCTACGGCA GAACAT	G	T				SILENT- NONCODI NG			
623- 624	cg20627797	207	CCATCGGCTACG GCAGAACATGGA C(A/C)GCCAGCG AAACGACAAAA TCGCCA	A	C				SILENT- NONCODI NG			
625- 626	cg20628068	108	TTGCGATGGCTT CGTGGGCGATTT C(A/G)GTGGCAT CGGACTTCGATG TGCCCT	A	G				SILENT- NONCODI NG			
627- 628	cg20628068	123	GGGCGATTTCAG TGGCATCGGACT T(C/T)GATGTGCC CTGCGCCACACA GGGGTA	C	T				SILENT- NONCODI NG			

629-630	cg20628068	178	AATATTCCTCGGT ATTGGTCAACTC AIGAJCGATGAG GTTGTCGTCCTG GAAGAT	G	A				SILENT- NONCODI NG			
631-632	cg20628068	53	TGGCCACCCGA GACCTCGCCGG GGTG/AJGCGTC TGCCCAATGACT CGATTCCCT	G	A				SILENT- NONCODI NG			
633-634	cg20631839	221	AGGTGGAAGCC AGGATGGAGGG CAG[G/C]CCTCG CCTTCTGTCCGG GATCCGCC	G	C				SILENT- NONCODI NG			
635-636	cg20635329	94	GTGTTACATCAA ATGCAGTTTGT CT/CJTITTTACGT TGCTGTGTTGTA TTTCC	T	C				SILENT- NONCODI NG			
637-638	cg20635664	205	CTAGTGGTGCAG TTTTGTGTGT GT/gapJGGACGT GCTGGCCCCAGT GGTGCAGG	T	-				SILENT- NONCODI NG			
639-640	cg20636603	451	GCTGTAGGCACA ATCCATGGCTTT TIC/TACTTTGAAG CCAATGTGGCCT CTGAA	C	T				SILENT- NONCODI NG			
641-642	cg20638203	282	CGCATAGTACGT GTGGGCGGGTG GC[C/gap]AGCTC ATCAGCAGGGA GCGCGGCTC	C	-				SILENT- NONCODI NG			

643-644	cg20705188	109	TCCCCTCTTGAA TCTCAAGGCCTG G[C/gap]CTGTTT GGGGCCTGTTT GGGCCTC	C	.				SILENT- NONCODI NG		
645-646	cg20705880	309	CCGCCCCGGCT ATCAACCAGGGA GGT[C]TCATTCC TGTCATATCCCGG CCGGCG	T	C				SILENT- NONCODI NG		
647-648	cg20709811	220	AGTGGAGTGATC TCAACTCACTGC A[G/A]CCTCTACC TCCTGGTCTCAA GCAGT	G	A				SILENT- NONCODI NG		
649-650	cg20710663	53	CAAAACCAGTG CGGAGACGACTA C[C/T]GACGTCCA GCACCCGGCTTT TTCCG	C	T				SILENT- NONCODI NG		
651-652	cg20719026	175	CGTGTCTTCCC AAAGCGCGGG AG[C/gap]TCCAG ATCCATGACGAG GAGGTCCT	C	.				SILENT- NONCODI NG		
653-654	cg20721343	127	GCCCGCAACGT GTTAGGTCGTTG GT[A/G]TTTGTGA CTTGTGCTCGGC GCGAGC	A	G				SILENT- NONCODI NG		
655-656	cg20721343	134	ACGTGTTAGGTC GTTGGTATTGT G[A/G]CTTGCT CGGCGGAGCA AACCTC	A	G				SILENT- NONCODI NG		

657- 658	cg20721343	141	AGGTCGTTGGTA TTTGTGACTTGT G/C/TTCGGCGC GAGCAAACCTCC TGCCAG	C	T				SILENT- NONCODI NG		
659- 660	cg20721343	149	GGTATTTGTGAC TTGTGCTCGGCG C/G/AJAGCAAAC CTCCTGCCAGGA TGACGT	G	A				SILENT- NONCODI NG		
661- 662	cg20721343	151	TATTTGTGACTT GTGCTCGGCGC GA[G/gap]CAAAC CTCCTGCCAGGA TGACGTGC	G	.				SILENT- NONCODI NG		
663- 664	cg20721343	191	GGATGACGTGCT CAGCACCAACAC TTT/C/CTCAGGT CGTCACCAAGCTC CGATG	T	C				SILENT- NONCODI NG		
665- 666	cg20723457	516	CTTTGAAATCA CACACAACCCAT C/C/TJGGGTTTTC TGCTATGGAAG GCTCT	C	T				SILENT- NONCODI NG		
667- 668	cg20724478	291	GAGGCTGGGA GCTCGGCCTGG CTG[G/A]GATAC GCGATGTCGTCA ACGCCAGC	G	A				SILENT- NONCODI NG		
669- 670	cg20724478	295	CTGGGGAGCTC GGCCTGGCTGG GATIA/TJCGCGAT GTCGTCAACGCC AGCCCGT	A	T				SILENT- NONCODI NG		
671- 672	cg20724478	388	AAGACGTAGCCC GGGTGGGATGT GA/C/TJGGCCTG AGCGTCGTCG GCGATT	C	T				SILENT- NONCODI NG		

673-674	cg20724478	52	GAGGGGTGCC CTCATATTGAT GAT/CJCGCGTA CATCTCGTTGCC GAAATTG	T	C				SILENT- NONCODI NG		
675-676	cg20727018	67	CACGTGCACATC TGCGGTGAGGTT GJAGJGGGCTGC AGTGATATTGAA AGTCTC	A	G				SILENT- NONCODI NG		
677-678	cg20728358	419	GATGAAACCCCG TCTCTACTAAAA A/T/CJACAAAAAT TAGCCGGGTGT GATGGC	T	C				SILENT- NONCODI NG		
679-680	cg20730743	11	ACGCGTACTG[G] A/JCGGATCTCAG TAGGATAACCCA CCA	G	A				SILENT- NONCODI NG		
681-682	cg20730927	124	ATCTGAACATCT TTTTATCGACTA CT/CJGGCCCCA GTGAACCTATGC AACGTC	T	C				SILENT- NONCODI NG		
683-684	cg20738127	60	TCGATGTCGAAG TTCGCTTCGATG GJG/CJCCCGGAG GATAGCGCGTCA GGTGGC	G	C				SILENT- NONCODI NG		
685-686	cg20744814	103	CCATGGCCACCC ACGAAGCTCTCC CT/CJGCCCCCT CCGTCGCCCAAC TCCTGG	T	C				SILENT- NONCODI NG		
687-688	cg20744814	80	GAGGGGCACCC GGGTGCTGCTG GCC[A/GJTGCC ACCCACGAAGCT CTCCCTGC	A	G				SILENT- NONCODI NG		

689-690	cg20745811	21	NACGCGTGGG CATGTCAGA[G/A] CTTCAGATGTGC ATTGCGAACATG C	G	A				SILENT- NONCODI NG		
691-692	cg21132570	166	GTATGTACGAGT GTGCACGTGTGT G[C/gap]GTGTGC ACAGAGGGTGT GGTGCCAG	C	-				SILENT- NONCODI NG		
693-694	cg21132570	173	CGAGTGTGCAC GTGTGTGCGTGT GC[A/gap]CAGAG GGTGTGGTGCC AGCTTGAGT	A	-				SILENT- NONCODI NG		
695-696	cg21147609	420	AGTGCAGAGCCA GGATCCACCTGA G[T/C]CCCCCGG CTGGCTCCAGAT CCCACA	T	C				SILENT- NONCODI NG		
697-698	cg21147771	119	GACTGGCTTATT CCACTTAGCATA AT[C]GTCCTCAA GGTGTGTTCAAC CATGT	T	C				SILENT- NONCODI NG		
699-700	cg21147771	340	GTITGACAGAGT ATCACTCTGTCA C[C/T]CAGGCTG GAGTGCAGTGAT GCAATC	C	T				SILENT- NONCODI NG		
701-702	cg21147771	369	GCTGGAGTGCA GTGATGCAATCT CG[G/A]CTCACT GCAACCTCCGCC TCCCAGC	G	A				SILENT- NONCODI NG		
703-704	cg21148047	147	TGCTTATATTCT GTTGGTGGGAAT [A/G]TAAACCGT ACATCTAGTATG GAAA	A	G				SILENT- NONCODI NG		

705-706	cg21148047	372	ATTGAGGGATGA ATGGA AAAACAA A[A/G]TCTGACAT ATACATACATAC AGTGG	A	G				SILENT- NONCODI NG		
707-708	cg21148047	464	CATATAGACATA TGCTATAACATG G[A/C]TGCACCTT GAGTACATTATG CTAGG	A	C				SILENT- NONCODI NG		
709-710	cg21148047	487	GGATGCACCTTG AGTACATTATGC T[A/G]GGTGAAAT AAGCCTGTCACA AAAAAC	A	G				SILENT- NONCODI NG		
711-712	cg21148047	497	TGAGTACATTAT GCTAGGTGAAAT A[A/G]GCCCTGTCA CAAAAACAAATA CTGCA	A	G				SILENT- NONCODI NG		
713-714	cg21148047	534	AAACAAATACTG CATGATTCATT T[A/G]AATGAGG GGCCTAGAATAT TCAACT	A	G				SILENT- NONCODI NG		
715-716	cg21148047	535	AACAAATACTGC ATGATTCATTTA [A/G]ATGAGGG CCTAGAATATTC AACTT	A	G				SILENT- NONCODI NG		
717-718	cg21150410	494	GGCGGAGGTTT CAGAGTAGAAGG TG[A/G]TGTACGC TCCAGCTCCCT CTGTCG	A	G				SILENT- NONCODI NG		
719-720	cg21150410	98	GAATAAGAAGAT GAAGTTTGCAGT C[G/A]AATTCATG TTCTCCTACCCC TGCTC	G	A				SILENT- NONCODI NG		

721-722	cg21405503	50	GAAAGACTTCTA GTTACACAGGG CTG/CJTATCTGA ACCCTAAACAG GCCCAG	G	C				SILENT- NONCODI NG		
723-724	cg21415668	139	GGACTGGTCTAG GGAGGAGTTAG GGC/A/TJGGAGG ACTGGTCAGGGA GGAGTTAG	A	T				SILENT- NONCODI NG		
725-726	cg21415668	168	GGACTGGTCTAG GGAGGAGTTAG GGC/A/TJGGAGG ACTGGTCAGGGA GGAGTTAG	A	T				SILENT- NONCODI NG		
727-728	cg21417734	147	TCCTGGCCGTTT TCGACAGGAGC GC[A/gap]TCATG GACCAGCCCG CAATCTGTT	A	-				SILENT- NONCODI NG		
729-730	cg21424662	113	TGAGGAAGAGG AAATACAGAACT CAIG/CJCTGTCC CGGGGTGCGC CCGTGTGT	G	C				SILENT- NONCODI NG		
731-732	cg21424662	181	GTGCTGTGCCG CGAGCGCGCGC GAG[G/A]CGGCG TGTGTGTGTGT TGIGIGIG	G	A				SILENT- NONCODI NG		
733-734	cg21424662	214	GTGTGTGTGTGT GTGTGTGTGTGT G[gap]/TJGTGTGT GCGCGCGCGCG TATGTAATG	-	T				SILENT- NONCODI NG		

735-736	cg21424662	222	TGTGTGTGTGTG TGTGTGTGTGT G/C/TJGCGCGG CGTATGTATGTG TGTGTG	C	T			SILENT- NONCODI NG			
737-738	cg21424863	166	GGACCGTTCGC GTCGACCTGGG CTC[G/A]TTGGAG GGCATTATGCCT CCGGCGG	G	A			SILENT- NONCODI NG			
739-740	cg21424863	189	TCGTTGGAGGG CATTATGCCTCC GG[C/gap]GGAAC AGGTTCCCGGG GAGAAATAT	C	-			SILENT- NONCODI NG			
741-742	cg21424863	40	CAACTGCCCGG CAGGTCAATTTT CA[A/G]CGGCTG CGCGAGGCCGA GGACGAGC	A	G			SILENT- NONCODI NG			
743-744	cg21424863	83	GGACGAGCAGA AATACGGTCATT TTT/GJCCGCCGT TGAGGGTGACGT CATCAC	T	G			SILENT- NONCODI NG			
745-746	cg21424863	88	AGCAGAAATACG GTCATTTTTCG C[C/G]GTTGAGG GTGACGTCATCA CCGGAG	C	G			SILENT- NONCODI NG			
747-748	cg21424863	94	AATACGGTCATT TTTCCGCCGTTG A[G/A]GGTGACG TCATCACCGGAG TCGTCC	G	A			SILENT- NONCODI NG			

749-750	cg21425684	233	TGCACCTGACGC GGTTCGACGTGC AIG/ATCGAGG CCITCGAAGAGC CCCTCC	G	T				SILENT- NONCODI NG		
751-752	cg21425684	474	AGAAGGCATCCG TGAGGATCCGA CIA/GGCCAGGG CCAGGGCGATTT CCTTGA	A	G				SILENT- NONCODI NG		
753-754	cg21425687	417	CCCCAGAAGAG GGAGGGCGCTC TCTG/CCCAGG AGACCTGCTGTG CTCCCAT	G	T				SILENT- NONCODI NG		
755-756	cg21428753	206	CCCTCCCTCTGT ACCTGTGTCTG AIC/AJCCCCCTTT CTTATAAGGACA CCGGT	C	A				SILENT- NONCODI NG		
757-758	cg21428762	125	CATCAGAGGTGA AAACGATGAGCG GIG/ITGTGCTCG GACGCAGACGA GCGATAC	G	T				SILENT- NONCODI NG		
759-760	cg21428762	65	ACACCGGGGTAA CGACGGCGTGA GCIG/gap]CCCCA GACCCAGGCCGA GGGTCTTGG	G	-				SILENT- NONCODI NG		
761-762	cg21433543	102	TACGCCTCCCTC ACCACTCCGACG CIG/AJTACCTTCG TCGTGCGCCGTGA CAGCA	G	A				SILENT- NONCODI NG		

763- 764	cg21433543	119	TCCGACGGGTAC CTTCGTGTCGC CIG/AJTGACAGC AGCCGTATGCG GGGCCGC	G	A				SILENT- NONCODI NG			
765- 766	cg21433543	268	CACTGAAGTTAT GGCGTCGCTGC GTIACIGCCGAG GCTGGGGTAGC GCTCCIGG	A	C				SILENT- NONCODI NG			
767- 768	cg21433543	98	CGGGGCTCTG GCCTGGCAGCC GCA[G/gap]GACC CAATGGATCGGG CGCTCAGCG	G	-				SILENT- NONCODI NG			
769- 770	cg21433589	63	TCATTTGTGCC AAGATACACTGT CIG/AJTGCTGT ATCCGGAATGGT CTGTGT	G	A				SILENT- NONCODI NG			
771- 772	cg21628871	350	GCCCGGACCCT GTACCCGACCA GGIAGJACACAGC CCATCACTAATC AATGATA	A	G				SILENT- NONCODI NG			
773- 774	cg21628871	373	GGACACAGCCC ATCACTAATCAA TGIAGJTATTCC ATAAACCAAGA GAATTC	A	G				SILENT- NONCODI NG			
775- 776	cg21632268	130	AAGAACACCCCGT GACAAAAGAAG A[G/gap]GGCCGG CAGAAATGACCCG CCGGCCC	G	-				SILENT- NONCODI NG			

777- 778	cg21632268	210	GACGGTCGTCAC TTCTCCTCTTTG G[G/gap]CAGCCG CCACTGGTCGTG CTCGGIG	G	-				SILENT- NONCODI NG			
779- 780	cg21632268	268	GCGGACGCGGG CCGTGATAATCA GG[G/gap]CCGTA GGCTCCCGGAG CGGGGCGGAC	G	-				SILENT- NONCODI NG			
781- 782	cg21632288	34	GTGTGAGGGC GCGGCGCCCC TAG[C/G]CGGCC CTGCGCCGGG TCTCAGAG	C	G				SILENT- NONCODI NG			
783- 784	cg21632288	69	GCCGGGGTCTC AGAGGGCCGGC CCG[G/gap]CGG GGCGCCCGCG GGCCAGGACT	G	-				SILENT- NONCODI NG			
785- 786	cg21632288	81	GAGGGCCGGCC CGCGGGGGGC GCC[G/gap]CGG GCCAGGACTGC GCTCAGGATC	G	-				SILENT- NONCODI NG			
787- 788	cg21634562	112	CCTGGCTCAGCA GAGCCGCTTCC T[G/A]CTGCAGAA GCTGATGTCGCC CCACC	G	A				SILENT- NONCODI NG			
789- 790	cg21638303	323	CAAGCCCTGTTAT ACAACCCAGATCT C[AC]TGAGAACT CACTATCACAAG GTCAG	A	C				SILENT- NONCODI NG			

791-792	cg21638303	349	TGAGAACTCACT ATCACAAGGTCA G[C/T]ATCAAGAA GATGGTGCTTAA CCATT	C	T			SILENT- NONCODI NG		
793-794	cg21638303	362	TCACAAGGTCAG CATCAAGAAGAT G[G/T]TGCTTAAC CATGGTGAAAG ATCCG	G	T			SILENT- NONCODI NG		
795-796	cg21638638	374	GAGGGAAGGCC TCCCATGTACCC GT[C/T]ACTCCTC TCTTCTCCATCA AGGCCA	C	T			SILENT- NONCODI NG		
797-798	cg21639240	125	TTGCCACGTTGC CTAGGCTGGTCT C[A/G]AACTCCTG GGCTCAGATGAT CCACC	A	G			SILENT- NONCODI NG		
799-800	cg21639652	343	AAACCCATGCA CTCCTGTGGAT T[G/A]CCCCCTGA GCTCCACAGTCT CTCCC	G	A			SILENT- NONCODI NG		
801-802	cg21640260	209	TGTCACCCAGGC TGAAGTGCAGTG G[T/C]GTGATCTT GGTCACTGCAA CCTCC	T	C			SILENT- NONCODI NG		
803-804	cg21640260	242	TGGCTCACTGCA ACCTCCACCTCC C[A/G]GGTTCAA GCAATTCTCCTG CCTCAG	A	G			SILENT- NONCODI NG		
805-806	cg21640260	252	CAACCTCCACCT CCCAGGTTCAAG C[A/G]ATTCTCCT GCCTCAGCCTCA GCCTC	A	G			SILENT- NONCODI NG		

807-808	cg21642593	307	CGGCCACCCCG GACCCAGCCCG CAC[G/A]CCCAG GGCGTACCCATC GGTCATCG	G	A				SILENT- NONCODI NG			
809-810	cg21643872	249	CCGAAGACCCA GCCAAGCCGTC CAA[G/A]ATCTTC GCTCCCAGTGGT CTCATGC	G	A				SILENT- NONCODI NG			
811-812	cg21646394	197	AGGAAGCAGAGT CTATACAAAATTT [A/G]AGAGAATGA GACAGAAGACG CTCCT	A	G				SILENT- NONCODI NG			
813-814	cg21651520	181	GCATCCCCGCAC AGCACGTGGTGT G[T/C]GGACATG CCACAGCATCCG CGGGAG	T	C				SILENT- NONCODI NG			
815-816	cg21652256	97	ACTGCAGCGTGA GCCCTGGGACG CA[G/A]TCGAAG CAGAGCAAAGTC TCCCCCG	G	A				SILENT- NONCODI NG			
817-818	cg21655657	197	CAACATACATGG CGTTTGCCTCAC A[G/A]TTGGAGTC AGATGTGAGCCC GGAGG	G	A				SILENT- NONCODI NG			
819-820	cg21656849	174	CACCCAGAACCA CGGATTACGCAA CIG[A/C]ACGCTG CCACCAGGGAC GACGCGC	G	A				SILENT- NONCODI NG			

821-822	cg21656849	50	AGGACTGGTTGG TGATCCCGGGA TIG/AJACACCTT CTGACCTTGCTG CTCGA	G	A				SILENT- NONCODI NG			
823-824	cg21656849	69	CGGGATGACAC CCTTCTGACCTT GCT/CJGCTCGA CCTCAGTATCGG CATGCAC	T	C				SILENT- NONCODI NG			
825-826	cg21659091	292	GTTCAAAACCAAA TCCTGCTCCTGA G/G/TAACACAGA AGGGGCAGGAC TTCCAGA	G	T				SILENT- NONCODI NG			
827-828	cg21659216	13	ACGCGTGTGTCC T/CJGTGACTACA AAACAGCACTGG GGT	T	C				SILENT- NONCODI NG			
829-830	cg21659216	139	AAGGATGCTGG GACCTGGAGTCA GG/C/TAAGTTGC AGCCAAGCTCAG CCTTG	C	T				SILENT- NONCODI NG			
831-832	cg21659349	238	ACATTGCGCTCA ATGGAGACCCG GT/C/TAACCCCT CCCACGCCGTG AAACCCG	C	T				SILENT- NONCODI NG			
833-834	cg21659349	252	GGAGACCCGGT CAAACCCCTCCA CG/C/AJCGTGAA ACCCGGCGGATAC CGTCACC	C	A				SILENT- NONCODI NG			
835-836	cg21659349	278	CGTGAACCCCG GCGATACCGTCA CC/G/AJTCACAC CCCCGGATGGG ACCGGGT	G	A				SILENT- NONCODI NG			

837-838	cg21659349	304	TCCACACCCCGG GATGGGACCG GTTTCCTCCAGG TCATCAACCCGA TCACGA	T	C				SILENT- NONCODI NG		
839-840	cg21660290	100	AGGTGGAACGG GCACCTGGACCTG TGCTATGGCGT GCAAAGGGTGC GCCCGAG	C	T				SILENT- NONCODI NG		
841-842	cg21660634	167	CCCACACCAGGA AACAGATACCAA TTAGJAGGTCC ACGTGACGACC GGAACAT	A	G				SILENT- NONCODI NG		
843-844	cg21660687	159	CTCAACCGCCTG ACGCGCTCGCT GC[ap/G]CCGCG CGCGCACCGTG GAGTTGCC	-	G				SILENT- NONCODI NG		
845-846	cg21660975	293	GCAGGGGCATT GGGTAATAGCC TTTCCTAGCCCT TTTGAGGGAAA CACATG	C	T				SILENT- NONCODI NG		
847-848	cg21661807	69	TGCCCTCAGGAG CAGACCCCCACA CIGCTATGAGC CGTCGCTGCGT GACGTTT	G	C				SILENT- NONCODI NG		
849-850	cg23217486	352	GCTATGGCTGTG GATTCGGAGTG CIGTGGGAAGT GTGGAGGAGGT GTTGGGG	G	T				SILENT- NONCODI NG		

851-852	cg23217486	363	GGATTTCGGAGT GCGGGGAAGTG TGjG/CjAGGAGG TGTGGGGGCT GGAGAGAT	G	C				SILENT- NONCODI NG			
853-854	cg23295774	352	GCCCTCCTGAG TGCCAAAGGAGG CGjG/AjGCGTCT ACACTTGCCGTG CACACAA	G	A				SILENT- NONCODI NG			
855-856	cg23295774	413	GCCAACTCTACG TCAATACGCGTG GjC/AjGGTGGCA GCAACCGGGCC CCCAAAA	C	A				SILENT- NONCODI NG			
857-858	cg23298372	112	CGCGTGATAGG CTCAGGAGCCTG CCjT/CjGTGTACA CAGACAGCACAC ATGACA	T	C				SILENT- NONCODI NG			
859-860	cg23298372	136	CTGTGTACACAG ACAGCACACATG A/CjTjAGGCCCG GGAGCCTGTCTG TGTACA	C	T				SILENT- NONCODI NG			
861-862	cg23299043	208	AGTACGACATCC GACACGCTTCAG A/CjGjCGACCCAG AGTGAAGAAATTT CGCGTA	C	G				SILENT- NONCODI NG			
863-864	cg23299248	220	CCAACCTATTAG ATATATATACCC CjgAp/CjTACCCCC AGTGAAGAACAA TCTGCTA	-	C				SILENT- NONCODI NG			
865-866	cg23305320	199	TGCTGCATACCA GGTGCCAAATGG CjG/AjTCCTATAA ATGGAAGCTCTT GjGjG	G	A				SILENT- NONCODI NG			

867-868	cg23306056	323	TCCAGTATGACT TTATCTCGATTA C[A/gap]CCTGTA AAGACCTTAAGC CATATT	A	-				SILENT- NONCODI NG		
869-870	cg23306056	332	ACTTATCTCGA TTACACCTGTAA A[G/T]ACCTTAAG CCATATTTAAG GTTC	G	T				SILENT- NONCODI NG		
871-872	cg23309108	23	ACGCGTGCCCG TTACGTTGACC[A] /GGCTGGTTGT AAACTCCTGGGC TCA	A	G				SILENT- NONCODI NG		
873-874	cg23309108	66	TGGGCTCAAGTG ATCCACCTGCCT C[A/G]GCCTCCA AAAGTGCTGGGA TTACAT	A	G				SILENT- NONCODI NG		
875-876	cg23331833	74	ACAGCGCTACT TTGGGCTCCGG GA[T/G]TCGCTCC GCGCCCGCGGT TGAGCA	T	G				SILENT- NONCODI NG		
877-878	cg23332230	234	TTGTGGGAGTAT TAGGGGAAGTTG C[C/gap]ACTAAG GCTGGCAGGTC CTGGAGTT	C	-				SILENT- NONCODI NG		
879-880	cg23333370	141	TTGGGGGCTCA GAGGCACGGTTA AC[G/A]CAGCAG CAGCGCAAACCT CACACTC	G	A				SILENT- NONCODI NG		
881-882	cg24109555	43	AATATAATGGGT TTATATGACTATA [T/C]CAAAGGAG GGAAGAAGGCC CCCAGC	T	C				SILENT- NONCODI NG		

883-884	cg24110526	247	GCACTGAGACAG CATCAGGAGAC T[G/A]TGCCTGCC CCGCATGCCTCT TGCCA	G	A				SILENT- NONCODI NG			
885-886	cg24113982	197	TACTTAGTTATGT TTTTAAACACAC[A/G]TCTGAGCTC AAAGCCCAAGAAA GGGA	A	G				SILENT- NONCODI NG			
887-888	cg24114224	275	AATGGGCCAGG CTGGAGCTACGT TG[A/C]GTTTGT GAGTTTTTGTCT TATTGC	A	C				SILENT- NONCODI NG			
889-890	cg24114456	167	ATCCTGACGTGT AGACTCCTATGG A[G/T]ACCTACTT AATTCACACCGG GTGTC	G	T				SILENT- NONCODI NG			
891-892	cg24114456	203	TTACACCCGGGT GTCCTGATGTGT A[G/A]ACCCCTGT GGAGACCTACTT AATTC	G	A				SILENT- NONCODI NG			
893-894	cg24115035	207	GAGGTGAAAGG GAAGAAAAGCTA AG[G/A]TCGACCT TAGAAAAGCATTG AGTCAA	G	A				SILENT- NONCODI NG			
895-896	cg24115035	505	AGAACTGTTGCT TTTTGTTTAACCC [A/C]CGTGCAAGT AAAGTTCAATAA AGTT	A	C				SILENT- NONCODI NG			
897-898	cg24121961	196	ACAGGCCACACC CCCATCTCAGAG A[T/A]GGCAGCG ACTTCATCCAAG GGGCAG	T	A				SILENT- NONCODI NG			

899-900	cg24132746	296	CCTGTGGTGTG CTTCTCCAAATG CIC/TGCCCTTG GCTGTTTCCCAG GAGTCA	C	T				SILENT- NONCODI NG		
901-902	cg24141481	529	GTGTAAAGAAGT ATAATTTCTCTG CIC/TGACTCCAT TTAATCCACTGC AAGGC	C	T				SILENT- NONCODI NG		
903-904	cg24144955	33	GCACGCGTGTG TGGCTGGAAGG GC/G/T/CAGTGC TCTGGAGGGGG AACTGAG	G	T				SILENT- NONCODI NG		
905-906	cg25132332	107	AAGTAAGTTGCT TAATCAGGTCCA A/G/A/CAGTAATT GAGAGAAGAGA GTAGCT	G	A				SILENT- NONCODI NG		
907-908	cg25132807	340	TGAACGTGCACC ATTCITTAATGAC [G/A]GTAGAGAT TTGCAGTTTACT GCAC	G	A				SILENT- NONCODI NG		
909-910	cg25147161	324	CTGCAATATGCC ACCAGCGCCATG G[C/gap]GAACCG CATCTACGCTCC AATTCCC	C	.				SILENT- NONCODI NG		
911-912	cg25153589	518	TCCCAGCACTTC TGGGAGGCCAA AGT/C/IGGGAGG ATCGCTTGAGCC CAGGAGT	T	C				SILENT- NONCODI NG		

913-914	cg25153589	528	TCGGGAGGCC AAAGTGGGAGG ATC[G/C]CTTGAG CCCAGGAGTTCG AGACCAG	G	C			SILENT- NONCODI NG		
915-916	cg25153589	545	GGAGGATCGTT GAGCCAGGAG TT[C/T]GAGACCA GCCTGGGCAAC ATAGCGA	C	T			SILENT- NONCODI NG		
917-918	cg25154211	117	GGCCACCCAGC TGCCTATGCTGG GG[A/T]CGGGGC CGCTCAGGTCCC CACCGGG	A	T			SILENT- NONCODI NG		
919-920	cg25154211	119	CCACCCAGCTGC CTATGCTGGGA C[G/C]GGGCCGC TCAGGTCCCCAC CGGGCC	G	C			SILENT- NONCODI NG		
921-922	cg25154211	145	GGGCCGCTCAG GTCCCCACCGG GCC[T/gap]GTGC CACCGGCTGCG GTCCTCTCGC	T	-			SILENT- NONCODI NG		
923-924	cg25154916	208	GATAATAAAACC TGCCCCACAATT T[A/gap]AAAAAAA AAATCATGTCAT GTTAGT	A	-			SILENT- NONCODI NG		
925-926	cg25155258	358	TGCTGAGCTGA GTCTAAAGGAGG A[A/gap]GAAAGG GGACCTAGGCAA AGGGACC	A	-			SILENT- NONCODI NG		

927-928	cg25167383	78	TGACTGTGTGTC CGGGCCACGTG TG[G/A]CTATGTG TCCGGGCCACG TGIGACT	G	A				SILENT- NONCODI NG		
929-930	cg25171115	118	GACCACCTCCG GTACCCCGGCT GG[C/T]TGCTG ATATCCCGCCGG CCTCTCTG	C	T				SILENT- NONCODI NG		
931-932	cg25171115	181	GCCAAGCGTTCA CCCACGCTGCT G[C/T]CTGCAAGA CCTGAGGAACG CGCATG	C	T				SILENT- NONCODI NG		
933-934	cg25171136	145	TGCAAGGCCAGT CGGCTGGGGA AA[C/T]GGATGCC CTGCAGGGGGA CGGGAAC	C	T				SILENT- NONCODI NG		
935-936	cg25171709	274	GCATTGTCAACG AAACCTGCGACT C[T/C]CTTGCCTT CTGTGCCTGCAG CATGG	T	C				SILENT- NONCODI NG		
937-938	cg25173882	234	TGCAAGTCCAGC TTTCTCTCACCTT IC/TACCGTGTTT TGTGCGCACCCAC TGAG	C	T				SILENT- NONCODI NG		
939-940	cg25174416	132	ATGCTGGACACA GGGCTCGACAAA C[A/C]CAAGAGA CGATCCTCGGAC CATCCT	A	C				SILENT- NONCODI NG		

941-942	cg25184184	331	CAGTGGGAGCG GGAAGAGGCCG GAG[C/T]TCCTGC CCCACACGTGAG CAAAGGG	C	T				SILENT- NONCODI NG			
943-944	cg25237193	246	CTTCCAAATGA ATCCCAACTTCA C[C/T]TGACTAG TTTACAGTCCTT ACAC	C	T				SILENT- NONCODI NG			
945-946	cg25239764	53	CATAAGCTCAAG AAGCTGTGGA GC[G/A]CAACCT CCAGGACGATTT CCCTCAT	G	A				SILENT- NONCODI NG			
947-948	cg25244087	153	TCGTACCCACTG GCGTTGTCGACG TTT[C]GTCAAACC GAGGAGGTTTCAT GCGCT	T	C				SILENT- NONCODI NG			
949-950	cg25244087	204	CGATCGTTCCCC CTCCCGCTCCTT A[AC]GAGCCTTG TAGGCGCACCGT CTGCC	A	C				SILENT- NONCODI NG			
951-952	cg25244087	39	CGAGCCGGACC GCTCGGCGAGC ATC[G/A]GAGTAC CAACACCGATGT CGCCCGC	G	A				SILENT- NONCODI NG			
953-954	cg25244087	42	GCCGGACCGCT CGGCGAGCATC GGA[G/A]TACCAA ACACGATGTCGC CCGCCTC	G	A				SILENT- NONCODI NG			

955-956	cg25244087	90	CTCTCTTGTAAC TGGGGACCCGA CG[C/T]CCGAG CGAGGACAGCG GCCCCTCA	C	T				SILENT- NONCODI NG			
957-958	cg25248402	237	AGAAAGGCACAG AGGAAGGGCAA AG[C/gap]CCCAG GGGAGAGAAAA CCAGTGACC	C	-				SILENT- NONCODI NG			
959-960	cg25257592	201	GAGGACGACAC CGATCTGGCGG ACG[C/T]CGCCC GTTTCATGGCGCA GATACCTC	C	T				SILENT- NONCODI NG			
961-962	cg25257592	280	CTGTCCTGGAC TAGGCATTTTCG G[G/C]TATCTTGC GTGGTGGTCATT GTGGC	G	C				SILENT- NONCODI NG			
963-964	cg25257592	38	TGGTCACATCCA TGTCGATGGTGT G[A/C]GCGTAAT GAAGGTCTACAT CGCCCT	A	C				SILENT- NONCODI NG			
965-966	cg25257592	475	TCCCGGCTGTTT TCATCGTCGCCG G[C/T]ATCTTTT CTGGCTCGCCGT CTAAG	C	T				SILENT- NONCODI NG			
967-968	cg25257592	59	TGTGAGCGTAAT GAAGGTCTACAT C[G/A]CCCTGGT GAAGGCCTGCA CCACTAG	G	A				SILENT- NONCODI NG			

969-970	cg25257592	73	AGGTCATACG CCCTGGTGAAG GC/C/TTGCAACA CTAGCGTCGGCA CCATT	C	T			SILENT- NONCODI NG		
971-972	cg25261577	58	TGATAATAGCGC TTGCCGGTTAGT G[G/A]TAATACAC AGCTTGAAATTT GGTGA	G	A			SILENT- NONCODI NG		
973-974	cg25263948	141	GGGGCGATTTC AGCAGAACTCA C[G/A]ACGACCTT CACTGCGGGCT CCGGGC	G	A			SILENT- NONCODI NG		
975-976	cg25263948	168	CGACCTTCACTG CGGGCTCCGGG CT[G/A]CCCGAC CTTACCGGCGTC AAGGGCG	G	A			SILENT- NONCODI NG		
977-978	cg25263948	27	CCGGTGACGCTA AGAAGCTCGTCC T[G/A]TGGATGTG GCCAGAAGGCTT CGACA	G	A			SILENT- NONCODI NG		
979-980	cg25263948	65	GAGGCTTCGAC AAGCAGACGTTA GT/C/JGCCGTC GCCAAAGCGCA GCCGTCT	T	C			SILENT- NONCODI NG		
981-982	cg25268662	248	CCCTTGAGCTTT GAGCTCAGGTCT A[G/gap]AGGTGA ACAGAGCAGTCA CCGGGGCG	G	-			SILENT- NONCODI NG		

983-984	cg25268662	253	GAGCTTTGAGCT CAGGTCTAGAGG T[G/A]AACAGAGC AGTCACCGGGC GACTCA	G	A				SILENT- NONCODI NG		
985-986	cg25268662	282	AGAGCAGTCACC GGCGACTCAG AC[G/C]GGCCAG CGCTCAGGGTC CTTGGTAA	G	C				SILENT- NONCODI NG		
987-988	cg25268662	305	ACGGGCCAGCG CTCAGGGTCCTT GG[T/gap]AATAT ATGCCCTAGAGAA AGGCCATG	T	-				SILENT- NONCODI NG		
989-990	cg25268662	306	CGGGCCAGCGC TCAGGGTCCTTG GT[A/gap]ATATAT GCCTAGAGAAAG GCCATGC	A	-				SILENT- NONCODI NG		
991-992	cg25310296	48	AACTCCATCTC AAAAAAAAAAAA A[A/gap]ATTAGTT TGGGATACCAG TAATTT	A	-				SILENT- NONCODI NG		
993-994	cg25310296	49	AACTCCATCTCA AAAAAAAAAAAA A[A/gap]TTAGTTT GGGATACCAGT AATTC	A	-				SILENT- NONCODI NG		
995-996	cg25311248	218	CACAGGCAACCC GTCCAGCCAAGC A[G/T]AAGCCGT GGCGTAGCCGA CAGGCCT	G	T				SILENT- NONCODI NG		

997-998	cg25311248	230	GTCCAGCCAAAGC AGAAAGCGTGG CGT/CJAGCCGA CAGCCTTCGAC CCAACCC	T	C				SILENT- NONCODI NG		
999-1000	cg25311248	60	TCGTGTGTCT TCCTCACCCCTCA TT/CJCCATTGAC GGTCATTGGTG GGCCA	T	C				SILENT- NONCODI NG		
1001-1002	cg25311248	75	TCACCTCATTC CATTGACGGTCA TT/CJGGTTGGG CCAACAACAAGG ACCTCC	T	C				SILENT- NONCODI NG		
1003-1004	cg25311248	78	CCCTCATTCCAT TGACGGTCATTG GT/GJGGGCCA ACAACAAGGACC TCCGAT	T	G				SILENT- NONCODI NG		
1005-1006	cg25314764	120	TATGGAAGAAA GTCACTCGGAAG T/A/GJCCGTAAAT CACCCAGCGC CTCATC	A	G				SILENT- NONCODI NG		
1007-1008	cg25314764	130	AAGTCACTCGGA AGTACCGTAAAT C/A/GJCCCCAGC GCCTCATCCCCC GAATCT	A	G				SILENT- NONCODI NG		
1009-1010	cg25314764	140	GAAGTACCGTAA ATCACCCAGCG C/CJGTCATC00C CGAATCTGTTCG CCATC	C	G				SILENT- NONCODI NG		
1011-1012	cg25314764	151	AATCACCCAGC GCCTCATCCCCC G/A/GJATCTGTTC GCCATCTGCTGT CGCCC	A	G				SILENT- NONCODI NG		

1013-1014	cg25314764	180	TGTTGCCATCT GCTGTCGCCCT GCTGCTTAAGG CATCACCCCACT AGACT	C	T			SILENT- NONCODI NG			
1015-1016	cg25314764	185	GCCATCTGCTGT CGCCCTGCGC TTTGGAGGCATC ACCCCACTAGAC TGACCG	A	G			SILENT- NONCODI NG			
1017-1018	cg25314764	53	GGCGACATCACCC GGTGACGGTTCA A/GA/GTGGCAG CCCGAGGGCCCC GCCGTGA	G	A			SILENT- NONCODI NG			
1019-1020	cg25314764	77	AGTGGCAGCC CGAGGGCCCCG CGT/GC/JAACTTA TTGTGTCGTCTT ATGGAAG	G	C			SILENT- NONCODI NG			
1021-1022	cg25314764	81	GGCAGCCCCGAG GGCCCGCCCGTG AACT/AJTATTGT GTCGCTTTATGG AAGAAA	T	A			SILENT- NONCODI NG			
1023-1024	cg27297262	540	CACACACACACA CACACACACACA C/A/gap/CTCACC CAAGAGTGTTC AACAGAA	A	-			SILENT- NONCODI NG			
1025-1026	cg27355682	114	GAGACAGGCTTG TACATAAAAAA A/A/gap/TACTTAG ATTAATTCCTGG CCCTGT	A	-			SILENT- NONCODI NG			

1027-1028	cg27360908	229	GTGCGGTATCCA GCGTGAGAAGAA A/T/C]GCCGAAG GTCACGGCGAT GACCGCG	T	C				SILENT- NONCODI NG		
1029-1030	cg27364539	198	CGCTCACTGTGT TGTCCTTCCTTG G[G/gap]TATGTC TCGATGGTTTCA CGATGGA	G	-				SILENT- NONCODI NG		
1031-1032	cg27369798	67	CGACATCCTGTT CACCCAGGGTG AC[A/G]TCATCAG CAGTAAGTGTG CACAGG	A	G				SILENT- NONCODI NG		
1033-1034	cg27784915	37	CCATAGACACTC ACCTCCGAGTCC G[A/G]GATCTTCT CCTCGCTGCGG CCG	A	G				SILENT- NONCODI NG		
1035-1036	cg27794839	306	CCTTCACTCGCA AATGCCCTCTCT C[C/T]CCACCTCC CCAGGCCCTC CTGGGA	C	T				SILENT- NONCODI NG		
1037-1038	cg27802892	188	TTGCTACTGCTA ACATCCCTTAGG C[A/gap]CTGGGA CTATTCTAATG CCTGGCA	A	-				SILENT- NONCODI NG		
1039-1040	cg27804759	21	ACGCGTGCCGA GGCGCTGGG[C/g ap]GGCGGCTGT GTGAGTTGGTG CCCA	C	-				SILENT- NONCODI NG		
1041-1042	cg27804759	52	CTGTGTGAGTTG GTGCCCCAGAC GA[A/G]CAGCTT GTGCGAGACTCT GGGCATT	A	G				SILENT- NONCODI NG		

1043-1044	cg27805688	380	CCAGCACCAGTT CTGCTGGCCAC GC[G/gap]CCTTG TCGGCATGCAGC ACAGGGTC	G	-				SILENT- NONCODI NG			
1045-1046	cg27806958	168	AGCAGTGAAG GGCAGCGGCGC ACA[G/A]GCATAT CCACAGCCCAT TGACCCA	G	A				SILENT- NONCODI NG			
1047-1048	cg27807001	120	ACAATGCCGTTA ACACTGCCGCTG G[C/gap]ACCAAGC ATCGGCTGAACC GTGACCA	C	-				SILENT- NONCODI NG			
1049-1050	cg27807001	170	ACCGACTTTAGC CTTAACCTTGAG AT[G]CCGCCCTTA CCTTTGACATCG ACTTC	T	G				SILENT- NONCODI NG			
1051-1052	cg27807001	217	CTTCTACTGTCC TCGAAGTCGAAG A[G/A]AGCCGAG AGTTGGGGACAT CGGGGG	G	A				SILENT- NONCODI NG			
1053-1054	cg27807001	223	CTGTCTCTGAAG TCGAAGAGAGCC G[A/G]GAGTTGG GGACATCGGGG GCACTGC	A	G				SILENT- NONCODI NG			
1055-1056	cg27807001	242	GAGCCGAGAGTT GGGGACATCGG GG[G/gap]CACTG CCAAGATGCATG ACCGCCAG	G	-				SILENT- NONCODI NG			
1057-1058	cg27807001	277	GATGCATGACCG CCAGCGCACGTT C[C/T]CGAGCGT ACTTGTCAAGT TGTCCC	C	T				SILENT- NONCODI NG			

1059-1060	cg27807001	296	ACGTTCCCGAGC GTACTTGTTCAA GTCJGTGTCGGA TCGCGCGAGC GGCGGC	T	C				SILENT- NONCODI NG			
1061-1062	cg27825769	55	CTGTATCTTTAA CAGTAAAGCGT AIGCJGAAGCAC ATAGCCCCAATG TATTTA	G	C				SILENT- NONCODI NG			
1063-1064	cg27826716	158	CGTTGGTTGAGA AGGATGTCACCA AIC/TTGAGGTAT CGAGATCTCATG CCCCAC	C	T				SILENT- NONCODI NG			
1065-1066	cg27831266	55	TAAGGCTGTGGA GGAGCCAGATG GGIG/AJACTAGC CTCTGGACTTCT GCTTAGG	G	A				SILENT- NONCODI NG			
1067-1068	cg27831595	128	GGCCTCAGGG TAAGCTGGAGTT GCIG/gapJGGCCA CCGCCCCAGGA GTTGAGTGG	G	-				SILENT- NONCODI NG			
1069-1070	cg27834324	75	CATGGAGTCACT CAGATCACGCAT CIG/AJAGGAAAG CACTAAGGTAAC ACCCAG	G	A				SILENT- NONCODI NG			
1071-1072	cg27835768	90	CAGCTGTTGTGT GCCTGGCAGCG CTIG/gapJCTTTC AGCCCCATTTCAT TTCCAACT	G	-				SILENT- NONCODI NG			

1073-1074	cg27837446	438	TGTTTGCTATTT ATTTTTGAGAC[A/G]GGTCTCATT CTGCCATTACGG CTGA	A	G				SILENT- NONCODI NG		
1075-1076	cg27837446	543	TGTACGTGTGTG TGTGTGTGTGTG T[G/gap]TAAGTG TCTGTGTGTACG TGTAAGT	G	.				SILENT- NONCODI NG		
1077-1078	cg27838870	240	CGACAACTCGAT CGCACCAGGC GC[G/A]ACACCC GCCTGCCCCGTA CTTTCCC	G	A				SILENT- NONCODI NG		
1079-1080	cg27838870	283	ACTTTCCCGCCA TCCCAAGTCACC G[G/T]GTGTGCG CTCGTCAGCATC GCCTCA	G	T				SILENT- NONCODI NG		
1081-1082	cg27840665	274	TGATACGAAGGA TGCGCAGATTGT T[G/A]GTCTTACC CGGAATATCCAT CGGGG	G	A				SILENT- NONCODI NG		
1083-1084	cg27840665	289	GCAGATTGTTGG TCTTACCCGGAA T[AG]TCCATCGG GGAACCGGACA ACACGA	A	G				SILENT- NONCODI NG		
1085-1086	cg27840665	330	GACAACACGACG ACGCGGTCACC GA[C/T]CGGCAC GAAACCCTTGTC GCGCAGG	C	T				SILENT- NONCODI NG		

1087-1088	cg27842663	37	CTAGCCTGGAGT CAGGAGACAGC AA[<i>gap</i>]/A]GAGTA GGGGCTGAGGT TGTGGGGCC	-	A				SILENT- NONCODI NG		
1089-1090	cg27842663	37	CTAGCCTGGAGT CAGGAGACAGC AA[<i>gap</i>]/A]GAGTA GGGGCTGAGGT TGTGGGGCC	-	A				SILENT- NONCODI NG		
1091-1092	cg27842663	53	GAGACAGCAAGA GTAGGGGCTGA GGT/G]TGTGGG GCCCAGGGTCC CAGTGTAG	T	G				SILENT- NONCODI NG		
1093-1094	cg27843594	522	AGGTACAGCTCA GGGAAGGGAGC AG[C/ <i>gap</i>]/CCCTT GCTCACGGTCCT TTCTGGCA	C	-				SILENT- NONCODI NG		
1095-1096	cg27843890	222	CGTGGTTGACGA TCTCGCCGGTG GA[G/A]GCGTCC TTGACGACGATC TGGCCAC	G	A				SILENT- NONCODI NG		
1097-1098	cg27843890	38	TGGACTTCGTGG GTCTGCGGTACG A[C/T]GAAGGC TCAACATTGCCG GTGGCA	C	T				SILENT- NONCODI NG		
1099-1100	cg27843890	62	ACGAAGGGCTCA ACATTGCCGGTG G[C/ <i>gap</i>]/ATCGAT GATGAGTTTGCT CGCCTGG	C	-				SILENT- NONCODI NG		

1101- 1102	cg27843890	96	TGAGTTTGCTCG CCTGGGCAACAC CTT/CJAGCAGCAA TGGCATCGATAG TCCCT	T	C				SILENT- NONCODI NG			
1103- 1104	cg27844015	234	GGTAATGCGGAA CGCACGTGCCT GC[G/A]TTCAGAC TCCATTATCTTC ACCGT	G	A				SILENT- NONCODI NG			
1105- 1106	cg27845127	104	GAGCGTGCGCC ATGATGCCGCGA CT[G/C]ACACCAC CTGCGGTCCAG CCCCAAA	G	C				SILENT- NONCODI NG			
1107- 1108	cg27845127	151	AAATCGGGTGC TTCTTCATACCA A[T/C]CACGAGG AGGTCAACGTTG CCCGAG	T	C				SILENT- NONCODI NG			
1109- 1110	cg27845127	168	CATACCAATCAC GAGGAGGTCAA CG[T/C]TGCCCG AGAGGTCGACTA AGCGTC	T	C				SILENT- NONCODI NG			
1111- 1112	cg27845127	188	CAACGTTGCCCG AGAGGTCGACTA A[G/A]GCGTCGA CGGGTTCTCCG GACAGCA	G	A				SILENT- NONCODI NG			
1113- 1114	cg27845127	200	AGAGGTCGACTA AGGCGTCGACG GGT/CJTCTCCG GACAGCACGCG GGTCICGA	T	C				SILENT- NONCODI NG			
1115- 1116	cg27845127	22	ACGCGTCTGAA GCCGCCGAC[G/ A]CGACGAGAAC AGCAGGCCCAGC AGCT	G	A				SILENT- NONCODI NG			

1117- 1118	cg27845127	224	GTCTCCGGACA GCACGGGGTC TC[G/T]ACCTCGA CATGGGGATGCT TATTAG	G	T				SILENT- NONCODI NG			
1119- 1120	cg27845127	244	GTCTCGACCTCG ACATGGGGATGC TT[C/T]ATTAGCGA GCGGCTTGACG ACCTCG	T	C				SILENT- NONCODI NG			
1121- 1122	cg27845127	248	CGACCTCGACAT GGGGATGCTTAT T[A/G]GCGAGCG GCTTGACGACCT CGTTGA	A	G				SILENT- NONCODI NG			
1123- 1124	cg27845127	263	GATGCTTATTAG CGAGCGGCTTG AC[G/A]ACCTCGT TGAGTCGTTTGA GGGCT	G	A				SILENT- NONCODI NG			
1125- 1126	cg27845621	23	GGATCCTGTGCC AGCCGAGGAGG[gap/C]TCCCTCCC AGGCTCTCTCAA GGGTC	-	C				SILENT- NONCODI NG			
1127- 1128	cg27845788	28	GCGTTTGGTAA TGAGCCTGAGCA G[T/C]CATGCTG GACCGCCCCAGG CTCCCAG	T	C				SILENT- NONCODI NG			
1129- 1130	cg27846188	112	TTCAAATCCAGT TCCTCCACAGCA A[C/T]CAGCCCAT AGTTGTTCTGTG TTCTT	C	T				SILENT- NONCODI NG			
1131- 1132	cg27846188	126	TTCCACAGCAAC CAGCCCATAGTT GT[C/T]CTGTGT CTTCCACAGCTG TTTAC	T	C				SILENT- NONCODI NG			

1133-1134	cg27846188	156	TGTTCTTCCACA GCTGTTTACGGT A[G/A]CCTCCTAG CCACTCTCCTCA GCAAG	G	A			SILENT- NONCODI NG		
1135-1136	cg27846188	278	TACCTCACITCC TCCACCCGCTCTT C[A/G]GCCCTTT GATGTCCTCTCA GAGAA	A	G			SILENT- NONCODI NG		
1137-1138	cg27846188	91	ACTAGATCCACT GTGCTTTCTTTC A[A/G]ATCCAGTT CTCCACAGCAA CCAGC	A	G			SILENT- NONCODI NG		
1139-1140	cg27847752	21	GCGGCCCTCC CTGGGTGAC[A/G JGGCTGTACTTCT TTCACAAAAGGA C	A	G			SILENT- NONCODI NG		
1141-1142	cg27847752	259	TGAGGCCATTCT TGCACCTGCTATA A[A/C]GAAATACC CGAGACTGGGTA ATTAA	A	C			SILENT- NONCODI NG		
1143-1144	cg27850121	29	CGTCGCCGAAAA GCCAGGCCCGG AG[G/gap]TGCCT AAGTCAGGGACC GAGACGCA	G	-			SILENT- NONCODI NG		
1145-1146	cg27922967	72	CGCGTGGTACCA GGGAAGGGGAC AG[G/A]ATTCTT GCACITTTACCC CITTCT	G	A			SILENT- NONCODI NG		

1147- 1148	cg27926321	105	CATCACCTCCCT GACTGCCTCTCC TIA/CJCCACCTCC CATCACCTCCCT GACTG	A	C			SILENT- NONCODI NG		
1149- 1150	cg27926378	261	ATGGGATGTTCT GTTTTGCTGT A/A/GJAGGGAAA GGGATCATTTAT GTTCAA	A	G			SILENT- NONCODI NG		
1151- 1152	cg27926378	327	TTAGGGAAGTAA TTAAGAGGCTGT G/C/gap/CCTCTG TCACATCCAAGT TTCGGC	C	-			SILENT- NONCODI NG		
1153- 1154	cg27926378	329	AGGGAAGTAATT AAGAGGCTGTGC C/C/gap/JCTGTG ACATCCAAGTTT CTGCCCCA	C	-			SILENT- NONCODI NG		
1155- 1156	cg27926927	141	ATCTTAAGACCC TCGATGGATGT G/A/TJGCGGC CGCCCGGTGCG CGAAGG	A	T			SILENT- NONCODI NG		
1157- 1158	cg27928117	71	GTGGTGGAGGT CGGGGCATGGG GTG[C/gap]CCCA GCCATGTTTCAGA TTCCTGTAG	C	-			SILENT- NONCODI NG		
1159- 1160	cg27928408	609	ACCTTGGGGAG GGCGGGTAGAG GCC[G/A]AGGAA TCTGCAGGCGCA GAGGACAG	G	A			SILENT- NONCODI NG		

1161- 1162	cg27930889	298	ACAATTAGATGT ATGGTTAGTCTG A[CT]GATGTGAT AAGAAACCTCC CCAGC	C	T			SILENT- NONCODI NG			
1163- 1164	cg27931448	157	AACCACACCTT CGCCGCCCCG CG[C]AGCCAGC CAGCCCGTACG CGCTCACC	C	A			SILENT- NONCODI NG			
1165- 1166	cg27931448	186	AGCCAGCCCGTA CGCGCTACCCA C[AG]GGAACCC CCTCGTCCAGTC CCTCAC	A	G			SILENT- NONCODI NG			
1167- 1168	cg27931448	193	CCGTACGGCGTC ACCCACAGGAAC C[C]CCTCGTCC AGTCCCTCACTA CCCCCT	C	T			SILENT- NONCODI NG			
1169- 1170	cg27931448	199	GGCTCAGCCACT AGGAACCCCTC G[T]C]CCAGTCC CTCACTACCCCT CAGGCC	T	C			SILENT- NONCODI NG			
1171- 1172	cg27931448	205	ACCCACAGGAAC CCCCTCGTCCAG T[C]CCTCACTA CCCCTCAGGCC CTGTCA	C	T			SILENT- NONCODI NG			
1173- 1174	cg27931448	207	CCACAGGAAGCC CCTCGTCCAGTC C[C]C]CACTACC CCTCAGGCCCTG TCAAG	C	T			SILENT- NONCODI NG			

1175- 1176	cg27931448	222	CGTCCAGTCCCT CACTACCCCTCA G[G/A]CCCTGTC AAGCCGGCGCC GGCGCAG	G	A			SILENT- NONCODI NG			
1177- 1178	cg27933823	275	CGTTAACCTCCC ACCTCTGCAATC TT[A]GCCCCGACA CCTAGATACCTG CGTGC	T	A			SILENT- NONCODI NG			
1179- 1180	cg27955069	108	AAAAAAGAAAA AAGAAAAA A[A/gap]GAATGC AGTCTGTCCATT TTTGTGC	A	-			SILENT- NONCODI NG			
1181- 1182	cg27957329	398	GCCGCGGGCTG AGATTTTCGTCC TG[C/gap]CCCCC TCCCTGCCGCCCC AGCGCCTA	C	-			SILENT- NONCODI NG			
1183- 1184	cg27958374	94	GATTGGCTGTAC AGGATAGCGAAT G[C/gap]TGTGGT TGGAGGGCACA GTCTTCCC	C	-			SILENT- NONCODI NG			
1185- 1186	cg27958800	121	AGTGGCAGGAG AGAGGAGATGG GGG[C/T]GTGGC AGTGAGCGATGA GGTCAATC	C	T			SILENT- NONCODI NG			
1187- 1188	cg27958800	136	GAGATGGGGGC GTGGCAGTGAG CGAT[C]GAGGT CAATCTGACGAG GCCTGTGG	T	C			SILENT- NONCODI NG			

1189-1190	cg27958800	201	TTTGGCTTCAGC TAAGGGAGATGG C[C/A]GCCACTGT GGAGTTTTGGGG CAGAG	C	A				SILENT- NONCODI NG		
1191-1192	cg27958800	225	CCGCCACTGTG GAGTTTTGGGC AG[A/G]GGGACA TGCTCTGACTTC CCTTTAA	A	G				SILENT- NONCODI NG		
1193-1194	cg27958800	260	TCTGACTTCCCT TTAAATGGGTCA T[C/G]ATGGCTCC TACGCTGAGGGA CTACA	C	G				SILENT- NONCODI NG		
1195-1196	cg27958800	285	CATGGCTCCTAC GCTGAGGGACTA C[A/gap]GGGGAG AAGGGGAGAAA GACCCAGTT	A	-				SILENT- NONCODI NG		
1197-1198	cg27958800	91	CTTGAGCGCGC CAGGGACAGTG GAG[A/G]CCAGA GTGGCAGGAGA GAGGAGATG	A	G				SILENT- NONCODI NG		
1199-1200	cg27961578	351	TATGGAAGAGAG AGAGAGAGAGA GA[G/gap]TTTTT TTTCACATCTGA ATTGATG	G	-				SILENT- NONCODI NG		
1201-1202	cg27962034	156	GCCCCCCCGAC CAAGCGTCGGA CGC[G/gap]GCCC GGCGCCGAGCC ATGGAGCCTG	G	-				SILENT- NONCODI NG		

1203- 1204	cg27963505	62	CCCTTCGAGGCCA CGGGAAGACCT CC[A/G]ACCCCG CTGACAAATGCTG GGCCCTC	A	G			SILENT- NONCODI NG		
1205- 1206	cg28098037	253	GAATGGAGATAA AAGGGAATAACA AATCTCAACTAG AAGGAGAAGAAG TCCTG	T	C			SILENT- NONCODI NG		
1207- 1208	cg28104192	300	TAACTACCGAGA GTGGGTATTTAT CTTAAAGAGAGAT AGAGGCTTTTGG AGCAG	T	A			SILENT- NONCODI NG		
1209- 1210	cg28117507	52	AGGCGGAAGCT GCTCCGGTGTG TTG[A/G]CCTCAGT GTGCCGATGCC GGCGTCA	G	A			SILENT- NONCODI NG		
1211- 1212	cg28117507	82	AGTGTGCCGATG CCGGCGTCAAG CCT[C/T]TGTGG AGGGTCCAGACT GGGGT	T	C			SILENT- NONCODI NG		
1213- 1214	cg28117507	94	CCGGCGTCAAG CCTTGTGGAG GGT[C/G]CCAGAC TGGGGTTTATTG GATCGAC	T	C			SILENT- NONCODI NG		
1215- 1216	cg28350841	107	GGGACTTGGACA GGCACGGGCCC TG[G/gap]CATGG CGGGCCAGGTC CACCTCGGC	G	-			SILENT- NONCODI NG		

1217- 1218	cg28375854	192	GCGGGGGGCCCA GCCATCTTGCAC TTA/GATGGATG GCACACGAGGC CAGCTGC	A	G				SILENT- NONCODI NG		
1219- 1220	cg28376296	283	AACGGAGTAAGC GATAAAGAGTCC GTT/gapJAGATGA ACACCGCGCCG CTGAGGAT	T	-				SILENT- NONCODI NG		
1221- 1222	cg28388611	181	AGATAGATAGAT AGATAGATAGAT GTA/gapJTAGATA GATAGATAGATA GATAGAT	A	-				SILENT- NONCODI NG		
1223- 1224	cg28388611	183	ATAGATAGATAG ATAGATAGATGA TAA/gapJGATAGA TAGATAGATAGA TAGATAG	A	-				SILENT- NONCODI NG		
1225- 1226	cg28389525	124	TCGACCTGGAG TCACGAAGCGTT TGAJGGAGTGG ATCGGAAAGTG TACATA	G	A				SILENT- NONCODI NG		
1227- 1228	cg28389525	136	TCACGAAGCGTT TGGGAGTGGAT GC[G]A/GAAAGT GTACATAAAACC AATCCGC	G	A				SILENT- NONCODI NG		
1229- 1230	cg28389525	213	TTCGGTCAAGAG GGGCGGTTCCG AA[A/G]TCGTCCC GCGTATGATCTC ATTGTA	A	G				SILENT- NONCODI NG		
1231- 1232	cg28389525	49	TAAATTTCAAAG ATCCCAAGGACC ATT/CJGAGCGTTT CATGAAGCTCGT TGAGC	T	C				SILENT- NONCODI NG		

1233-1234	cg28389807	127	ACCTTCTGTATG CTGGCATTGCAG A/C/TCCAGCAAG GAGCCAAACGAA TGAAA	C	T			SILENT- NONCODI NG		
1235-1236	cg28396311	373	GCACGAGGCCT GACACTTTGCGG GA[G/gap]CCCTG GAGGAAACAGGT GGTTGCTG	G	-			SILENT- NONCODI NG		
1237-1238	cg28397512	123	TTTGCTGTACG CAACCATAGCCA C[G/A]GGTATACC AGCTTCTGCATT TTCTG	G	A			SILENT- NONCODI NG		
1239-1240	cg28397512	321	GCCTCCACCTGT GCTAGGTGGC CC[C/gap]TCTGG GTTCTAAGGCAT CTCTGTAT	C	-			SILENT- NONCODI NG		
1241-1242	cg28399769	190	GGGTCCAGGGA GGAGAGCGCGG CGC[G/gap]GGCG GCTGAGCGCGA AGAGGGAGTG	G	-			SILENT- NONCODI NG		
1243-1244	cg28453626	458	GAGTGGTTCACC TTTTACTTGGTC A[A/G]TCAGGGG GTTTGTGTTCCC AGGAAC	A	G			SILENT- NONCODI NG		
1245-1246	cg28458642	205	GGAAGGTCAGA CCCCCGTCACC CGC[G/A]ACGA AATGGCCTCGGA TGCATCAG	G	A			SILENT- NONCODI NG		

1247-1248	cg28464065	198	TGTCACGAAAT ACACCCCAAACC C[G/A]AAGCCTTC TCTCCACCAAGT CCAAG	G	A			SILENT- NONCODI NG		
1249-1250	cg28464080	101	GTGGATGGCAG CCAGAGAGACTG CT[G/C]AGGTTCT GGATGTTAGGGC CTTGAT	G	C			SILENT- NONCODI NG		
1251-1252	cg28464080	285	GGGACAGCCG AGGGCGAGTGG TCT[T/C]GGAAGC GTGCCATGTGCA GGACACA	T	C			SILENT- NONCODI NG		
1253-1254	cg28473092	175	TGGCGAGGGTC AGCAGTCTTCTC GG[C/T]GTCGTC AGGTCGAGCATG GTACTCG	C	T			SILENT- NONCODI NG		
1255-1256	cg28473092	239	GACGGTTAAGGA TTTGGCAGCTAA T[A/G]ACGATCG GAGCGTCACCCCT CGAGCA	A	G			SILENT- NONCODI NG		
1257-1258	cg28473092	248	GGATTGCGAGC TAATAACGATCG G[A/G]GCGTCAC CCTCGAGCATCG TCACCT	A	G			SILENT- NONCODI NG		
1259-1260	cg28473092	254	GCGAGCTAATAA CGATCGGAGCG TC[A/G]CCCTCGA GCATCGTCACCT CGATGC	A	G			SILENT- NONCODI NG		
1261-1262	cg28473092	299	CGATGCTAATTA GAGCCATGTGCC G[A/G]TGAGTGA AGGAGACCATCC GCGAGG	A	G			SILENT- NONCODI NG		

1263-1264	cg28473092	367	TTGCCCGCCGG GGTGGCCCATAC CA[A/G]CTCCCG ACACAGGACACC CTCGCGG	A	G				SILENT- NONCODI NG			
1265-1266	cg28473092	431	GTTTATACGACT GGATCTCGTTGA T[A/G]CTGAGCA GGAGTGGTTCGT CATCCA	A	G				SILENT- NONCODI NG			
1267-1268	cg28473115	22	TCATGAAATGTT TGTTGGTAA[G/A] GTACCATTTAAC CTTTTTTCCAAT	G	A				SILENT- NONCODI NG			
1269-1270	cg28785423	228	GGGTTTAGCTAG CATGTAGCAAGC C[C/T]TTAATGAC TGCAGCTATTAT CATAA	C	T				SILENT- NONCODI NG			
1271-1272	cg28785423	241	ATGTAGCAAGCC CTTAATGACTGC A[G/A]CTATTATC ATAATTAGCTCT GTATG	G	A				SILENT- NONCODI NG			
1273-1274	cg28785423	267	CTATTATCATAAT TAGCTCTGTATG[A/gap]CTTTTTAC ATTCATCAGATC CCTTA	A	-				SILENT- NONCODI NG			
1275-1276	cg28786600	152	GGATGCACCCAC GCTGGCGCCCC AG[C/gap]GGCCT CTAACCGCGGCC CCAGCCCCA	C	-				SILENT- NONCODI NG			

1277- 1278	cg28790405	129	GGTATGCCTCAC TACCCGGGGCG TA[G/gap]CCGAC GCGACTTCGAG GAAACGTG	G	-				SILENT- NONCODI NG			
1279- 1280	cg28814812	86	TAATAACAGCAG AGTTACCCTAAG A[C/T]ATACAATC TGCTGCGGTAT GCTAA	C	T				SILENT- NONCODI NG			
1281- 1282	cg28821175	225	ACTATTGCCAAT ATTTAAACACT [A/T]ATTTGCCCT TAAACTAGAGAT TTAA	A	T				SILENT- NONCODI NG			
1283- 1284	cg28955364	101	CAATAACCGCGG TGGGTGTGCAG CA[G/A]GAAGTTT TCCAGTACCTGA TAGCCG	G	A				SILENT- NONCODI NG			
1285- 1286	cg28955364	117	TGTGCAGCAGGA AGTTTTCCAGTA C[C/T]TGATAGCC GTCACCTTCGGG TGCGT	C	T				SILENT- NONCODI NG			
1287- 1288	cg28955364	147	AGCCGTCACCTT CGGGTGCGTTG AT[C/G]TCGTAAT GGAATCGAGCG CTGTCAC	C	G				SILENT- NONCODI NG			
1289- 1290	cg28955364	203	CAGTTTTGAATC GCGATGGCCTTG G[C/T]TACGGGG GTAGATTTCCCC TTGATA	C	T				SILENT- NONCODI NG			

1291-1292	cg28955364	243	TCCCCTTGATAA TTCGGTTAGTTA A/C/G/TCCCCCTAT GTCGGATGGAAC GTGG	C	G				SILENT- NONCODI NG		
1293-1294	cg28955364	248	TTGATAATTCGG TTAGTTAACTCC C/C/T/TATGTCGG ATGGAACGTTGG CAGGG	C	T				SILENT- NONCODI NG		
1295-1296	cg28955364	253	AATTCGGTTAGT TAACTCCCCTAT G/T/C/CGGATGG AACGTTGGCAGG GACTTC	T	C				SILENT- NONCODI NG		
1297-1298	cg28955364	267	ACTCCCCTATGT CGGATGGAACGT T/G/A/GCAGGGA CTTCGGGTGTACA CCGAGT	G	A				SILENT- NONCODI NG		
1299-1300	cg28955364	296	GGGACTTCGGT GTACACCGAGTT AT/G/T/TGGGGT GCCGGCTTTCCG GTTATCG	G	T				SILENT- NONCODI NG		
1301-1302	cg28955364	309	ACACCGAGTTAT GTGGGGTGCCG GCT/C/TTCGCCGT TATCGAAGGTTA CTGGAT	T	C				SILENT- NONCODI NG		
1303-1304	cg28955364	48	ACGGAATACCTT CAAGTCGTGCCA T/G/A/JAGTGCCAT TGACGCCGCGA AATGGA	G	A				SILENT- NONCODI NG		
1305-1306	cg28955364	84	ACGCCGCGAAAT GGATGCAATAAC C/G/A/JCGGTGGG TGTGCAGCAGGA AGTTTT	G	A				SILENT- NONCODI NG		

1307-1308	cg28955364	94	ATGGATGCAATA ACCGCGGTGGG TG[T/C]GCAGCA GGAAGTTTCCA GTACCTG	T	C				SILENT- NONCODI NG		
1309-1310	cg28961882	39	AACAGAATGCAA ACAATCAAAAC A[T/gap]AGTCCA TTTAAACTATCTG GGCGAC	T	-				SILENT- NONCODI NG		
1311-1312	cg28961882	446	TGGCAGTTCTGC TGAGATTTTTTT [gap/T]AGGACTT TCCTGAAGCTTA GCITCA	-	T				SILENT- NONCODI NG		
1313-1314	cg28961882	61	ACATAGTCCATT TAAACTATCTGG G[C/T]GACAAAT GGGCACTTAATT TTACT	C	T				SILENT- NONCODI NG		
1315-1316	cg28970326	212	CATGGCCTGTCA TGCGGTAGTCTT C[C/T]ACGTCGTA AAGTATGAGACA ATCCA	C	T				SILENT- NONCODI NG		
1317-1318	cg28970326	357	GGGTCCATGAG GAGTTCGTCCAA GG[gap/G]TTCTGA ACTCATTACCGT CGAATACG	-	G				SILENT- NONCODI NG		
1319-1320	cg28972181	449	AGCTGGTTCTCT CCGAAATGCATT T[G/A]GGTGCAG CGTCGGGTCAAT ACGTCC	G	A				SILENT- NONCODI NG		
1321-1322	cg28972181	464	AAATGCATTGG GTGCAGCGTCG GGT/G[C]ATTACG TCCCGGGGGTA GAGCTAC	T	G				SILENT- NONCODI NG		

1323-1324	cg28972181	500	CGGGGGTAGAG CTACTGGATGCT TG[C/A]GGGCC GTATCGGGTACC AACAGCA	C	A				SILENT- NONCODI NG			
1325-1326	cg28986449	50	AGGGAAGAGCA AGTTGGTCTGGA AC[A/G]CAAAAAG GGCCGGGATCT CCTTGG	A	G				SILENT- NONCODI NG			
1327-1328	cg29004129	65	CGCAAGATTTCG AGGCAACTCGGT AT[C]CACTCACT GTGCTTGACCCAC GTGG	T	C				SILENT- NONCODI NG			
1329-1330	cg29012565	126	CCCATTCGGAAA ATCAATCCGGGG G[C/T]GTCGGCT GGTTAGTCACG GCGGGC	C	T				SILENT- NONCODI NG			
1331-1332	cg29012565	174	GGCAAAGCCAC GGTGTCCCTCC TG[A/G]ATGAGCT AGATTACCCTAC CCTACC	A	G				SILENT- NONCODI NG			
1333-1334	cg29141731	508	ATAGGGGGGATA TTTTGGGTGGT G[G/T]TAGTGGT GGTCTGTTTCC AGATAT	G	T				SILENT- NONCODI NG			
1335-1336	cg29141731	569	AATATTCAGTAA GCTTTTGAAGC T[C/A]CTTACACA TCCGTAAACTT CTCAG	C	A				SILENT- NONCODI NG			
1337-1338	cg29144273	410	ATGGGATAAGAT GTAAGTTTTTAAT [A/G]CTAGCAATG TACACTACTCTTT TTT	A	G				SILENT- NONCODI NG			

1339-1340	cg29144339	63	AAGCAAAACCCA TCGGGGGGGGG GG[gap]GJACATC TACATGCCATCT TTGGTGCT	.	G				SILENT- NONCODI NG		
1341-1342	cg29195033	59	CCGCTCATAGTG TCGTCAGTCAGA A[T/C]CTTCATCA TTGCCGATACGT GATCG	T	C				SILENT- NONCODI NG		
1343-1344	cg29202844	107	CGGCCACCCCA CTCTAGGCCCTCC CT[G/A]TGGTTCA GCATCCTCAACC CCGCTT	G	A				SILENT- NONCODI NG		
1345-1346	cg29207528	97	CGGGTCAGGGG CGTTCGGCGCG CCA[G/gap]CTGG CACAACTTCGCG ACCGGCGGAC	G	-				SILENT- NONCODI NG		
1347-1348	cg29207528	156	CTTCGACGCCAA CGAGCTTGCCGT A[G/A]CTCCTGAT ACTGACACCCGTC ATCCA	G	A				SILENT- NONCODI NG		
1349-1350	cg29207528	189	TACTGACACCCGT CATCCAGGGAGT C[G/gap]GGCCCCG CCCTAGCCCTCC TCGATCC	G	-				SILENT- NONCODI NG		
1351-1352	cg29207528	308	CCTCGTCGACAC ATGCCGATAACC C[G/A]ACAGCCC AGGCATGGCGC GATTTCG	G	A				SILENT- NONCODI NG		

1353- 1354	cg29207528	70	CTGCGCGTGGC AGATGCCGCACA GG[C/gap]ACGGG TCAGGGGCGTTC GCGGCGCC	C	-				SILENT- NONCODI NG			
1355- 1356	cg29210581	244	TTTTCTGAGTT ATGGAAGGAATG [G/A]TAATTGGGG AATTCAGGCTTA AAAT	G	A				SILENT- NONCODI NG			
1357- 1358	cg29216983	137	GCATTCTGTGAG GCTACCGCAGG CT[C/T]TGGCGTA AAGCAGTGGAG CCAGGTC	C	T				SILENT- NONCODI NG			
1359- 1360	cg29217243	188	GGCGCGGGCT CCATCCAAATCG AT[C/T]TGGGCAT CCGCCCTGTCA CCGCAA	C	T				SILENT- NONCODI NG			
1361- 1362	cg29217243	305	CAGCACCATTA CGACGAGCCGA GC[A/G]CCGTCC AGATAGGCCCC GCGATCCC	A	G				SILENT- NONCODI NG			
1363- 1364	cg29217243	323	GCCGAGCACCG TCCAGATAGGCC CG[G/A]CGATCC CATGCTCCGCAG CCACTGA	G	A				SILENT- NONCODI NG			
1365- 1366	cg29217243	374	TTCCTAGATCCG CCCAACCGCGA CG[G/T]CCAGCG TCCTCAATGAGG GTTCTCG	G	T				SILENT- NONCODI NG			

1367- 1368	cg29217243	392	CGCGACGGCCA GCGTCCTCAATG AG[G/A]GTTCTCG GCCCCGGCTGTCT CTACTA	G	A			SILENT- NONCODI NG		
1369- 1370	cg29234950	66	CAACCCAGGGG CCCCTCTCCGAG GGT[C/J]ACCCCA CAGGCCACACG GTGGCGAC	T	C			SILENT- NONCODI NG		
1371- 1372	cg29237731	36	CTCAATCCTGAC AGATACCGATCA TTA/GJAGGCAATG GCACTCCAGGA GTATT	A	G			SILENT- NONCODI NG		
1373- 1374	cg29237731	39	AATCCTGACAGA TACCGATCATAA G[G/C]CAATGGC ACTCCAGGAGTA TTTCCT	G	C			SILENT- NONCODI NG		
1375- 1376	cg29239003	414	GGATTCCACTTT CCCTGTCCCCTA C[C/T]TCCCCAAA CTCTTGCAAGAA AATAA	C	T			SILENT- NONCODI NG		
1377- 1378	cg29250853	77	CGTACGAGATCA CGTTCCTCACCC A[G/T]CTCCCCAA AGACCTCACGTG CAGCG	G	T			SILENT- NONCODI NG		
1379- 1380	cg29255997	226	AAACAAGGAAGA GTAGGATGGAAT C[G/gap]GAATAA AACAGTGAAGA ACATTAT	G	-			SILENT- NONCODI NG		

1381- 1382	cg29255997	240	AGGATGGAATCGA GAATAAACAGT G/A/GAAGAACAT TATTCITTTGTACC GTGA	G			SILENT- NONCODI NG		
1383- 1384	cg29256466	459	TGAATATAAGGC TAGATAATGGAG C/G/AJTTTGTGAT CCCTTGICTATT CTCAG	A			SILENT- NONCODI NG		
1385- 1386	cg29260975	109	CTGCAATGAGCT GTGACCCACGCCA C/T/CJGCACTCCA GCCTGGGCGAC AGAGCA	C			SILENT- NONCODI NG		
1387- 1388	cg29260975	140	CCAGCCTGGGC GACAGAGCAAGA CC/A/GJTGATATT TCAAGAAAAGTC CTTGAG	G			SILENT- NONCODI NG		
1389- 1390	cg29264501	280	CTCCCCAACCCA CTCCCCAGTAAC A/G/CJAGGGTTTT CCCCGATTCTCA CAGTG	C			SILENT- NONCODI NG		
1391- 1392	cg29337682	533	GTGGTGCATGCC TGTAATCCCAGC A/C/AJTTGGGAG GCTGAGGCAGG AGGATC	A			SILENT- NONCODI NG		
1393- 1394	cg29345077	171	ACTCCCGACCTC AGGTGATCCGCC C/A/GJCTCGGC CTCCCCAAAGTGC TGGGAT	G			SILENT- NONCODI NG		
1395- 1396	cg29345273	97	CTTATGGCACGG GGGCTGCAGCC TG/G/CJCTCCTC CTCCAGGTGGG ATGCCTC	C			SILENT- NONCODI NG		

1397- 1398	cg29345769	181	CTGTATTAAGAC TTAACTCCTGC C/G/A/CACCTGG AGTAATAAACTT GTGGGA	G	A			SILENT- NONCODI NG		
1399- 1400	cg29346973	70	AGTTATCTCATA ATTAAAAA [A/gap]CTAGCTC GTTAGAATTAGA ATCTAA	A	-			SILENT- NONCODI NG		
1401- 1402	cg29348101	147	CCGCTCAGGCT GCTGCTGCGGG CGC/C/T/GTGTG GTACTCCGCCGA AGCGGATA	C	T			SILENT- NONCODI NG		
1403- 1404	cg29348101	183	CCGCCGAAGGC GATAAGTGGAAG GT/C/T/GATACCA ACGGTGACAAGA GCAAAG	C	T			SILENT- NONCODI NG		
1405- 1406	cg29348101	195	ATAAGTGAAGG TCGATACCAACG G/T/C/GACAAGA GCAAAGTTGTTG CCGATT	T	C			SILENT- NONCODI NG		
1407- 1408	cg29348101	262	CGACGACAAGA GCGCTGTCACTG AC/C/G/CCCGTT GGAGCGACGCG T	C	G			SILENT- NONCODI NG		
1409- 1410	cg29348101	66	TGCTTTCCTCCG CCAAGAAGGCTG C/C/T/GCCAAGG GCAAAGTACATCC TCGGAT	C	T			SILENT- NONCODI NG		
1411- 1412	cg29348101	69	TTTCCTCCGCCA AGAAGGCTGCC GC/C/T/AAGGGC AAGTACATCCTC GGATTG	C	T			SILENT- NONCODI NG		

1413-1414	cg29348230	70	TCAGAGGGTGA GAAAGCCCAGA GCAIT/gapJTTTAC ATGTTTAGGATT TTGACTTT	T	-				SILENT- NONCODI NG		
1415-1416	cg29348328	110	TGCATTACCAAG AGCTGACGATCT CTTCJGGAGGAT CGAATGCCAGTC GGGCAG	T	C				SILENT- NONCODI NG		
1417-1418	cg29348328	131	TCTCTGGAGGAT CGAATGCCAGTC G[G/A]GCAGACG TTCACCGGGCG GTCGACA	G	A				SILENT- NONCODI NG		
1419-1420	cg29348328	181	ATGCTCGGACG GGGAAATATCGA CG[G/A]GACCCC CATTGTCACCTCA CACTTTT	G	A				SILENT- NONCODI NG		
1421-1422	cg29348328	182	TGCTCGGACGG GGAAATATCGAC GG[G/A]ACCCCC ATTGTCACCTCAC ACTTTTG	G	A				SILENT- NONCODI NG		
1423-1424	cg29348328	227	CTTTGGCCTGT CCCAGTGGACC GA[G/A]GCTGTT GACGCCGTGCG CGGTCACG	G	A				SILENT- NONCODI NG		
1425-1426	cg29348328	253	GCTGTTGACGCC GTGCGCGGTCA CG[C/T]CGGCGT CAAGATCGCTAT CGATCCC	C	T				SILENT- NONCODI NG		
1427-1428	cg29348328	257	TTGACGCCGTGC GCGGTCACGCC GG[C/T]GTCAAG ATCGCTATCGAT CCCCGCC	C	T				SILENT- NONCODI NG		

1429-1430	cg29348328	47	GACGCGTGAGTT GGTTTGCTGGTT TTTCJCCCAAGG GATCAACGACGA CCATCA	T	C				SILENT- NONCODI NG		
1431-1432	cg29348397	76	TTATGTTATTTAT AAAACGACCAAG [G/A]AAATGAATG TAATTTGGTCTT CATA	G	A				SILENT- NONCODI NG		
1433-1434	cg29348993	225	GTTTGTTTGTTTT AACTTTTTTTTTT /gap]TCATTCTCG CTGTAGATAGCC TGAA	T	-				SILENT- NONCODI NG		
1435-1436	cg29348993	226	TTTGTTTGTTTTA ACTTTTTTTTTT /gap]CATTCTCG TGATAGATAGCCT GAAT	T	-				SILENT- NONCODI NG		
1437-1438	cg29348993	257	TCGCTGTAGATA GCCTGAATCCAA A[G/A]AAACCAA AAGGGTTATCC AAGTA	G	A				SILENT- NONCODI NG		
1439-1440	cg29349829	450	CATAGGCACCGC GTGAAGGGCAC CGT/gap]AAGAA TCTTCCCGAATG CTCTGTC	T	-				SILENT- NONCODI NG		
1441-1442	cg29349990	184	TCCGGGTGGG AACGGCGATCAG CGC/TJCAGCTTG GCGCTTTCGACG TTGGTC	C	T				SILENT- NONCODI NG		
1443-1444	cg29351920	178	TCAGGAGTTTGA GACCAGCCTGG CC[A/G]GCATGG CGAAACCCCATC TCTACTA	A	G				SILENT- NONCODI NG		

1445- 1446	cg293352964	127	GGAAGGTGTGC GGATACATTATTG TC[G/A]GTGCGG CATCGTCCATCC ACACCGT	G	A			SILENT- NONCODI NG		
1447- 1448	cg293352964	243	GCCGTCACTCCA TTGATCCCCGAG T[C/T]CGGATCCA TCTGGCCCCACA CGGCG	C	T			SILENT- NONCODI NG		
1449- 1450	cg293352964	252	CCATTGATCCCC GAGTCCGGATCC AT[C]CTGGCCC CACACGGCGGG AAGGCAA	T	C			SILENT- NONCODI NG		
1451- 1452	cg293352964	378	CGACCGGTTATG GTCTGCTCGCTC G[T/C]CTTGCCCA TATTGACGCCCC GACGC	T	C			SILENT- NONCODI NG		
1453- 1454	cg293352964	420	CCCCGACGCTG CTGTCGGTGTGG GG[G/A]AGTGAC GTTTACGATTCC CCCCGGG	G	A			SILENT- NONCODI NG		
1455- 1456	cg293354835	145	GGGGCCTTCCT GTTGTACACTTC C[C/T]GTGAGGG TCTCAGACCCCT TGCAGA	C	T			SILENT- NONCODI NG		
1457- 1458	cg293357657	434	TATCCGCGGGGAC GCCGCGAATTCG TT[Gap]CGCGAC CGCACGTTCTAC GAGGGCG	T	-			SILENT- NONCODI NG		

1459- 1460	cg29357938	156	TTGCTATCGCTC GCGCTTTGCGCT C[T/gap]GAACCC AAATATTGTTTG CGGATG	T	-			SILENT- NONCODI NG			
1461- 1462	cg29360589	250	GCCCGCTGTGA CACCATTGGTAC TC[C/G]GGTCCG TCTGACCTTCGA CCCAGAA	C	G			SILENT- NONCODI NG			
1463- 1464	cg29360589	92	CGATGGGGCGT GACGAATTGCCC CT[G/gap]CCGAC GGCGACCTCTCT GGCTCTGT	G	-			SILENT- NONCODI NG			
1465- 1466	cg29363109	161	TAATCCAGTGCT CCCGGCTGTACC A[C/A]CCTGCCTA TTCACAGTGGGC ACACT	C	A			SILENT- NONCODI NG			
1467- 1468	cg29495773	379	AGGAGCTGTCCA GGTTCTCTGGAGA C[G/T]AAACGGA GCCCGCTGGGA ACTGTCC	G	T			SILENT- NONCODI NG			
1469- 1470	cg29498780	60	AGAGGGAGCCA CAGAAAGCCCG ACG[T/C]TGACA GCCCTGCAGGC AGGGGCTG	T	C			SILENT- NONCODI NG			
1471- 1472	cg29513153	101	TCTCGAGAAAA AAACAACCGGAG A[G/A]ACTCTAGT GAAGGTCTCGAC AAGAC	G	A			SILENT- NONCODI NG			

1473- 1474	cg29513153	198	GCGGCAGGAAC CTGCCACTCCTG GG[A/G]GCAAAA AGCTGCTCTCGG GAACCCCT	A	G				SILENT- NONCODI NG		
1475- 1476	cg29514688	136	GTAGTTTTAGTA NGGACGGGTT TC[G/A]CCATGTT GCCAGGCTGG TCTTGAA	G	A				SILENT- NONCODI NG		
1477- 1478	cg29514688	154	GGTTTCGCCAT GTTGCCCAGGCT G[G/T]TCTTGAAC TCCTGGGCTCGA GTGAT	G	T				SILENT- NONCODI NG		
1479- 1480	cg29514688	181	CTTGAACCTCCTG GGCTCGAGTGAT C[C/T]ACCTGCCT CAGCCTCCCAAT GCGCT	C	T				SILENT- NONCODI NG		
1481- 1482	cg29689883	148	GGCCACTTTTCT TTTTCTTGTTTG [T/gap]TTTTTTTT TCTTTTTTCTTT TTTT	T	-				SILENT- NONCODI NG		
1483- 1484	cg29689883	176	TTTTTCTTTTT TTCTTTTTTTTTT /gap)CTTCTCTTT TTGAGACATTCT CACT	T	-				SILENT- NONCODI NG		
1485- 1486	cg29692482	311	TTTCTCCACCT CCCTCCACTCAT TTC/TAGGTCAGG CATCGAATGTCA CTTTC	C	T				SILENT- NONCODI NG		
1487- 1488	cg29694531	19	TTGCAAAAATAA CCCCTT[G/gap]G GGCTCTGTCTCC CTCAACTATTGC	G	-				SILENT- NONCODI NG		

1489-1490	cg29694531	22	TTGCAAAATAA CCCCTGGG[G/g ap]CTCTGTCTCC CTCAACTATTGC TCT	G	-				SILENT- NONCODI NG		
1491-1492	cg29694613	106	AGTAGGTATCCC CGCTCCCCCACC A[gap]/C]ACCCCC AATTTGAATGCA CATTGA	-	C				SILENT- NONCODI NG		
1493-1494	cg29694613	94	TCCAGTGTTTT CAGTAGGTATCC C[C/]GCTCCCC CACCAACCCCCA ATTGA	C	T				SILENT- NONCODI NG		
1495-1496	cg29694879	149	GTTGCAGTGAGC CGAGATCGTGCC A[C/]TGCACTCC AGCCTGGGTGA CAGAGC	C	T				SILENT- NONCODI NG		
1497-1498	cg29970826	210	GTTGTCCTGGC ACGGAACAGGA GA[C/]TATACGTA AGCAGCTAAGTC TCTTCC	C	T				SILENT- NONCODI NG		
1499-1500	cg29970826	248	CTAAGTCTCTC CAAGGAACGGT GG[A/G]GACACC AATCACCATGTC GAGGTGA	A	G				SILENT- NONCODI NG		
1501-1502	cg30123222	141	CTATGACATGAC ACTATTACATTT [G/A]GTTTTTAGC ATTTTTAAAGAG GAAG	G	A				SILENT- NONCODI NG		

1503- 1504	cg30144940	111	CCCCGGGACAA GTCAAGATCTGT GA[gap/T]TTTGG CGTCAGTGGCAA CCTAGTTG	-	T				SILENT- NONCODI NG		
1505- 1506	cg30144940	71	CATCCATCGCGA CGTCAAAACCGAC C[G/A]ATATCTTG GTCAACACCCCGC GGACA	G	A				SILENT- NONCODI NG		
1507- 1508	cg30148429	399	ATGACAGAAATG CTACAGTAAGGG A[G/C]AGGAGAT GGGGGAAGGCA AAAGGGG	G	C				SILENT- NONCODI NG		
1509- 1510	cg30148429	415	AGTAAGGGAGA GGAGATGGGG AAG[G/A]CAAAAG GGGTTCTCTACT TATTAAG	G	A				SILENT- NONCODI NG		
1511- 1512	cg30148429	426	GGAGATGGGG AAGGCAAAAGG GGG[T/C]TCCTAC TTATTAAAGTCAAA TAGATC	T	C				SILENT- NONCODI NG		
1513- 1514	cg30154402	201	TATGTGAAGTAA AACAAAAACAAA A[G/C]TTGTTACA ATTTTTCCTTC TAAT	G	C				SILENT- NONCODI NG		
1515- 1516	cg30177428	111	GTGTGAGGGTG CAGGTTCTCCCC AA[G/gap]GGCCC ATTTCTGCACC AGAAAGCT	G	-				SILENT- NONCODI NG		
1517- 1518	cg30179644	127	CCTTGGTGGGG AGAAAGTGA AAA A[gap/A]GAGGAT CTGAAGACTCAT TAGTTGT	-	A				SILENT- NONCODI NG		

1519- 1520	cg30275403	45	GTGGGCAGCAG GAATTGGGAGGA GG[A/gap]GGTGG GGGTGGGGCAC AGAGCGGGG	A				SILENT- NONCODI NG		
1521- 1522	cg30373246	335	AGCCGGCCCT ATTTCCTGCCG GA[C/A]GCCCTCTC GCGGCCTTCAG CGCGACC	C	A			SILENT- NONCODI NG		
1523- 1524	cg30386365	122	GACCCAGTTAG GCAGCTCAGTT ATT[C/T]ATTGCAG CTTGATGGCCCC TGGGA	T	C			SILENT- NONCODI NG		
1525- 1526	cg30386365	54	AGGCTTCACTC CTCAGTGGCTA G[A/G]TGCAATTC TAACCAAGGGG CAAGTT	A	G			SILENT- NONCODI NG		
1527- 1528	cg30420313	93	AGTACAATAATG ACCGGCACCAG GG[C/G]ACAGCT GAAATGGCACTG ACTGATA	C	G			SILENT- NONCODI NG		
1529- 1530	cg30421261	250	TAGTCCCCTTCT TTGTCAACGCTT TIG[C/T]ATGTTCTG GGTAGTGGACAA TTTCC	G	C			SILENT- NONCODI NG		
1531- 1532	cg30421963	396	AGGCACGTGCCCC TTGTCGCCCTTCC C[A/G]GACAACTT GTACCCCTCCAGG CCACC	A	G			SILENT- NONCODI NG		

1533- 1534	cg30453852	76	CGGTGCCTGGAT TCCTTTGATGAA A/A/GJGGCAAAG CCTTGAACCTAA GTCATC	A	G			SILENT- NONCODI NG		
1535- 1536	cg30489596	128	AATAAGTATAGC AAGTTTATAAAG G/A/GJAAAAGATA AAATACAGTTCC AGTAT	A	G			SILENT- NONCODI NG		
1537- 1538	cg30489596	307	GCCTTTAATCCT GGGAGATAAAGC C/A/GJAGATCTCT GAGTTCAAGGCC AGCAT	A	G			SILENT- NONCODI NG		
1539- 1540	cg30490648	64	ACAGGTACAGCC TGCGGTCAGACA C/A/GJACCACAA GGCACATGAAC CCCCAG	A	G			SILENT- NONCODI NG		
1541- 1542	cg30575906	179	TTTTCTGGTAAA TGGTCCTAAAT G/AJAAACCTGGC GTTTAACATGGA CACT	G	A			SILENT- NONCODI NG		
1543- 1544	cg30578763	234	GAGGTCTGGTTC GGGTTGCCAT GTG/AJAGGGC AAGAGGTGTCTG CCCCCTC	G	A			SILENT- NONCODI NG		
1545- 1546	cg30630643	267	GTCTTGGCTGG GGGTAGGATGA CTG/CJCAAGAAT TGGGTCTGTATT TAATAA	G	C			SILENT- NONCODI NG		

1547- 1548	cg30748852	117	AACCAGGGAACA TTATGGCCTGAG G[C/gap]CCCAGA GGAGTGGGACA GTTACCCA	C	-				SILENT- NONCODI NG			
1549- 1550	cg30749846	71	GGTCGAGCAGG GTTTACITTTAG TTT[G]GGATCTGT CGTGTGACTTGC CTCTA	T	G				SILENT- NONCODI NG			
1551- 1552	cg30750319	255	GGCTTACTCCTT TGATGGAAAGTG G[G/A]GACAAAA GGCTAGAGTGCA GCAGTT	G	A				SILENT- NONCODI NG			
1553- 1554	cg30750319	440	AGCATCAGTGGT GCCCCCGACCC AG[G/gap]CCTTG CCACCCAGAAC AGATAGGA	G	-				SILENT- NONCODI NG			
1555- 1556	cg30750659	197	AGGACTAAATGT AAGAGAGAGGG ATT[G]GCAAAAGC TTGAGGAAAAGA AACTCC	A	G				SILENT- NONCODI NG			
1557- 1558	cg30750659	470	TAGGACCCCATG CCTCAAATCGCT C[A/G]ACACCCAT CCCTGACTCTGA AAATC	A	G				SILENT- NONCODI NG			
1559- 1560	cg30783885	167	GCGGCCAGAA CCTTGGGCCC GCT[A/G]CTCACT GGGGCATTGGC TGCATACC	A	G				SILENT- NONCODI NG			

1561- 1562	cg30783885	176	AACCTTGGGCCC GGCTACTCACTG G[G]GCAATTGG CTGCATACCTGA CCCACG	G	A				SILENT- NONCODI NG			
1563- 1564	cg30784771	449	TTTATTTCTATAG AACAAAAAAA A[gap]GTTAAGAG ATTAGTAGAGAC GGGTC	A	-				SILENT- NONCODI NG			
1565- 1566	cg30785174	123	CGTTTCTCTGGT TTTTCTGGTCTC C[G]A[AAATTCAA GGATTCTACAG TTAGC	G	A				SILENT- NONCODI NG			
1567- 1568	cg30785603	636	AAGTCCCTTAG CTGAGAACCAAA G[A]gap]AGTGGT CCCGACTGTGCA GGCAGCT	A	-				SILENT- NONCODI NG			
1569- 1570	cg30785603	637	AGTCCCTTAGC TGAGAACCAAG A[A]gap]GTGGTC CCGACTGTGAG GCAGCTT	A	-				SILENT- NONCODI NG			
1571- 1572	cg30785603	656	CAAAGAAAGTGGT CCCGACTGTGCA G[G]C]CAGCTTG AAAGAAAGAAACA GGCCCG	G	C				SILENT- NONCODI NG			
1573- 1574	cg30785957	684	TTCGCGAATGTG TGTGTGGCATAAC CT/C]TGGCCCC ATCGTCTGTCCC ATAATC	T	C				SILENT- NONCODI NG			
1575- 1576	cg30786264	412	CTCAAAACCCCTT GAACTCCCTCAGT G[G]A]ITCCCTCC CCCATGCAGCTG TACTC	G	A				SILENT- NONCODI NG			

1577-1578	cg30786450	230	TCACAGCAGCCA ATTCTTTCTCCCT [T/C]AGCCTCATC GCGTTCCAGTCA GCCT	T	C				SILENT- NONCODI NG			
1579-1580	cg30787589	182	CGTCTGGAGCCT TCTTTTTTTTTT[gap/T]GAGACAG GATCTCGCTCCG TCCTCC	-	T				SILENT- NONCODI NG			
1581-1582	cg30787589	182	CGTCTGGAGCCT TCTTTTTTTTTT[gap/T]GAGACAG GATCTCGCTCCG TCCTCC	-	T				SILENT- NONCODI NG			
1583-1584	cg30787705	111	GAGTAACACCCT TTTTCAAAAAA [A/gap]GTTACCA TTTTCTGTAATAG GAAAA	A	-				SILENT- NONCODI NG			
1585-1586	cg30787705	256	AAATGTGAAAGA CTCTTTAGGACA A/T]TATACCAAG TGGAAGAAGACAG GAATA	A	T				SILENT- NONCODI NG			
1587-1588	cg30787816	192	TAAAAACATCAC TCTTGAGCTGC A[G/T]GGAAAAG GAGTTGAGAAGC ATGGAA	G	T				SILENT- NONCODI NG			
1589-1590	cg30788422	198	GATTGCATGGAG GCCCCGCCCCC CC[C/gap]AACCA ATCTTTGATAAT AGCACAG	C	-				SILENT- NONCODI NG			
1591-1592	cg30788717	28	ATCATATCATGA AAGCTATCATAA A[G/T]GAAGAAA ATAGGGATTGA CTATC	G	T				SILENT- NONCODI NG			

1593-1594	cg30790895	303	GTCCTGGGCAG GAAGATGAGGCA AACTTACAAAGCA CATGGATGCACG CACACA	C	T				SILENT- NONCODI NG		
1595-1596	cg30790895	311	CAGGAAGATGAG GCAACACAAAGC A[CA]ATGGATGC ACGCACACACTC GTGCT	C	A				SILENT- NONCODI NG		
1597-1598	cg30792591	247	TTGGATATTGGC TTTAAATGTTTT [C/T]ATTTAATAC CCCCCTCCCCAC ACAC	C	T				SILENT- NONCODI NG		
1599-1600	cg30793374	154	AATTGAACTGCT GTTCCCTGTGTG C[CT]GGGCCCC ATAGCTAGCACT GGGAAC	C	T				SILENT- NONCODI NG		
1601-1602	cg30794324	290	TCCTAAATGAGT GTTTGAATAGT T[AG]TTTCATTG GAAACAAAGTCA AAACA	A	G				SILENT- NONCODI NG		
1603-1604	cg30794324	523	TCTACCACAATT ATTGATCAACT A[G/A]TTATCAAC CCTGACTGCAG	G	A				SILENT- NONCODI NG		
1605-1606	cg32073644	381	ACCCTCCTGGCA CATCTCTGCTCA C[CT]CTGCGAG CAACCGACCCC GACGTGG	C	T				SILENT- NONCODI NG		
1607-1608	cg32119723	510	TGGATCGCCAG GGCTACGGCCA GAT[CT]AAGGTG GTCCGCGCCGA TGGGGACA	C	T				SILENT- NONCODI NG		

1609- 1610	cg32119813	362	GCCCGTCGTAC GTGGGGCGCTC GCGC/GJTG GT GCAGACGCGCTT GATTGGTT	C	G			SILENT- NONCODI NG		
1611- 1612	cg32120097	123	TGGCCTGCACGT CCCCGACGCTCA G[C/gap]TCCCCG TGGCCCCGGCT GTACAGGA	C	-			SILENT- NONCODI NG		
1613- 1614	cg32126043	267	CCTGTGGCATCC GTTCTGATGGAA A[C/T]GTGCAGTT GTATTTGGAAGT TCAGA	C	T			SILENT- NONCODI NG		
1615- 1616	cg32149436	145	AGGGCGCCCGG AGTGGCTCCAG GAA[C/G]GACGG AAACCCCTCAGG GCITTTGG	C	G			SILENT- NONCODI NG		
1617- 1618	cg32149517	503	TGTGCGTGTATG TGCGCTTGCTCT G[gap/T]CATGCG TGGTGTGTGTAT GTGTGTG	-	T			SILENT- NONCODI NG		
1619- 1620	cg32149517	89	TGGTGGTGTGCG CAGAGAGTGACC T[G/C]CCTGTCTG GGTGGAGGAA AAGCCA	G	C			SILENT- NONCODI NG		
1621- 1622	cg32150747	324	CAGAACTTCGGC AGTAAAGAATAA A[A/gap]GGCCAG ACAGAGAGGCA GCAGCACACA	A	-			SILENT- NONCODI NG		

1623- 1624	cg32152942	114	CACAGCTGTGCA TGTCGACTTAGG T[G/A]GCCTGCC AGTCATCTCCG GCGGCA	G	A				SILENT- NONCODI NG		
1625- 1626	cg32152942	136	GGTGGCCTGCC AGTCATCTCCG GC[G/A]GCACGG TCAACGACGTCG AGCTGCC	G	A				SILENT- NONCODI NG		
1627- 1628	cg32152942	139	GGCCTGCCAGC TCATCTCCGGCG GC[A/C]CGGTCA ACGACGTCGAG CTGCCGCG	A	C				SILENT- NONCODI NG		
1629- 1630	cg32152942	205	TCACTTGTTTCCAG ATTGCCCATGGA T[A/G]GTCACTG ATCCCAACGAT GTGGG	A	G				SILENT- NONCODI NG		
1631- 1632	cg32152942	220	GGCCATGGATAG TCACCTGATCCC C[A/G]ACGATGT GGCTAGCTGA CTAGCGG	A	G				SILENT- NONCODI NG		
1633- 1634	cg32152942	232	TCACCTGATCCC CAACGATGTGGG CT[C/G]AGCTGACT AGCGGTAACCTG AGCTC	T	C				SILENT- NONCODI NG		
1635- 1636	cg32152942	61	CGCGATCCTCGT TGAGGCGCTGAA G[A/G]CGCTGGG ATGCAGCACGAA ACTCCG	A	G				SILENT- NONCODI NG		

1637- 1638	cg32153241	133	ACCCGGGCTCCG GTCCCGAGGTC CCA[C/T]AGCAGT TGACCAGGCATG GGCCGCA	C	T			SILENT- NONCODI NG		
1639- 1640	cg32153241	172	GCATGGGCGC AGGGCTGCCAG CGC[G/A]ACAGC TCGTACCCGCGT CTTGGTGA	G	A			SILENT- NONCODI NG		
1641- 1642	cg32153241	199	CAGTCGTACCG CGTGCTTGGTGA T[A/G]AGTCCGTC GTGGGCGAAAT GCTCCT	A	G			SILENT- NONCODI NG		
1643- 1644	cg32153241	217	TGGTGATAAGTC CGTCGTGGCG AA[A/G]TGCTCCT CGGCCAGGCG GGGTAC	A	G			SILENT- NONCODI NG		
1645- 1646	cg32158391	719	TGCATACCATGC TCCAGAGGAAGC A[G/gap]ATAAAT CTGATCCTAAAC CTGGGGT	G	-			SILENT- NONCODI NG		
1647- 1648	cg32168122	292	CATGCGCGCTG GCCTCCATGGGT GG[C/G]GGGACC GACTGTGTGACG CACTTGC	C	G			SILENT- NONCODI NG		
1649- 1650	cg32168828	346	TGATTGCGCGCA CAGTTCGTTTAG G[G/A]CAACGCC AAGTTCGAAGAC GTCCCC	G	A			SILENT- NONCODI NG		

1651- 1652	cg32177197	255	CACCGTGTGCG GAAAGGTCGCT C/A/GCCTCTACC ACGATCCGGTG GTTACC	A	G				SILENT- NONCODI NG			
1653- 1654	cg32177197	618	GGGGAAGGAAT GAAAGCGGTG GGG[T/C]CGTCG GTCGTCGGGGC AGTGCCCA	T	C				SILENT- NONCODI NG			
1655- 1656	cg32177584	20	CCGACGCGTG AGCCACCG[T/C] GCCTGGCCAC GTGACACTGTTA AA	T	C				SILENT- NONCODI NG			
1657- 1658	cg32180618	414	AATCAGCACGGT GCGCGTGAGGG GC[G/A]GGCGCG CTTCTCACACAT GCTGTGC	G	A				SILENT- NONCODI NG			
1659- 1660	cg32195480	136	CTTTCCCTTGC GTACACTCTGGA CT[C]CCAGGCA GGAAATCAAGG CCTCAC	T	C				SILENT- NONCODI NG			
1661- 1662	cg32195480	224	GCATTAGTCCAG GACAGCAGACC CC[ap/C]TCTGG ACGCTGACTCGG GATGGGGT	-	C				SILENT- NONCODI NG			
1663- 1664	cg32308743	129	TTTCCGTACGCG TGAACGTCTGTG T[T/C]GTCTGTGG AATCCCCTCGGG ACGTT	T	C				SILENT- NONCODI NG			

1665- 1666	cg32338390	455	GAGCCATAAGG GAGGACTTGGCA GC[G/A]TGCTTG CTCCCTGAGTGA CGTTGTG	G	A				SILENT- NONCODI NG			
1667- 1668	cg32544064	536	CAGGAGTTCATG ACCAGCCTGGC CA[A/G]CACAGT GAGACCCCGTCT CTACTAA	A	G				SILENT- NONCODI NG			
1669- 1670	cg32544064	539	GAGTTCATGACC AGCCTGGCCAAC A[C/T]AGTGAGAC CCCGTCTCTACT AAAAA	C	T				SILENT- NONCODI NG			
1671- 1672	cg33193895	38	TCTCTCCTNTGC CAAGATAAAAAT A[A/gap]TATTCTC CCTGGGCTTTCT TAACTA	A	-				SILENT- NONCODI NG			
1673- 1674	cg33193895	40	TCTCCTNTGCCA AGATAAAAATAA T[A/gap]TTCCTCCC TGGGCTTTCTTA ACTACA	A	-				SILENT- NONCODI NG			
1675- 1676	cg33194116	210	GTGTCACTAGTG TGAAAAAAGTTG T[A/gap]GTGGAG AGCTTGGTATGT CAGGCAA	A	-				SILENT- NONCODI NG			
1677- 1678	cg33199608	302	GATTCTCCTGTC TCAACCTGCCAA G[T/C]AGCTGGG ACTACAGGCGCA CGCCAC	T	C				SILENT- NONCODI NG			
1679- 1680	cg33199608	347	CGCCACCACGA CCGGCCCAATTC TG[C/T]ACTTTTA GTAGAGACAGG GCTTCAC	C	T				SILENT- NONCODI NG			

1681- 1682	cg33208319	148	CCTTGATGAGGC TGCTTTTAAGC TTC/TAATTGAAG GTAGTAACAACA ATCCT	C	T				SILENT- NONCODI NG			
1683- 1684	cg33208319	229	GAAATGTGTAGA TTCTGGAACAGT GIC/TCTAGCAG GTTGCAGATACT TACTAG	C	T				SILENT- NONCODI NG			
1685- 1686	cg33208319	280	AAGTTTCTGAG TGAATGAAAAGT CIA/GJAAAATGAA TGTATCCTTCCA AGCAT	A	G				SILENT- NONCODI NG			
1687- 1688	cg33265890	32	TCGTGCTTGGAA TCAGCAGGCAG GG[C/gap]CACATT CCCTCTTGAAGC TCACATCT	C	.				SILENT- NONCODI NG			
1689- 1690	cg33271693	103	GTTGCGGAGAAA GCTACGACCAAG TIA/gap]CGCCCA GCTCGGGCCTTA GAAC TTC	A	.				SILENT- NONCODI NG			
1691- 1692	cg33899283	171	CCCTTCGGGATT GGAGTTCGACCT GIA/TJAGCATGG ATAATTATTCACA TTTC	A	T				SILENT- NONCODI NG			
1693- 1694	cg34078594	191	AGAGACAAGGCT TCCTCATAGGAC G[G/gap]CAGAGC CACCTTTAGGAA CAGCTTG	G	.				SILENT- NONCODI NG			

1695- 1696	cg34078594	67	TCAAAGTGAAGA AGCAGGAGGCG GGG/CJAGTTCC GCCTCTCCCAGC CCAAGGG	G	C				SILENT- NONCODI NG		
1697- 1698	cg34078713	199	TGAAATAGTGT GCTGAGCCCTG GA/GJCATTAAA AATGTGTTCTA TGTGGA	A	G				SILENT- NONCODI NG		
1699- 1700	cg34096681	178	AGACTTGAAAC AACTGGAAGAGA G/GA/GTTCCTCA AGGGAGAAGAC ACGAGA	G	A				SILENT- NONCODI NG		
1701- 1702	cg34098766	315	CTCAGCCTCATG AGTAGCTGGAC A/G/gapJCAGACA TGACAAACCACA CCTGGCT	G	-				SILENT- NONCODI NG		
1703- 1704	cg34098766	356	ACACCTGGCTAA TTTTTTTTTTTTT T/gapJTGCGGTG GAAATAGAAATCT CACTGA	T	-				SILENT- NONCODI NG		
1705- 1706	cg34098766	357	CACCTGGCTAAT TTTTTTTTTTTTT T/gapJGGGTGG AAATAGAAATCTC ACTGAT	T	-				SILENT- NONCODI NG		
1707- 1708	cg34107938	217	CACAAATGCTCT GTAGGCACGTGT G/GA/JCTAGTGA CTGCCCTACGGT CGGCAT	G	A				SILENT- NONCODI NG		
1709- 1710	cg34108088	127	ATATTAAACCAT GAATGAAGTATG GT/CJTATCCTCC CCTCTTTTTTGAT AATC	T	C				SILENT- NONCODI NG		

1711- 1712	cg34126415	194	ATGCTAGGAAGC TAGCTCCTGGGG GIGAJTTCAGATC TAGTGAGGGTGC CTTTC	G	A				SILENT- NONCODI NG		
1713- 1714	cg34126415	423	AAGTAAAAACAA ACAAGATAACTT TT/CJTITTTTCT GAGATGAATTTT CACTT	T	C				SILENT- NONCODI NG		
1715- 1716	cg34147197	176	GGCTCAAGCAAT CCTCCCGCTCA GT/CJCTCCCAAG CAGCTGGGACTA CAGGC	T	C				SILENT- NONCODI NG		
1717- 1718	cg34387835	106	TGTATTTTGTAGTA GAGATGGGGTTT T/CJACCATGTGG GCCTGGCAGGT CTCGA	T	C				SILENT- NONCODI NG		
1719- 1720	cg34387835	183	CCTCGGCTCCCT AAATTCCTGGGA CT/CJACAGGCG TGAGCCACTGCA CCGGC	T	C				SILENT- NONCODI NG		
1721- 1722	cg34387835	74	ACCGGTGCGTG CCACCACACCCG ACIC/TJAATTTT GTATTTTGTAGTA GAGATG	C	T				SILENT- NONCODI NG		
1723- 1724	cg34387835	83	TGCCACCACACC CGACCAATTTT GT/CJATTTTGTAG TAGAGATGGGGT TTTAC	T	C				SILENT- NONCODI NG		
1725- 1726	cg34390673	390	TAAACTTCGATC TTTCCCTGTGCT C(gap/T)AACATTG CTATTTGGATCC CGGICT	-	T				SILENT- NONCODI NG		

1727- 1728	cg34405904	373	AGTTCGCTGTTG ATTGCTATAATTT [T/gap]CTCTCTAA AATCTGGATTTT CATCT	T	-				SILENT- NONCODI NG			
1729- 1730	cg34407516	356	CACATATATCTC AACAAACCATGC A/C/TJATCATCTG TTCAGAACTGGG AAACG	C	T				SILENT- NONCODI NG			
1731- 1732	cg34407558	260	CCAAGCTCCTGC CTCGCAATTGCC T/T/C/JGTAGGCC AAGATCATGCCG TGAAG	T	C				SILENT- NONCODI NG			
1733- 1734	cg34407558	293	CAAGATCATGCC GTGAAGTGGCCT T/T/C/JCCTAGCCT AACTTTTGCTTTT TGAT	T	C				SILENT- NONCODI NG			
1735- 1736	cg34407558	318	TCCTAGCCTAAC TTTTGCTTTTTGA [T/C]GCATACTCC AGTCCCAAACCT TCCT	T	C				SILENT- NONCODI NG			
1737- 1738	cg34407558	416	GGCCAAAATCGT CGTGAAGTCACC C/T/A/JCTGCAGG CCTAGCTCCTGC GTCCGA	T	A				SILENT- NONCODI NG			
1739- 1740	cg34407558	425	CGTCGTGAAGTC ACCCTCTGCAGG C/C/G/JTAGCTCCT GCGTCCGAGTG CTGTGT	C	G				SILENT- NONCODI NG			
1741- 1742	cg34407558	436	CACCTCTGCAG GCCTAGCTCCTG C/G/C/JTCCGAGT GCTGTGTAGGCC AAGCTA	G	C				SILENT- NONCODI NG			

1743-1744	cg34407558	440	CTCTGCAGGCCT AGCTCCTGCGTC C[G/A]AGTGCTGT GTAGGCCAAGCT AATGC	G	A				SILENT- NONCODI NG		
1745-1746	cg34407558	481	AAGCTAATGCCT CACAGCACACTT T[T/C]GAGGCTGA GCGTTTCCTTT GTGCA	T	C				SILENT- NONCODI NG		
1747-1748	cg34407558	492	TCACAGCACACT TTTGAGGCTGAG C[G/A]TTTCCTTT TGTCATCCTCT CCAAG	G	A				SILENT- NONCODI NG		
1749-1750	cg34407558	539	CAAGCCCTGAAC TTACTCCAGTTG G[C/T]CTCTCCAG ACCAAGCTCTCC CTCCC	C	T				SILENT- NONCODI NG		
1751-1752	cg34409256	223	TTACTATATATGA TGAGTCTAATA[A/C]TTTCTATCC TATTTTATTCCT TT	A	C				SILENT- NONCODI NG		
1753-1754	cg34409256	227	TATATATGATGTA GTCTAATAATTT[T/gap]CTATCCTA TTTTATTTCCCTT TTTT	T	-				SILENT- NONCODI NG		
1755-1756	cg34411960	137	ATGGTGGAGATG CTTCTGGTTTATT [C/T]GTGGCTAC CGCTGTTACTGC TTGG	C	T				SILENT- NONCODI NG		
1757-1758	cg34664360	363	AGCTAGACATAG AGCCCTGACCGT G[T/C]GATTCCAA CTGTGGAATTCA CACAA	T	C				SILENT- NONCODI NG		

1759- 1760	cg34750113	385	TTTTATTGTTTG AGACAGAGTCTC [A/G]CTCTGTTGC CTAGGCTGGAGT GCAG	A	G			SILENT- NONCODI NG		
1761- 1762	cg34750113	423	GGCTGGAGTGC AGTGGTGCAATC AC[A/G]GCTCACT GCAACTTCACCC TCCIGG	A	G			SILENT- NONCODI NG		
1763- 1764	cg34888218	312	AAATGTTGGGAT CAATATCTAAAT C[G/A]AACTCCAA ATTACAGCCTCC AGGA	G	A			SILENT- NONCODI NG		
1765- 1766	cg34888218	408	CAGGCTGTATGC CTGAAGTCCCA A[G/A]TACCAAGT GCATGTACTCTG CTCTG	G	A			SILENT- NONCODI NG		
1767- 1768	cg34888218	422	GAAGTCCCCAAG TACCAAGTGCAT G[T/C]ACTCTGCT CTGGTCTAAGGA TGAAA	T	C			SILENT- NONCODI NG		
1769- 1770	cg34896418	199	AAACAAGGATTA AATCTGGTCCTG G[T/C]GGTTGTAT GGGATAAACATG GATT	T	C			SILENT- NONCODI NG		
1771- 1772	cg35001967	195	TGAGCAGAGAAC ACTGACCTGGTT T[G/T]GCAGGGA CAGGAGATACGC TGGGT	G	T			SILENT- NONCODI NG		
1773- 1774	cg35001967	197	AGCAGAGAACAC TGACCTGGTTTG G[C/T]AGGGACA GGAGATACGCTG GGTTGG	C	T			SILENT- NONCODI NG		

1775- 1776	cg35001967	232	AGATACGCTGGG TTGGTATGGATC A[G/A]CAAGAGG GTACTGCTAATG GGAACA	G	A			SILENT- NONCODI NG		
1777- 1778	cg35001967	273	AATGGGAACAGG GAGGGAAGGCT CA[A/gap]CCCCA TTCCCGTATTTC CCTGATTC	A	-			SILENT- NONCODI NG		
1779- 1780	cg35003947	474	TGTTCTGGTGA TGGGAACTTAAC A[T/C]GTCTTTGC CGTTACATATTC TTTGA	T	C			SILENT- NONCODI NG		
1781- 1782	cg35003951	210	TTGAACTCCTGA CCTCAAGTGATC C[A/G]CCCGCCT CAGCCTCCTAAA GTGCTG	A	G			SILENT- NONCODI NG		
1783- 1784	cg35013956	66	CAGAATCCAGCC CTGCTTGATGCA A[T/C]CCTCTTCA GCCAGGCGTTG CTGAAT	T	C			SILENT- NONCODI NG		
1785- 1786	cg35014502	212	GAGCAGTTTCTG TTTTCTAGTTAA [G/T]ATGTACTGC ACATCCCCCTAC TGTT	G	T			SILENT- NONCODI NG		
1787- 1788	cg35017611	152	GCAGGCAGACG GGCAGGGCCAG AGG[C/gap]GCTA CCGGGTCTCCT GCACTGTAT	C	-			SILENT- NONCODI NG		

1789- 1790	cg35019280	286	ATAAACTGTGTC AGACATGGGCG AC[G/gap]CGGGG ACCGCTGGAGG GAGGCGCGC	G	-			SILENT- NONCODI NG			
1791- 1792	cg35019280	52	TCCGCTGGGAG CAGGAGGGGCG GGG[C/gap]CGG GCTTGAGGAGTG GCTGGCCGCC	C	-			SILENT- NONCODI NG			
1793- 1794	cg35023126	244	AGAAATACCAT CTGGACATAAGA CTT/GTGGCTAAA ATTTCATGATGA AGATA	T	G			SILENT- NONCODI NG			
1795- 1796	cg35049067	193	TCTCCCTGATGG ACGGGGAAGTCT TIG/CJTITGTGGA AGACACTGAGCC ACGCT	G	C			SILENT- NONCODI NG			
1797- 1798	cg35049067	339	CACCACCACCG GCATCCGGGGA GGA[G/C]TGTC AACGGGTGACTC GGCCAGGA	G	C			SILENT- NONCODI NG			
1799- 1800	cg35049067	526	TCCGGGCACCC TCCTGCGGGTG GAC[A/G]ATGAG CGCCTGGGAGG CCGTTGTCC	A	G			SILENT- NONCODI NG			
1801- 1802	cg35049628	353	GCTGGAGGATTG CTTGAAGCCAGG A[A/G]TTCAAGAC CAGCCTGGGCA ACATAG	A	G			SILENT- NONCODI NG			

1803- 1804	cg35063579	216	GCAGATCACTGG AGGTCAGGAGTT C/A/GIAGACCAG ACTGGCCAAACAT GGTGAA	A	G			SILENT- NONCODI NG		
1805- 1806	cg35066497	174	GCGTGGCACGC CCGTCAGGGGC AGGTT/A/GCCCC AGGTACTCCTA CGGTGCTC	T	A			SILENT- NONCODI NG		
1807- 1808	cg35066497	202	CCCAGGGTACTC CTACGGTGCTCG G/G/A/C/TCCCAC CGTGGGAGTGC CGAGAC	G	A			SILENT- NONCODI NG		
1809- 1810	cg35066497	233	CACCGTGGGAG TGCCGAGACACT GAT/C/CGATGG GTCTTACAGGTA TGGCATT	T	C			SILENT- NONCODI NG		
1811- 1812	cg35066497	263	GGGTCTTACAGG TATGGCATTTTA C/G/T/GACAGTG AGGAAGATAGAC GAGGGA	G	T			SILENT- NONCODI NG		
1813- 1814	cg35066497	271	CAGGTATGGCAT TTTACGGACAGT G/A/G/GGAAGAT AGACGAGGGAT GGCGCTC	A	G			SILENT- NONCODI NG		
1815- 1816	cg35066497	543	GGCCTGATTCTT GATGTCGTCCTG G/C/T/GGTCGCT GATGGCGTCCTT GGCCTT	C	T			SILENT- NONCODI NG		

1817- 1818	cg35068462	202	TGGCACAGGAG CCCGAGATCTTA TTT/CJCTTGACG AGCCGACAAATC ACCTTG	T	C				SILENT- NONCODI NG		
1819- 1820	cg35072832	317	TTTGGATAATAT GTAACCTCTCCACI A/TATGTCGCTT CCGTAGCAATTG TAGA	A	T				SILENT- NONCODI NG		
1821- 1822	cg35074019	478	TGCAGAAAGGAAC TGGACTCGCTGC A/GTJGGAGAGA AAGTACACCTGA AGGAGA	G	T				SILENT- NONCODI NG		
1823- 1824	cg35097790	97	TCCCTCAGTTTG CTCATCTGTAA GIC/TJAGGAATAA GGCTGATACCTT CTCAG	C	T				SILENT- NONCODI NG		
1825- 1826	cg35097892	283	GTATTTTCAGTA GAGACGGGGTTT T/A/GJCCATGTTG GCCAGGCTGGT CTCGAA	A	G				SILENT- NONCODI NG		
1827- 1828	cg35098722	220	TATGCTCTCTTC GTTGGTTAGTGG [C/GJTGACGGAT ATTTGAGCAGC ATAA	C	G				SILENT- NONCODI NG		
1829- 1830	cg35098722	228	CTTTCGTTGGTT AGTGGCTTGCAG G/A/GJTATTTTGA GCAGCATAAAAC TGTTA	A	G				SILENT- NONCODI NG		
1831- 1832	cg35106817	164	ATGCAGGTGCC GGGTGAGGACG GCA/C/TJCATGCC GAACTGTTCGG ACGGATC	C	T				SILENT- NONCODI NG		

1833- 1834	cg35111750	314	ATATTGGATCTTTT CCCTGTTTTTTT T/gap]GTATCTAG CAGACCTTCATG GTTAT	T	-				SILENT- NONCODI NG			
1835- 1836	cg35137271	253	AGCCAATGGTGC ACAGTGATGATA C[G/A]AATGTCAA TCTTTGCTCGGT CAGTG	G	A				SILENT- NONCODI NG			
1837- 1838	cg35137271	290	TTGCTCGGTCAG TGAGGATGTCGC C[C/T]TGACCTT CTGCTCCCCAG AAAGG	C	T				SILENT- NONCODI NG			
1839- 1840	cg35138283	434	TGAAGTATAAGA ATATTCTGCTGC T[G/T]TGAGTGG TATGTAATGTATA TGTC	G	T				SILENT- NONCODI NG			
1841- 1842	cg35138283	552	GTTTATACATTA TTGAAAGTGGAA T/C]ATTAGATTCT ACCACTAGT	T	C				SILENT- NONCODI NG			
1843- 1844	cg35350458	350	TTCTCGTCTAGC AGTATTCAGATA C[C/T]CCTTCTGC TCAGCCTGCTTG GCGTT	C	T				SILENT- NONCODI NG			
1845- 1846	cg35354409	378	TTTCCGGAGTT ATTTAAAAAAA [A/gap]CAAAACAG ATGCCCTTTTAAG GGTAT	A	-				SILENT- NONCODI NG			
1847- 1848	cg35364749	33	CCCATCACCAAC GCCACCTGGA CC[G/A]GGTGAG TGCTGGGCTAG CCCTGTC	G	A				SILENT- NONCODI NG			

1849-1850	cg35354849	79	GTTGATGCTTGA TTTAAGAGTAAG T(GA)TTATCGTG TTCAGTTTTTATA TC TC	G	A				SILENT- NONCODI NG		
1851-1852	cg35817789	462	CTCTTAGCAACC AATAATTTTTTTT T(gap)CAATAATT AAGTACCAATT. CCTGC	T	-				SILENT- NONCODI NG		
1853-1854	cg35817789	502	CAATTCCTGCT AATGGGCAGGC CC(A/C)CCTTTAT TTC TTTTTTTTC CATT A	A	C				SILENT- NONCODI NG		
1855-1856	cg35817789	512	CTAATGGGCAGG CCCACCTTTATT T(C/T)TTTTTTTT CCATTAGAACGA GCAT	C	T				SILENT- NONCODI NG		
1857-1858	cg35907288	182	GAAGAGCACTTG CAGCCGCATCAG G(T/C)GAACATCA AACTGCAAGGCC ACCTG	T	C				SILENT- NONCODI NG		
1859-1860	cg35927209	161	CCCCCTTGTTAG TGGCGGCACGA AT(C/T)AGTCTTC TTCGCGGTCCAT GGTGAC	C	T				SILENT- NONCODI NG		
1861-1862	cg35927209	33	CCACGGGATCAC CGGCATCGCGC AG(A/G)CCGACG AAGTTAACCCCT TTAACGA	A	G				SILENT- NONCODI NG		
1863-1864	cg35927209	39	GATCACCGGCAT CGCGCAGACCG AC(G/A)AGTTAA CCCCTTTAACGA CCCGCC	G	A				SILENT- NONCODI NG		

1865- 1866	cg35929317	73	GCCGAGCATGG TGCGGGGCACC TGT[A/G]GTCCCA GCCACCTGGGA GGCTGAGG	A	G				SILENT- NONCODI NG			
1867- 1868	cg35933276	125	ATGAGTTCCTGC GATAACCCGGTA GT[C]CTCGAAAA TCTGGGCTCCG GTATAC	T	C				SILENT- NONCODI NG			
1869- 1870	cg35933276	132	CCTGCCGATAACC CGGTAGTCTCGA A[A/G]ATCTGGG CTCCGGTATACG ACGAGA	A	G				SILENT- NONCODI NG			
1871- 1872	cg35933276	167	CCGGTATACGAC GAGATAGTGGAT A[T/C]ACCCATCT TGCTCATCGTCT TAAGG	T	C				SILENT- NONCODI NG			
1873- 1874	cg35933276	213	TAAAGACGCCCT TGCCAAGAGCCT T[G/A]TAAACGTT ATGGATAGCAGT TTCAG	G	A				SILENT- NONCODI NG			
1875- 1876	cg35933276	239	TAAACGTTATGG ATAGCAGTTTCA G[G/A]GTCACTA GACACCCACACC TCGCGC	G	A				SILENT- NONCODI NG			
1877- 1878	cg35933276	306	CTGACTCGAAGA GCAAATACGGGT T[G/A]ACAGCCG AAGCACCATAAC CCATGA	G	A				SILENT- NONCODI NG			

1879-1880	cg35933276	315	AGAGCAAATACG GGTTGACAGCC GAJAGJGACCA TAACCCATGAGG AGGGCGA	A	G				SILENT- NONCODI NG			
1881-1882	cg35933276	64	AGCGATCTCGGT CAGGCCGACCC CCJTGJCGATGC GACTCGTCGTT CGGCCGA	T	G				SILENT- NONCODI NG			
1883-1884	cg35933276	86	CCCTCGATGCGA CTCGTCGTTCCG GJCJGAGTACT CATCAATGAGTT CCTGC	C	T				SILENT- NONCODI NG			
1885-1886	cg35980513	266	AAATGAGCCGG GCGTGGTGACA CAJGJGCTGTG GTCCAGCTACT TGGGAG	C	T				SILENT- NONCODI NG			
1887-1888	cg36173201	463	GCCTCCAGAACT GTGAGAGATAA AJGJGTCCTG TTTTAAGCCATT CAGTT	C	T				SILENT- NONCODI NG			
1889-1890	cg36180692	435	GAGGACTGCTTG AGCCCAGGAGTT CIAJGAGACCCAG CCTGGGCAACAC AGTGAG	A	G				SILENT- NONCODI NG			
1891-1892	cg36190410	155	ACAGGCGTGAG CCACCATGCCCA GCJGJTTGAATA CTGAATCTAAGT ATTTTT	C	T				SILENT- NONCODI NG			
1893-1894	cg36190410	175	CCAGCCTTGAAT ACTGAATCTAAG TJATTTTTTGCT AGTTTTAAATAA TTA	A	T				SILENT- NONCODI NG			

1895- 1896	cg36190410	256	TCTAGCATATGT TAAATGAAGTAG A[T/gap]TTTTTTT TTAACTCTCCATT TGATA	T	.				SILENT- NONCODI NG		
1897- 1898	cg36504297	309	CGTTTTCTTCAG TGCTTCATTTTAT [A/G]CCTCAAATT CTGCTGAAGTGA TTTA	A	G				SILENT- NONCODI NG		
1899- 1900	cg36517624	172	CCTCCTCGTCGC GGAACGGGCTC TC[C/G]CCGAAG CGCTCCTCCAGC TGCCGGC	C	G				SILENT- NONCODI NG		
1901- 1902	cg36517624	215	CTGCCGGCGAA GCTTCTGGGAAC TG[G/gap]CCCAG CCAAACTCTTCA AGCTGCTG	G	.				SILENT- NONCODI NG		
1903- 1904	cg36588981	543	AGGAGCACCTCA AGGCTGTGACC C[G/A]AGCACCAT GTCGGGGTGTG GCTGCA	G	A				SILENT- NONCODI NG		
1905- 1906	cg36603177	233	TGAGATCAGGAG TTCGAGACCAGC C[C/T]AGCCAACA TAGTGAACCCCT GTCTC	C	T				SILENT- NONCODI NG		
1907- 1908	cg36618790	179	CAGGCACGGTG GTTACAGTCTGT AA[C/T]CCCAGCA CTTTGGGAGGCT GAGGAA	C	T				SILENT- NONCODI NG		

1909- 1910	cg36618790	207	CAGCACTTTGGG AGGCTGAGGAA GGT/CJGGATGA CTTGAGCCGAGG AGTTTGA	T	C				SILENT- NONCODI NG		
1911- 1912	cg36618790	212	CTTTGGGAGGCT GAGGAAGGTGG ATG/CJACTTGAG CCCAGGAGTTTG AGACCA	G	C				SILENT- NONCODI NG		
1913- 1914	cg36618790	227	GAAGGTGGATGA CTTGAGCCGAGG A/G/AJTTTGAGAC CAGCCTGGGCA ACATGG	G	A				SILENT- NONCODI NG		
1915- 1916	cg36623778	70	TGTGCCTATCAA GGTTGTGGTCGA C/C/GJGTTGGAA CGTGCCCGTCAC CGTCAC	C	G				SILENT- NONCODI NG		
1917- 1918	cg36733186	183	GCTCCACAGGAC AATGACCTTGGC C/C/GJGTGGCCC ATCCTCTCTGGC CTCCAT	C	G				SILENT- NONCODI NG		
1919- 1920	cg36753762	402	CAGGAGTTCAAG ACCAGCCTGGC CA/A/GJCATGATG AAACCCTGTCTC TACTAA	A	G				SILENT- NONCODI NG		
1921- 1922	cg36753762	446	CTACTAAAAATA CACAAAGTTAGC C/A/GJGGCGTGG TGGCACGTGCCT GTAATC	A	G				SILENT- NONCODI NG		
1923- 1924	cg36999717	240	CCTGCGCCTTCG GATACGATCAGC G/T/CJCTAGAGG CATTGGGGCCG ACGGCA	T	C				SILENT- NONCODI NG		

1925- 1926	cg36999717	264	GTCTAGAGGCAT TTGGGGCCGAC GG[C/gap]ATGCT TAGTGCCGACAA CCTCACCG	C	-				SILENT- NONCODI NG		
1927- 1928	cg37003369	300	GTGAGTTTCAGT TGATTTAAGGAA T[A/gap]AAAAA GACCATTTTGCT AAACACT	A	-				SILENT- NONCODI NG		
1929- 1930	cg37028403	405	CAGGTAACCCGC ATATTGTTGCTG GTT/CIGGAGTGC CCAAACACGGCAC TTGGAA	T	C				SILENT- NONCODI NG		
1931- 1932	cg37056126	109	CTGGGGCTCAG GCCCTATGACCC AA[C/T]GGCCATT GGTGGCCTGTC CTCATGG	C	T				SILENT- NONCODI NG		
1933- 1934	cg37056126	255	CAAACCAACAATA GCAGTTCTGGGT T[A/T]TGGGTTTG GTAAACCCACCT CAGGG	A	T				SILENT- NONCODI NG		
1935- 1936	cg37418902	172	ATCCACCTCACA AAGAAATGCAAC A[C/T]CCATTAGC GGTCACTCTCAT TCTCC	C	T				SILENT- NONCODI NG		
1937- 1938	cg37418902	182	CAAAGAAATGCA ACACCCATTAGC G[C/T]CACTCTC ATTCTCCTTGTC CAGCC	G	C				SILENT- NONCODI NG		

1939- 1940	cg38034239	137	GGCCTGGAACA GGAGAGCGGC GTA[G/gap]CTCG GGCTTCTATGAA GATCCCAGC	G	-			SILENT- NONCODI NG			
1941- 1942	cg38068769	193	TTATGCTCCTCA TCTTTCTAGATT G[G/A]TTCAGATG CCCCTTCTAGGA AGCCT	G	A			SILENT- NONCODI NG			
1943- 1944	cg38068769	209	TCTAGATTGGTT CAGATGCCCTT CT/C]AGGAAGC CTTCCCAGATT TCGCCC	T	C			SILENT- NONCODI NG			
1945- 1946	cg38070669	294	ACTGTTATGCCA CTGAAAAA A[A/gap]CAAAAA AACAAAAACCCAA AGCCAAA	A	-			SILENT- NONCODI NG			
1947- 1948	cg38206730	306	AGGTGTGCCACA TGTTCAATTTTCG G[T/C]TCAAGGC GTACACGTGCAG GTGTGT	T	C			SILENT- NONCODI NG			
1949- 1950	cg38206730	319	GTTCAATTTTCGG TTCAAGGCGTAC A[C/T]GTGCAGGT GTGTTACGTGTT CATT	C	T			SILENT- NONCODI NG			
1951- 1952	cg38276118	283	TTTGAATTAG CCAAAAA A[gap/A]TCAAAC CTTAAACATTGTT CAATTC	-	A			SILENT- NONCODI NG			

1953- 1954	cg38277495	482	CAGCACCTTGGG AGGCTGAGGTG GG[C/T]GGATCA CCTGAGGTTGG GAGTTCGA	C	T			SILENT- NONCODI NG		
1955- 1956	cg38278604	289	CAGGAATGTGAT AGAAAGTGGCTG G[C/T]AAGAGGG AGCTGAGGCTG GTGGGTC	G	C			SILENT- NONCODI NG		
1957- 1958	cg38279706	469	TGCAGCTCCATG GCTCAACAAGGT G[C/T]GGATGCC TGCTGGACCTGG CTGCCT	C	T			SILENT- NONCODI NG		
1959- 1960	cg38318472	52	CCACGTGTCATG ACTGCTGTGCT T[C/T]TCCAAGGC AGCATTTCAGACA CCCCG	C	T			SILENT- NONCODI NG		
1961- 1962	cg38323872	178	CGCCCGCCTCG GCCACCAAAAT GC[T/C]GGGACC ACAGGCTGTAAT TTATTT	T	C			SILENT- NONCODI NG		
1963- 1964	cg38323872	183	GCCTCGGCCAC CAAAATGCTGG GA[C/T]CACAGG CTGTAATTTATTT TTTTCA	C	T			SILENT- NONCODI NG		
1965- 1966	cg38323872	184	CCTCGGCCACCA AAAATGCTGGGA C[C/T]ACAGGCT GTAATTTATTTT TTCAT	C	T			SILENT- NONCODI NG		
1967- 1968	cg38326936	62	TGCGCGGCTG CGCACGCTGCT GGC[T/C]AAGAA CAACCGGCTCG GCGGGCCCA	T	C			SILENT- NONCODI NG		

1969- 1970	cg38338993	233	CTGTAGCCTAAG CAACAGAGCAAG AT/CJGCCGTCTC TGAAAAGGAAAG AAAC	T	C				SILENT- NONCODI NG		
1971- 1972	cg38341382	51	GGTGCTTAAGAC AGCAGACTGCTG C/T/CJTTCCTGGG CCAGGCCTGGG TTTATT	T	C				SILENT- NONCODI NG		
1973- 1974	cg38345418	404	TGGCCGCCTTCT CCAGTTGATGGG A/C/TAATGACA AGACCTCCAGCA TCTTC	C	T				SILENT- NONCODI NG		
1975- 1976	cg38350552	420	TCCTGGGCTAGG ATGACAGCTTCC T/C/AJCTCGTTCT CATCTGCTTCTG CCCAG	C	A				SILENT- NONCODI NG		
1977- 1978	cg38403226	113	CGCTGGGTGGC GCCATCGATAAG TC/T/CJTTGAAG CCGTCAAGATGG CTCCCG	T	C				SILENT- NONCODI NG		
1979- 1980	cg38403226	122	GGCCCATCGATA AGTCTCTTGAAG C/C/JGTCAAGAT GGTCCCCGGGG GGTCTA	C	T				SILENT- NONCODI NG		
1981- 1982	cg38403226	185	CGGCCGCCATT GTCATGCTCAGT GA/C/JGGGAATA ATACCCAAAGCG GTCTC	C	T				SILENT- NONCODI NG		
1983- 1984	cg38403226	189	CGCCATTGTCAT GCTCAGTGACG GG/JGJATAATAC CCAAGGCGGTTT TCCCGT	A	G				SILENT- NONCODI NG		

1985- 1986	cg38403226	203	TCAGTGACGGGAC ATAATACCCAAAG G[C/T]GGTTCTCC CCTGGTGGCGG CCAACC	C	T				SILENT- NONCODI NG			
1987- 1988	cg38403226	249	CAACCGAGCTGC CGCGGCCAAAG TC[T/C]CGGTGTA CACCATCGCCTT TGGTAC	T	C				SILENT- NONCODI NG			
1989- 1990	cg38403226	297	TACCGAGACCG GGTATGTCGACC TT[G/A]ACGGGC AGCGAGAGAGA GTTGCACC	G	A				SILENT- NONCODI NG			
1991- 1992	cg38403226	366	TACTGTCGCCGA CCGTACTCACGC T[A/C]AATCGTGG ACCGCCGACTC GGCGGA	A	C				SILENT- NONCODI NG			
1993- 1994	cg38403226	41	GGATGCCACCGT CGACCGACCGG CCT[T/C]ACCGTGT TACGTGCTGTTG ACGGAA	T	C				SILENT- NONCODI NG			
1995- 1996	cg38403231	120	AACGGAGAAGCT CGAAGTATCAAA G[C/T]GGTTGGAT TCGTCCGATGG GGCTCG	C	T				SILENT- NONCODI NG			
1997- 1998	cg38403231	88	TGGCAACTGGAT CGGTGTCATTGG G[A/T]TCGACGAA CGGAGAAGCTC GAAGTA	A	T				SILENT- NONCODI NG			

1999- 2000	cg38403266	269	CGGTATGCCTTT GATGGTCAGTCA CIA/GJTTGACGG GGCTGGAACG CTCGIGC	A	G			SILENT- NONCODI NG		
2001- 2002	cg38403266	292	ACATTGACGGGC GCTGGAACGCTC GTT/CJGCTGCCC GCTGACACCCG CACCGAC	T	C			SILENT- NONCODI NG		
2003- 2004	cg38403266	298	ACGGGCGCTGG AACGCTCGTGCT GC/CJGCTGA CACCGCACCG ACGACGGG	C	T			SILENT- NONCODI NG		
2005- 2006	cg38403271	182	TCAACGGCCCCAG TCGGAATTTGGA AIG/CJGATGATC GAACTTGCTGA CGAACT	G	C			SILENT- NONCODI NG		
2007- 2008	cg38403271	212	ATCGAAACTTGC TGACGAACTCTC C/CJGATGGTTCT GATGCCGGGTTT AAGTA	C	G			SILENT- NONCODI NG		
2009- 2010	cg38403276	265	AGCAGATCGCC GCATCTGATCCG GA[G/A]CATTCCA AGCGGTTGTTCT CCTTTG	G	A			SILENT- NONCODI NG		
2011- 2012	cg38403276	292	ATTCCAAAGCGGT TGTTCTCCTTTG C/CJGATGATGAT CGCTGGTATGGC CAGCC	C	T			SILENT- NONCODI NG		

2013- 2014	cg38403276	38	CTCTCAGATCCT CGACATTCTGTC TIG/AICGGGCCT GATTTTCGTCCG GCTGCT	G	A				SILENT- NONCODI NG		
2015- 2016	cg38403276	413	TGGAAGACTCGC CGAGAAACTCGG GTC/TGGCCTCT GCGAGCCCGCG TGGAGT	T	C				SILENT- NONCODI NG		
2017- 2018	cg38403276	427	AGAAACTCGGT TGGCCTCTGCGA GTC/TCCGCGTG GAGTGATGTTCC CGGGGT	C	T				SILENT- NONCODI NG		
2019- 2020	cg38403276	445	CTGCGAGCCCG CGTGGAGTGATG TTC/TGCGGGG TCACCTGCTTGG ACTATCG	C	T				SILENT- NONCODI NG		
2021- 2022	cg38403276	493	TCGATACCGCCA AGACCCCTACGCG ATC/TCTCGATGT GCCGACTCTCAT CGTCA	C	T				SILENT- NONCODI NG		
2023- 2024	cg38403276	494	CGATACCGCCAA GACCCTACGCGA CIC/TTCGATGT CCGACTCTCATC GTCAC	C	T				SILENT- NONCODI NG		
2025- 2026	cg38403276	550	GTGCGTATGACC TGACGCGGCAC GTC/TAAAGCCG GTCGAGATGCG AGGCTG	C	T				SILENT- NONCODI NG		
2027- 2028	cg38403276	595	AGGCTGCGGAC TTTCTATCTGAAT ATC/TGCCACCG AAGATATGGACC TTGCCG	C	T				SILENT- NONCODI NG		

2029- 2030	cg38403345	143	GTGTTGACGTGT AACTTGGATTCT C/C/TGGCTAAGT CGGCAATCGTCA CTGGT	C	T				SILENT- NONCODI NG		
2031- 2032	cg38403345	155	AACTTGGATTCT CCGGCTAAGTCG G/C/TAAATCGTCA CTGGTCCCGCT GGAGC	C	T				SILENT- NONCODI NG		
2033- 2034	cg38403345	188	ACTGGTCCCGC GTGGAGCGATAC TT/C/TTTTGAGG ACTGACTGCTGG GCAGGG	C	T				SILENT- NONCODI NG		
2035- 2036	cg38403345	225	ACTGCTGGGCA GGGGTGAGCGA TGC/G/AJTGATG GTGAGAAATTCG CCTATTC	G	A				SILENT- NONCODI NG		
2037- 2038	cg38403345	229	CTGGGCAGGGG TGAGCGATGCGA TG/A/GJTGGTGA GAATTCGCCTA TTCCTTG	A	G				SILENT- NONCODI NG		
2039- 2040	cg38403345	280	CCGGCTCATATC ACCATCCGTAGT G/C/TGCGGACG AAGATCCCAGAT GGCCGT	C	T				SILENT- NONCODI NG		
2041- 2042	cg38403345	286	CATATCACCATC CGTAGTGCCCGC G/A/C/TGAAGATC CCAGATGGCCGT TCTTGG	C	T				SILENT- NONCODI NG		
2043- 2044	cg38403345	331	TCTTGGACCTGT ATATGACGTATG GT/C/CJTTGTGG GTAGCTTACTGG CGCAG	T	C				SILENT- NONCODI NG		

2045- 2046	cg38403345	53	CCCCAGTATGGA CGGCCCCGGCC TGTC/JTCTGG GAGTTTCTCGCG TTCCACC	T	C				SILENT- NONCODI NG		
2047- 2048	cg38403345	80	GCTGGGAGTTTC TCGCGTTCCACC A[G/A]CCCCAAG GACACCAGCAC GTTGAGG	G	A				SILENT- NONCODI NG		
2049- 2050	cg38403345	96	GTTCCACCAGCC CCAAGGACACCA G[C/T]ACGTTGAG GGGCTCCCGAAT CGTGT	C	T				SILENT- NONCODI NG		
2051- 2052	cg38403377	1123	AAATCTTCTTGA CGATGACGTGCC CTT/GTGTCTGAG CGATCCCTGCTT CGTCG	T	G				SILENT- NONCODI NG		
2053- 2054	cg38403377	1124	AATCTTCTTGAC GATGACGTGCCC TTT/GTGTCTGAG GATCCCTGCTTC GTCGT	T	G				SILENT- NONCODI NG		
2055- 2056	cg38403377	1155	AGCGATCCCTGC TTCGTCGTTGCG TTG/AJCCGTGAG CGATCCGGACGT TGCACC	G	A				SILENT- NONCODI NG		
2057- 2058	cg38403377	991	CCTCTGCGACAT ATCGCTGGGCC GATTC/JGAGGCA TCGACGATCTCC CCGCGGT	T	C				SILENT- NONCODI NG		
2059- 2060	cg38402054	172	TCCAGGAAAGGA CAATGTCCTGCG A[G/gap]AAAAATC AGGAGGCCTCC ACTTCCTG	G	-				SILENT- NONCODI NG		

2061- 2062	cg38420254	57	CAGTCAATAATT GTCTTTGTGGAT GTT/CJGATAATTT TGGAGATAACACT TCTGG	T	C			SILENT- NONCODI NG		
2063- 2064	cg38421034	153	GGTGACTCTGAG CAAGTTCTGGAG C/C/TGGACGCA CAAGGGGCTCCT GAACAG	C	T			SILENT- NONCODI NG		
2065- 2066	cg38421040	330	TTGGCCCGTGTG GTCACCCCTGTGT T/C/TATCTCTCT CCCAGCCCATGG CCTCTC	C	T			SILENT- NONCODI NG		
2067- 2068	cg38433776	289	AGGCGTCGTAGT GGGCCACGATG AC/G/AJATGGTG GGAAGGTCCTCT CCGCCCA	G	A			SILENT- NONCODI NG		
2069- 2070	cg38438371	122	ACCTCGCTGATT CGTGCAGATTGA G/C/TTCAGTGTG TCTGGGACTGAG CTAAA	C	T			SILENT- NONCODI NG		
2071- 2072	cg38438371	157	CTGGGACTGAG CTAACACAGTGAG AC/G/AJTTGGAC CGTCTTTGATGT ACAGAG	G	A			SILENT- NONCODI NG		
2073- 2074	cg38438475	233	GGAAGAGGGGA AGGAAAAGGCA GCC[gap/G]TAAG GGAAGGCGCTG GCCTGAATCA	-	G			SILENT- NONCODI NG		

2075- 2076	cg38438944	101	ACGCACACTTAC CTTGACGCTTCA T[G/C]TCAGAGA GCAGCTGAGCA GCCAGCA	G	C				SILENT- NONCODI NG		
2077- 2078	cg38439545	80	CCTGGGGGCCA GTACCAGAGCAC AGT[C/C]CCGGAG TCTTCCGGCGG GATGCATG	T	C				SILENT- NONCODI NG		
2079- 2080	cg38444370	209	GCATCGTTTCCA CGATGAACCCCA TTC/TCTGGGAG CAGATATGACGA CGTACC	C	T				SILENT- NONCODI NG		
2081- 2082	cg38444370	413	AGTTCACCTGGG ACCAGGTCGACC TTC/C]GCTACTGT CGCAGACACCG GTCGGG	T	C				SILENT- NONCODI NG		
2083- 2084	cg38446357	139	TCGAGGACTTCG TTTTATCGGAGG AT/C]TCGTCGCG CAACCGATCAAT CTCAG	T	C				SILENT- NONCODI NG		
2085- 2086	cg38446357	181	CAATCTCAGTAG CGAAGTCCTCGA T[G/A]GTGTTGTA GTTCAAGTAAAC GCTGG	G	A				SILENT- NONCODI NG		
2087- 2088	cg38446357	190	TAGCGAAGTCCT CGATGGGTGTTGT A[G/C]TTCAAGTA AACGCTGGCAAA CCTCA	G	C				SILENT- NONCODI NG		
2089- 2090	cg38446357	228	CTGGCAACCTC AGGTAAGCGATG G[A/G]ATCAAGTT CACGCAGTGGC CCCAAG	A	G				SILENT- NONCODI NG		

2091- 2092	cg38446357	235	ACCTCAGGTAAG CGATGGAATCAA G[T/C]TCACGCA GTGGCCCCAAG ATCGCCA	T	C		SILENT- NONCODI NG		
2093- 2094	cg38446612	47	GCGTTAGAGTCG TCTTGCCGGCGC C[G/A]TTGCGAC CCACTAGACCGA CCTTGT	G	A		SILENT- NONCODI NG		
2095- 2096	cg38446612	67	GCGCCGTTGCG ACCCACTAGACC GA[C/T]CTTGTC CCAGTAGCTACC TGGAAA	C	T		SILENT- NONCODI NG		
2097- 2098	cg38446612	74	TGCGACCCACTA GACCGACCTTGT C[C/T]CCAGTAGC TACCTGGAACT CACCG	C	T		SILENT- NONCODI NG		
2099- 2100	cg38446677	266	GATCGGCGGTTG CCGGTTCGATAG G[G/T]GGCGTTAT AGTCATGATCAC CACCT	G	T		SILENT- NONCODI NG		
2101- 2102	cg38446677	401	ATCATGGGTGAC GACGACGAGGG TG[C/gap]GTCCC CGCCCGGTCGT CGCCGAAAG	C	-		SILENT- NONCODI NG		
2103- 2104	cg38453366	386	TCTTCGAGTTTT GTTCAAGTCTGG [G/C]TCTTCTGAC TGATTTTCCAAT GTCC	G	C		SILENT- NONCODI NG		

2105- 2106	cg38453366	407	CTGGGTCTTCTG ACTGATTTTCCA ATT/AGTCCAAGG TGCTGAACCGAA TGCAA	T	A				SILENT- NONCODI NG		
2107- 2108	cg38453366	415	TCTGACTGATTT TCCAATGTCCAA GIG/TTTGCTGAAC CGAATGCAATCA CCATT	G	T				SILENT- NONCODI NG		
2109- 2110	cg38453366	420	CTGATTTTCCAA TGTCGAAGTGC TIG/TAACCGAAT GCAATCACCATT CAATG	G	T				SILENT- NONCODI NG		
2111- 2112	cg38453366	424	TTTTCCAATGTC CAAGGTGCTGAA CIC/TTGAATGCAA TCACCATTCAAT GACAG	C	T				SILENT- NONCODI NG		
2113- 2114	cg38453366	430	AATGTCCAAGGT GCTGAACCGAAT GIC/TAATCACCA TTCAATGACAGC TCAAC	C	T				SILENT- NONCODI NG		
2115- 2116	cg38453366	443	CTGAACCGAATG CAATCACCATT A/C/CTGACAGCT CAACTTCCAAAT TTCTT	A	C				SILENT- NONCODI NG		
2117- 2118	cg38453366	446	ACCGAATGCAAT CACCATTCAATG A(gap)/A/CAGCTC AACTTCCAAATTT CTTTGA	-	A				SILENT- NONCODI NG		
2119- 2120	cg38453366	455	CAATCACCATT AATGACAGCTCA A/C/TTTCCAAAT TTCTTTGAATTC TTTT	C	T				SILENT- NONCODI NG		

2121- 2122	cg38453366	496	AATTTCTTTTAACT AGAACAAATCCAA T/CATGAAATC AGAATCTCTTCT GACG	T	C			SILENT- NONCODI NG			
2123- 2124	cg38453366	504	TTAACAGAACAA TCCAATATGAAA AT/CJCAGAACT CTTCTGACGGTG GGAGA	T	C			SILENT- NONCODI NG			
2125- 2126	cg38606941	84	TACAGATATATA CAAGATTCCCAC CT/CJGTATGCAA TTCTCTGGGTCA TCTGT	T	C			SILENT- NONCODI NG			
2127- 2128	cg38624864	16	ACCGGTCCCAGAT CAGT/GJGGAT GCCAGGACCCC TTTTGCAGG	T	G			SILENT- NONCODI NG			
2129- 2130	cg38628815	298	GTTGCACAGGCT CTCCAACTCCCA G/C/TCTCCAGG AATCCTCCAGCC TCAGCC	C	T			SILENT- NONCODI NG			
2131- 2132	cg38683973	245	CTTCAAAGTCT TTAATAACAGGG A/C/TJGAGCAAA TAAATTAGATAAA GCC	C	T			SILENT- NONCODI NG			
2133- 2134	cg38683973	298	AGAGATCGTGCT AAATACCAGCTT C/C/TJAGCAGTG GCTATCTGTGTCAG TCTAGC	C	T			SILENT- NONCODI NG			
2135- 2136	cg38691768	323	CTCCCAAAGTGC TGGGATTACAGG C/AGJTGAGCCA CTGCGCCGAGC CTCAAC	A	G			SILENT- NONCODI NG			

2137- 2138	cg38753049	354	GCAGCCTTGACCC TCCTGGGCTCAA G/C/TGATCCTTC TGCCTCAGCCTC CCAAG	C	T				SILENT- NONCODI NG		
2139- 2140	cg38863525	140	GGGATCACCAAG ATGGAAGAGTCG G/C/TAGAGTAC GAGCAGCGCG GCATAAA	C	T				SILENT- NONCODI NG		
2141- 2142	cg38864699	141	GCTGCCGAGCC TGGGTCTGAGCA GG/C/TJGGGAT GAGGACCAGGT GCTGAGGC	C	T				SILENT- NONCODI NG		
2143- 2144	cg38866989	113	ACAGAACCATCC TGGCAGATGGCA A/C/TJGGCTGTAG AGAAGACCCGCA GGCCC	C	T				SILENT- NONCODI NG		
2145- 2146	cg38868761	464	TCTGGGGTAGG GGCTGCTCCCC CAA/G/AJCCCCTG GGGGACTGTCT GGGACATC	G	A				SILENT- NONCODI NG		
2147- 2148	cg38868761	504	TCTGGGACATCC AGGCCCTGTCT C/T/GJTGCTTAA CCACTCACAACA GAGAA	T	G				SILENT- NONCODI NG		
2149- 2150	cg38868761	574	AAGAAGGCCCCA CACTTCTCCCAT C/C/TJGGCCTCC ACGTAAACGCGT	C	T				SILENT- NONCODI NG		
2151- 2152	cg38879618	294	GCTGAGAGCAG GAGTAGAAGGTC TG/C/TJAGCAGC ATTGAGAAAGTC ATAGAA	C	T				SILENT- NONCODI NG		

2153- 2154	cg38879658	57	GATCAGAATAAC TCCAGAGCACTG C[G/T]GTGTTTCT GACTGGCTGAAA TTGAT	G	T				SILENT- NONCODI NG			
2155- 2156	cg38880100	197	TCAGTTACGCGA TTCCGTGATCGC A[AVG]AGCTTGAA AGACTCGAGCCT GGACG	A	G				SILENT- NONCODI NG			
2157- 2158	cg38880100	236	CGAGCCTGGAC GCCAGGTGATTG TG[A/C]GCTCGTT CAACCATGTGCT GTTATC	A	C				SILENT- NONCODI NG			
2159- 2160	cg38884905	691	CAAAGCAACTGT GACCGAAAACCA A[C/A]TGCAAGAT TCTCAAGAGCCC TGAAG	C	A				SILENT- NONCODI NG			
2161- 2162	cg38884905	755	AATCATCCAAGA ACACACTAAGCC C[G/gap]CCAAGG GCCACCCCTGAC CATGTGG	G	-				SILENT- NONCODI NG			
2163- 2164	cg38890535	29	CACACGCGTTGG CGGAGAAACACT TTC/TGCCCCACAG TGTAGGGCCTCG CTTGG	C	T				SILENT- NONCODI NG			
2165- 2166	cg38892055	241	CCGAGAGGGCTG GCGAGGGTGTG CAG[C/T]ACGGC GCAGTGTGGCA GGGTCCCAG	C	T				SILENT- NONCODI NG			

2167- 2168	cg38892055	329	GATGAAGTGTCT TCCACGGCCAC C[A/G]GGACGCC ACTCGCCGCTG CTGCCA	A	G				SILENT- NONCODI NG		
2169- 2170	cg38892771	95	TCCTCTCTGGTT TCCACGGCGTGT C[T/C]GCCCTCT GAAGGTTAGCT CTCCC	T	C				SILENT- NONCODI NG		
2171- 2172	cg38898718	32	GACGACCGTGC CCGTACAAGCCG AA[G/A]CAACCGT CCCAAAAAGTAC AGAAAG	G	A				SILENT- NONCODI NG		
2173- 2174	cg38898718	339	CCAGGACGCC TTCTCTCAACCC TT[C/T]TGCAAG ACTCCGGATGCT GGCTCT	C	T				SILENT- NONCODI NG		
2175- 2176	cg38898718	350	TTCTCTCAACCC TTCTGGCAAGAC T[C/A]CGGATGCT GGCTCTTCCTCA GTGGC	C	A				SILENT- NONCODI NG		
2177- 2178	cg38898718	360	CCTTCTGGCAAG ACTCCGGATGCT G[G/A]CTCTTCCT CAGTGGCACGC CCTTAA	G	A				SILENT- NONCODI NG		
2179- 2180	cg38898734	174	ACATGGTGTAC CTTGAATAGGAA T[C/T]TCAGGCAA TCGAGACAGAGA GAGCC	C	T				SILENT- NONCODI NG		
2181- 2182	cg38899892	544	GCCAAAGATGCCA ACGAGCAGGC CA[A/G]GATTTGG GGAAGAGGGAC CACCATG	A	G				SILENT- NONCODI NG		

2183- 2184	cg38902436	638	TGACCGGGCCT CTGTGGAGGATG AC[A/G]GACGTA GTGGCTGGCTTC CTAGCCC	A	G				SILENT- NONCODI NG		
2185- 2186	cg38907673	253	GAGCGCACAGA GTGCTGTCGGG GGC[G/C]ATGAA TGCCAGAAATTT CAGAGCTG	G	C				SILENT- NONCODI NG		
2187- 2188	cg38907673	397	GAGTAGCCGCA GGTGCAAGGAC ACA[G/T]AACAGG GTGAGGAAAGA GTTTGGTT	G	T				SILENT- NONCODI NG		
2189- 2190	cg38909281	301	AACCTCTTAGTT GAGTACCCTGTT T[G/T]CAGTCCAA TGGTTGGGTGTC AGAAAT	G	T				SILENT- NONCODI NG		
2191- 2192	cg38912763	416	AAGAAGGGGGTT TGTTTCAGGAA G[C/G]ACTGTTAG CATCTTTGTTTCA AAGT	C	G				SILENT- NONCODI NG		
2193- 2194	cg38912763	451	ATCTTTGTTTCAA AGTTAACCTGTA[G/A]ACTAAGTTC CTCCCAAAGTTA GTTT	G	A				SILENT- NONCODI NG		
2195- 2196	cg38916043	102	CAGAGGATGGAT ATGGCAGCCGC AG[C/T]ACGGGC ACATGTGGTTCG CTGAGCA	C	T				SILENT- NONCODI NG		
2197- 2198	cg38916043	149	AGCATGGCGCC GGAGTGACGTG CGA[T/C]GGTGAT GAGGTGACGCG GGGGGATT	T	C				SILENT- NONCODI NG		

2199- 2200	cg38916043	167	CGTGCATGGT GATGAGGTGAC GCG[G/A]GGGA TTCCCACTCTCC GGTTCGTG	G	A				SILENT- NONCODI NG		
2201- 2202	cg38916043	170	GCGATGGTGATG AGGTGACGCG GG[G/A]GATTCC CACTCTCCGGT CGTGCTG	G	A				SILENT- NONCODI NG		
2203- 2204	cg38916043	263	AATGGCGAATGG CGAAATGGTGCT GT[C]GCGGTGG ATTATCCGTTGG TGTGCC	T	C				SILENT- NONCODI NG		
2205- 2206	cg38916043	61	CACGGCGTCATG CTTGCTCAGCTC A[A/G]CCGCGGT GAAACAGTCAGA GGATGG	A	G				SILENT- NONCODI NG		
2207- 2208	cg38916043	65	GCGTCATGCTTG CTCAGCTCAACC G[C/T]GGTGAAA CAGTCAGAGGAT GGATAT	C	T				SILENT- NONCODI NG		
2209- 2210	cg38921869	216	ACGATGAGGGC CATCACCAGAGAA GA[C/G]AACGGC CACCCTCGCAG ACCACCT	C	G				SILENT- NONCODI NG		
2211- 2212	cg38921869	372	GGGAGGATCGC GGCCACTGACCA CG[C/T]CAGTACC GGCAGGGTCAG GATCAGC	C	T				SILENT- NONCODI NG		

2213- 2214	cg38922874	490	TACCCGGACAGT TACGAGTCCATG TTC/G/CGAGCG CCCATTTGCTCAC CTTTTG	C	G				SILENT- NONCODI NG		
2215- 2216	cg38923147	241	TCTGCCCCCAAGG GCGAGAAGACG GG[C/gap]TTCGC AGCGACCCCTCG GGGGTCCAT	C	-				SILENT- NONCODI NG		
2217- 2218	cg38925867	224	CGAGGCGGTAA GGCTCACCCCG GCA[G/gap]CCCA CATCATCATCGT GGAGACGAT	G	-				SILENT- NONCODI NG		
2219- 2220	cg39331132	188	ATGGCAAGAGCT GGCCACCCACC CC[C/gap]TCCCC TTCCTTCCCAA GGCTGTGT	C	-				SILENT- NONCODI NG		
2221- 2222	cg39331132	195	GAGCTGGCCAC CCACCCCTCCCC CTT[gap]CCTTC CCAAAGGCTGTG TTTTGTCT	T	-				SILENT- NONCODI NG		
2223- 2224	cg39331132	259	TGTGACATGCTG TTTTAATTCAGT [G/A]ACCTCTTGG AAGGCACTGTCC CCAA	G	A				SILENT- NONCODI NG		
2225- 2226	cg39357997	279	CCTCTAGGAACC CAACCTTCTGCG TT[C]CATACACG CGCTCGCGCGC ACACGC	T	C				SILENT- NONCODI NG		

2227- 2228	cg393357997	332	GCACACACACAC ACACACACACAC A[C/gap]AGCAAG CAAGCCATCTCC GGTCACA	C	-				SILENT- NONCODI NG		
2229- 2230	cg39386977	109	TGTTTTTACACC AGCAGTCAAAA G/CJAGTTACTTT GATATTGCATGT GTC	G	C				SILENT- NONCODI NG		
2231- 2232	cg39413590	181	AAAGGAATATCC TCTCACCAGAGA C/A[gap]CGCGGC GGCCAGGCAGG GCCGGAGC	A	-				SILENT- NONCODI NG		
2233- 2234	cg39413590	314	GAGCTCTTGGAG CCACACCTGCGT GT/CJGCACATGT GTCACCCCACTG CTGGG	T	C				SILENT- NONCODI NG		
2235- 2236	cg39434475	246	GCCCTGCTGTG GATGGAATCCGG AG[G/gap]ACCCC AGCTCCCTGAGC AGCCCTC	G	-				SILENT- NONCODI NG		
2237- 2238	cg39457156	316	CAGCGTTAAGTG GCATACCCGGAA G[G/A]AAACACA GCAGCTCTTGA TATGAT	G	A				SILENT- NONCODI NG		
2239- 2240	cg39457156	57	ACTATGGTGCCA TGGTCGTCGATG C/A/TGGCGCTGT CCTGCCACAGTC ACGAC	A	T				SILENT- NONCODI NG		

2241- 2242	cg394622273	301	GAACGGACGCT GCCTCCTAGTAT TA[G/A]AATACCC AACTCTTTGATAT CTCCC	G	A				SILENT- NONCODI NG		
2243- 2244	cg39466668	512	ATATACCTTATTA : GCATTTCCTTTC[gap/A]AAAAAAC AGTTGCTTTTGG ATTTT	:	A				SILENT- NONCODI NG		
2245- 2246	cg39466668	519	TTATTAGCATTTTC CTTTCAAAAAA[gap/A]CAGTTGTC TTTGGATTTTGAT TGTC	-	A				SILENT- NONCODI NG		
2247- 2248	cg39485034	598	GTAAGAACTTGG TAGGCAGGTTGC G[C/T]TGCCACAC ATTGCGGATGAA CGCGT	C	T				SILENT- NONCODI NG		
2249- 2250	cg39507328	760	CGAGGAGAGAC TAACTTTTCACCT T[G/A]TTTCACCT GTGATCTGGGTC TGCGC	G	A				SILENT- NONCODI NG		
2251- 2252	cg39507822	136	TCAGCTTTCCTT AAGCCCTCTTCC A[G/T]AACAAATG AGACACTTACAT GTTTC	G	T				SILENT- NONCODI NG		
2253- 2254	cg39507822	352	TCAAAATTCCCTA GAGTCAAGATCT GT[C/T]TCTTGAC TCTGGTGCACCG GGAGA	T	C				SILENT- NONCODI NG		
2255- 2256	cg39512670	418	AATTAAGATCCT CCATTCTTCTAT [G/A]AAAAGTCAG GGACAAGGCAA GACAT	G	A				SILENT- NONCODI NG		

2257- 2258	cg39515262	106	CACTTCCCACTG TGCTCTGCCAAG C[C/G]TCTGTGG AGAGGAGCCCT CCACCTG	C	G				SILENT- NONCODI NG			
2259- 2260	cg39515274	243	GAGCCATGGCC GAGCCCTGCTG GG[C/T]CGGCG CGGGCGGGAGC GGGACGCGG	C	T				SILENT- NONCODI NG			
2261- 2262	cg39515274	395	GCITTCCAGCGG CCGGGAGGAGC GG[G/A]TCCTCG GGCCACGGAAG GTGAGCGC	G	A				SILENT- NONCODI NG			
2263- 2264	cg39515274	437	GGTAGCGCAC CTTTCGCTGAGC AC[A/G]GGGCGG CACCAGCGGGG CGGACCCC	A	G				SILENT- NONCODI NG			
2265- 2266	cg39515274	568	TTCCTCTCTTCG CCCTGCCAACCA C[T/gap]TTTTTAG TTTCTTCTCATCT CTCGG	T	-				SILENT- NONCODI NG			
2267- 2268	cg39516519	212	TAGAGCAGGTAC GCACTGATTTGA A[G/A]AGTAGTTG GTGTGTCTCCCA TACTG	G	A				SILENT- NONCODI NG			
2269- 2270	cg39517070	220	CAGAACCAAGGAC GATTGCTCCGAA G[G/gap]CCCCAC CACGAGGAAGG CAGCCAGG	G	-				SILENT- NONCODI NG			

2271- 2272	cg39517771	393	ACGGCTCTCTCG ACGGACAGGTC GG[G/A]GTTTTCT TCGTGATGATCG TGGCAG	G	A				SILENT- NONCODI NG			
2273- 2274	cg39517771	456	TTGTCGGTTTGG CGATCATCGTCA CTT/CJATTTCCG TTCCCGTCGCAC CACTT	T	C				SILENT- NONCODI NG			
2275- 2276	cg39517771	563	AACCGGCTTGTT CAACGTGGCCTG G[C/T]TCATGATT GCGGTGCCACT GGTGGT	C	T				SILENT- NONCODI NG			
2277- 2278	cg39521356	232	CCCAGAGCAAG CTGCGGCTCATT CA[C/T]GGACCC CTCAGAACACGGC TGGATGA	C	T				SILENT- NONCODI NG			
2279- 2280	cg39522018	520	ATACTCTGTGTG TCTATGTGCTTA G[C/T]GGGGAAC CTCCAGAGGAG GTGGTGA	C	T				SILENT- NONCODI NG			
2281- 2282	cg39523840	136	TGGCATTTTAA GTCGTGTAGAAC TTC/TACAACTTT TTAAACACCTTC CCATA	C	T				SILENT- NONCODI NG			
2283- 2284	cg39524105	53	TCTTGGAGCCAG GCATAGTGCTGG G[C/T]ACTGGTG CAAGCGAAGTG GAAGTCG	C	T				SILENT- NONCODI NG			
2285- 2286	cg39524138	196	GCTGACGAGATG ATCGCCCGCGA CG[G/A]GTTTCATC TGGCGCAGGCC TTGAGGA	G	A				SILENT- NONCODI NG			

2287- 2288	cg39524138	201	CGAGATGATCGC CCGCGACGGGT TC[A/G]TCTGGC GCAGGCCTTGA GGAGGAGA	A	G				SILENT- NONCODI NG			
2289- 2290	cg39524138	255	GATCGTCACGCT CAACGACACAC C[G/gap]CCTCGA AGATTGGTGGG GCCATCGT	G	-				SILENT- NONCODI NG			
2291- 2292	cg39524138	308	AGCCCCGTCGTA CCGTTGGTTCTG G[A/G]TCTGGTT GGTTCACACCCT CATT	A	G				SILENT- NONCODI NG			
2293- 2294	cg39524728	131	AGCCACCCACC GCCGGGTACCT GCA[C/A]AGCCA CATATATGCAAG TACACACA	C	A				SILENT- NONCODI NG			
2295- 2296	cg39524728	180	CACAGGCACTCG CACGCATGCATG CT[C/G]CATGCAAC ACACATGTACAC TCTAC	T	C				SILENT- NONCODI NG			
2297- 2298	cg39524728	279	CACCAGCCACAC ACAAGTACTCAT A[C/T]GCATACAT GCCACACACAAA AGTAC	C	T				SILENT- NONCODI NG			
2299- 2300	cg39524728	314	CCCACACACAAA GTACACACACGT A[C/A]ACCATATG CATATGTATGCA CTCAT	C	A				SILENT- NONCODI NG			
2301- 2302	cg39524728	348	CATATGTATGCA CTCATACACTCA T[A/G]CATATGTG CCCCCTCAGAGA AGTAC	A	G				SILENT- NONCODI NG			

2303- 2304	cg39524728	481	CAAGACACAAAC ACATGTACACGC A/C/TACATGCGC ACACACACGTAC ATCTA	C	T			SILENT- NONCODI NG			
2305- 2306	cg39530012	216	GCGCGCCTACCT TGCCAGACCCCTG G[G/gap]CACGCC TGCCCTTCAGGGT CCCAGGC	G	-			SILENT- NONCODI NG			
2307- 2308	cg39530012	299	GCTACAGCCTGC AGTCCTGAGCGT G[A/G]GGTGCTA TACTTCCCAGGA GACATC	A	G			SILENT- NONCODI NG			
2309- 2310	cg39530051	204	AAATTCATTACT TTTTATGGCTGA[G/A]TAACATCCC ATCGTATGGATG GACT	G	A			SILENT- NONCODI NG			
2311- 2312	cg39535156	315	GCGGGTCGTGA CGTAGCCGGGC AGG[gap]C]GCAA ACCGGTACCGG GAAAACGATG	.	C			SILENT- NONCODI NG			
2313- 2314	cg39535310	313	TTGAAGCAGGGC AGTAAATTTACC A[G/A]CTTCTTGA TGAAACATAACT CCAGT	G	A			SILENT- NONCODI NG			
2315- 2316	cg39535310	376	ATACTGCTAATA AATGACAGTGGC T[G/A]CTAACATC TCTTGAGCACTG CCCTT	G	A			SILENT- NONCODI NG			

2317- 2318	cg39535310	756	GAAGGGACAGG ACTTGGCTGCTG ATT/CJCCATGTG GAGGAGCTGCT CACGGTG	T	C				SILENT- NONCODI NG			
2319- 2320	cg39536028	440	ATCAGTCAAGCC GTCATGATCATC GT/GJGGGAAA GAAGTAACCAGG CAGAAT	T	G				SILENT- NONCODI NG			
2321- 2322	cg39536028	682	AGCAGGTGAGG GTCACTACCTCC TC/CJTTTCTG CCTGCCCGGCG CTCTCCG	C	A				SILENT- NONCODI NG			
2323- 2324	cg39536028	752	AACCATGGGTTT AGTGTCACCCAG A/C/TJTTAAAGGA CCCAGGACCTTC TCACC	C	T				SILENT- NONCODI NG			
2325- 2326	cg39537504	612	CAGGTCGTGAA GCTTCTGGGCTC A/G/AJGAGAGTCT TGGCCGACGCTT GCTCG	G	A				SILENT- NONCODI NG			
2327- 2328	cg39537504	880	TCGGGAACCTCG CCATGCCGCGCG CC[ga]/GJACCTC CCTACCCACCC GCCAGTCC	-	G				SILENT- NONCODI NG			
2329- 2330	cg39537504	893	CCATGCCGCGCG CCACCTCCCTAC CC/C/TJACCCGC CAGTCCTTCGCC GGCGCTC	C	T				SILENT- NONCODI NG			

2331- 2332	cg39537504	914	ACCCACCCGC CAGTCCTTCGCC GGC/TGCTCGG GGCTCCCGAT GCAATAGG	C	T				SILENT- NONCODI NG			
2333- 2334	cg39540190	86	TCAGATCCATGA GAGCTGCAAAGT T/A/GJCGGAAGC GTGAGCGCCGC TGGAGGA	A	G				SILENT- NONCODI NG			
2335- 2336	cg39540317	357	GAAAGTCAAGCA GTGGGAAGTACA T/G/AJGAGCTCTC AGCCCTGCTCCC ATCTG	G	A				SILENT- NONCODI NG			
2337- 2338	cg39540317	419	TCAGCAGATGGG CCACTGACTGAG C/G/AJTCGCCC GTCCCTGGTGCT ACTGGT	G	A				SILENT- NONCODI NG			
2339- 2340	cg39540317	427	TGGCCCACTGAC TGAGCGCTGCC CC/G/AJTCGCTG GTGCTACTGGTC TTTCTAA	G	A				SILENT- NONCODI NG			
2341- 2342	cg39540317	449	CCCGTCCCTGGT GCTACTGGTCTT T/C/TJTAACCTTA GCACCCCTGGAG AGTCCA	C	T				SILENT- NONCODI NG			
2343- 2344	cg39540317	458	GGTGCTACTGGT CTTTCTAAACTTA [G/A]CACCCCTGG AGAGTCCAAGGA GGCAG	G	A				SILENT- NONCODI NG			
2345- 2346	cg39540409	152	CATGTTTCTTC CTGGAGAAAGTG T/C/TJAGAAAAGT GTACAGCCTGG GGCCAA	C	T				SILENT- NONCODI NG			

2347- 2348	cg39540537	338	ACTGGCGGCAG GAATGAATCAGC AG[AG]TAGTCAT TTTCCCGCAGCC CTTCTA	A	G				SILENT- NONCODI NG		
2349- 2350	cg39541853	247	CTTCCCCATTA GATTTGTGTGT GTC/TGTGTGTT ATTATTTGGTA GGCGG	C	T				SILENT- NONCODI NG		
2351- 2352	cg39543172	393	CAGCAGCCGGG AGTAGTGCCCGC TT[C/G]CCCCACA GGAAGTTCCTGT CTGCCG	C	G				SILENT- NONCODI NG		
2353- 2354	cg39543172	394	AGCAGCCGGGA GTAGTGCCCGCT TC[C/G]CCCCACA GGAAGTTCCTGT CTGCCG	C	G				SILENT- NONCODI NG		
2355- 2356	cg39543172	426	GGAAGTTCCTGT CTGCCGCCACC CA[G/C]GGGTTG GTGCTGAGCAG CTTCTCAG	G	C				SILENT- NONCODI NG		
2357- 2358	cg39543172	670	AGCAAGCCCCAC AGCTGTCCTGCA C[G/A]AGTGGAG GCTGCTCACACA GCCCTT	G	A				SILENT- NONCODI NG		
2359- 2360	cg39545387	258	GTAGAGAGGGC CAGTGTGGTGC GAT[T/C]TTGTGG GAGGAGTTGAGA TTGGATG	T	C				SILENT- NONCODI NG		
2361- 2362	cg39545387	409	GTAGAGGAGGA AGTGACTGTCGG CA[AT]GTGTGGA GAGAGGAGCCC CAGCTTC	A	T				SILENT- NONCODI NG		

2363- 2364	cg39545387	691	CTTCACCTTAAT GTGAGGCTGATT C[G/A]TGAACCCA TTTATCTTGTG GCAGA	G	A				SILENT- NONCODI NG		
2365- 2366	cg39545619	673	GAGGGGCCGAC GAGCTGGTCT GCG[C/T]AAAGC AGTGAAGGCCG AGTTTGGCG	C	T				SILENT- NONCODI NG		
2367- 2368	cg39545619	678	GCCGACGAGCT GGTCTGCGCA AAG[C/T]AGTGAA GGCCGAGTTTG GCGGGGGC	C	T				SILENT- NONCODI NG		
2369- 2370	cg39545619	704	AGTGAAGGCCG AGTTTGGCGG GGC[A/G]CCCCG GGCTTCTCCTGC GAGGAGGA	A	G				SILENT- NONCODI NG		
2371- 2372	cg39545619	830	GCTGCAGAAATT GCGTGCCCAAGC AG[G/A]GAGAAG CACTCCACAACG TGCGCTT	G	A				SILENT- NONCODI NG		
2373- 2374	cg39545648	419	CTAGAGTATAAT TAAGGAGACTGC C[T/C]GTGCTTGC TGCTGGAGGGT GTATGT	T	C				SILENT- NONCODI NG		
2375- 2376	cg39559225	53	TCCAGCTTTAAA AAAAACACACAC A[Gap/C]AAACTTT GCCACAGTGTG CATGAG	-	C				SILENT- NONCODI NG		
2377- 2378	cg39559225	78	AAACTTTGCCA CAGTGTTCATG A[G/A]AATATGCT TGCTTTCATGTG CTGGC	G	A				SILENT- NONCODI NG		

2379- 2380	cg39559767	176	GCAAACCGGGC ATGGAGACCCCA TC[T/C]CAGGTCT GTGCTTCTCTGG GGGCCA	T	C				SILENT- NONCODI NG		
2381- 2382	cg39560753	330	TCGGCTGTCTTC TGCTGCCGGCA GG[A/T]ACGGGG CCTCAACCTTCT CTGGGCA	A	T				SILENT- NONCODI NG		
2383- 2384	cg39564627	138	GAGGAGCCCG AACACTGGGG CTGT[?]gap]GCTA CTAGCACCATAG AATTCAGGT	T	.				SILENT- NONCODI NG		
2385- 2386	cg39564627	47	CATAACAAGCG TAGGGTATGG GT[G/A]ACATTTC TACATTGCAGCA GCACAT	G	A				SILENT- NONCODI NG		
2387- 2388	cg39564709	184	GTTGGTCAGTGG GGTGGGCGCTG GG[C/gap]CTAAC TTTTCAAGCTGA AGATGCTC	C	.				SILENT- NONCODI NG		
2389- 2390	cg39565239	55	TCAAGGGACCC GAAGACTAGGG GAG[A/G]AGCAG CGAGCGGGTCG CGGCCGCGCT	A	G				SILENT- NONCODI NG		
2391- 2392	cg39571018	214	CCTCTGGTCCCG GTGCTAAGAGCA G[G/A]GTTGGTC CTGCAGCTTCTT GGCTGC	G	A				SILENT- NONCODI NG		

2393- 2394	cg39571022	83	CTGCATCCGCTG GTGGCAGAGAC AC[A/G]GTTGGG GGAGGCAGAGG TGGCACTG	A	G				SILENT- NONCODI NG			
2395- 2396	cg39574041	258	TTTGGAGGCC GAGCGGGCGG ATG[A/G]CAAGAT CAGGAGTTTGAG ACCAGCC	A	G				SILENT- NONCODI NG			
2397- 2398	cg39574041	260	TGGGAGGCCG GGCGGGCGGAT GAC[A/G]AGATCA GGAGTTTGAGAC CAGCCTG	A	G				SILENT- NONCODI NG			
2399- 2400	cg39575681	488	GCATTGGGTCTG CCCCGATCGTCG G[G/T]GCGTAGG GGTCCCAGACAT GACGTC	G	T				SILENT- NONCODI NG			
2401- 2402	cg39575791	187	AGCACACAAATG CCCACGTATGTG C[A/G]TGCATGAA AACACATGAAC ACACA	A	G				SILENT- NONCODI NG			
2403- 2404	cg39575791	444	GCACACGTGCAC ACACACAGCCAC A[T/C]GCACACAT CCACACGCACG CACACA	T	C				SILENT- NONCODI NG			
2405- 2406	cg39575852	270	GATGCGGACCTC AGTGGCCTGCA GG[C/gap]GCAGC GGGAAGCCACG CGT	C	.				SILENT- NONCODI NG			
2407- 2408	cg39575854	168	GACGCCCGCAG TTCCGGAAGATT CT[C/T]GGGGTTC GTGTAGCTACCC AGGCGG	C	T				SILENT- NONCODI NG			

2409- 2410	cg39575897	220	CTCTGTTAAGCT CCTCACCAGCCA TTC/TJTCCAGC GCCTCTCTCCCC TGGGC	C	T				SILENT- NONCODI NG		
2411- 2412	cg39581994	260	GAGATCAAGACC ATCCTGGCTAAC A/C/TJAGGAAAA CCCCGTCTCTAT TAAAA	C	T				SILENT- NONCODI NG		
2413- 2414	cg39581994	61	CTAGCCTGACCT GACTGTTAGAGT G/C/TJCAATCACT GTAAGCCACCAA GCTGC	C	T				SILENT- NONCODI NG		
2415- 2416	cg39582114	60	AAGACGGGTGCG GGTGGGTAGCC GAC[G/A]TCGCC GCCGACCCCGT GCGCTCGCT	G	A				SILENT- NONCODI NG		
2417- 2418	cg39582195	115	GTTCACTGTGAA AGCATTCTGCAC C/C/TJCCACAAC CCGCCTCTGGC CTGGCC	C	T				SILENT- NONCODI NG		
2419- 2420	cg39584802	451	ATCTAACGAGCT CAGCCGGCAGC TG[C/gap]ACGTG GGACCAGCCCT CTGAGCTTC	C	-				SILENT- NONCODI NG		
2421- 2422	cg39584802	525	GAACCAATACG AAGATAAAATGG G[A/gap]AAAAA AAATGCCATTCA CGGCACA	A	-				SILENT- NONCODI NG		

2423- 2424	cg39584802	534	ACGAAGATAAAA TGGGAAAAAAA A[A]gap]TCCCATT CACGGCACAGC CTGCCGA	A	-				SILENT- NONCODI NG			
2425- 2426	cg39585484	247	AGACATGGACCC ACACACAAACAT AT[C]GTGGACAC ACATGTACAAAC ATGCA	T	C				SILENT- NONCODI NG			
2427- 2428	cg39587361	228	CACATGCATACA TGCCCCACACACA C[A]gap]CTCATA CAGGTATACACA CCCATAT	A	-				SILENT- NONCODI NG			
2429- 2430	cg39587933	169	ACACAGCCAGAA TACAGCAAATAC AIG]TAGGCGAAT GCCAGCAGCAAA CCACT	G	T				SILENT- NONCODI NG			
2431- 2432	cg39587933	173	AGCCAGAATACA GCAAATACAGAG G[C]TGAATGCCA GCAGCAAACCAC TGAAC	C	T				SILENT- NONCODI NG			
2433- 2434	cg39587933	205	CAGCAGCAAACC ACTGAACTGAGA AT[C]AGGTCCCC TATTGAAGGAAT CAGAG	T	C				SILENT- NONCODI NG			
2435- 2436	cg39587933	209	AGCAAACCACTG AACTGAGAATAG G[T]A]CCCCATT GAAGGAATCAGA GAAAG	T	A				SILENT- NONCODI NG			

2437- 2438	cg39587933	214	ACCACTGAACGTG AGAATAGGTCCC CTT/CJATTGAAG AATCAGAGAAAG AACIG	T	C				SILENT- NONCODI NG		
2439- 2440	cg39587933	235	CCCCTATTGAAG GAATCAGAGAAA GJAGJACTGGAA GAGCTTGAAGG GGCTCGA	A	G				SILENT- NONCODI NG		
2441- 2442	cg39587933	282	TCGAGACCCCAA AAGTACAACAAT GIC/TJCAAGCAAC CAGAGCTTCCAG GGACT	C	T				SILENT- NONCODI NG		
2443- 2444	cg39587933	290	CCAAAAGTAGAA CAATGCCAAGCA AIC/TJCAGAGCTT CCAGGGACTAAG CCACT	C	T				SILENT- NONCODI NG		
2445- 2446	cg39592883	354	TGTCACITTTG CTTTCAGAGTCA C/T/CJGCTGCTGT AATAATCCTTGT ACATG	T	C				SILENT- NONCODI NG		
2447- 2448	cg39597328	382	TTCTTCTATACT ACAATTTTTTTTg ap/TJCATTTTTT CCTAATGTAGCG AAGC	-	T				SILENT- NONCODI NG		
2449- 2450	cg39597389	270	TTGGGGGACTAG AGGAGGGATAG CAT/TCTAGGAGA AATACCTAAAA AAGAAA	T	C				SILENT- NONCODI NG		
2451- 2452	cg39597389	406	TTCCCTTTTGAG TCCTGAACCCCG AIC/TJGTGCAAAA CCATCCCTTATC GATGA	C	T				SILENT- NONCODI NG		

2453- 2454	cg39602141	348	GAGGGCTAGTC CAGCCTTGTACA GG[C/T]TCCGCC CTTGACACCCGT	C	T				SILENT- NONCODI NG			
2455- 2456	cg39602254	226	GAGACAGGGTTT CACCATGTTGAC C[G/A]GGCTGGT CTCGAACTCCTG ACCTCA	G	A				SILENT- NONCODI NG			
2457- 2458	cg39602496	443	CCTCCGGTCCAG ACCTCGCCCCAG G[G/C]TTGCCCA GAGATGTAATCC AGGCTA	G	C				SILENT- NONCODI NG			
2459- 2460	cg39607243	212	ATGCTGTGTGTG TGTGTGTGTGTG T[gap/G]TTTTTGG GGGATGTGGGG GCCTGGA	-	G				SILENT- NONCODI NG			
2461- 2462	cg39607243	217	GTGTGTGTGTGT GTGTGTGTGTGT T[gap/T]GGGGGA TGTGGGGGCCT GGAGCCTG	-	T				SILENT- NONCODI NG			
2463- 2464	cg39607270	245	CCCCAGCGGCC TGGCGCCCATG GCA[G/A]TTCGG CAGCCGCTCACC GATACTCG	G	A				SILENT- NONCODI NG			
2465- 2466	cg39612908	688	TCTATGCAGGAC GCCGGTTCTGAA GT/CITGACAGAT ACACCATCAATG AGCAA	T	C				SILENT- NONCODI NG			
2467- 2468	cg39612908	701	CCGGTCTGAAG TTGACAGATACA C[C/gap]ATCAAT GAGCAAAACCGA TTTGACA	C	-				SILENT- NONCODI NG			

2469- 2470	cg39660253	182	ACCCTCCCCCGC CAGGTCCTGGCA G A T CTCGATGC ACAGAAAGGCTGT GAGCG	A	T				SILENT- NONCODI NG		
2471- 2472	cg39660253	195	AGGTCCTGGCA GACTCGATGCAC AG A C JAGGCTG TGAGCGGACCT GGCTGGGG	A	C				SILENT- NONCODI NG		
2473- 2474	cg39666355	179	TTCTGGGATTAC GCAGGTGTGAG CC A C CCGTAC CTGGCCCTTTT TTTTAT	A	C				SILENT- NONCODI NG		
2475- 2476	cg39666355	202	CCACCGTACCTG GCCCTTTTTTTT [T/gap]ATTTTAA GACAAGGTATTG CTCTG	T	-				SILENT- NONCODI NG		
2477- 2478	cg39667412	396	TGTGTTCCACA CCCAGGATGT GT G A GGCGGG TGCATGTGCACC ATGGCGT	G	A				SILENT- NONCODI NG		
2479- 2480	cg39667412	448	CACGTGCACCAT GGCGTGCACAC AA[G/gap]GGGA CTGTCAATCACA GGCTTTCA	G	-				SILENT- NONCODI NG		
2481- 2482	cg39667412	452	TGCACCATGGCG TGCACACAAGGG GG[gap]ACTGTC AATCACAGGCTT TCATATG	G	-				SILENT- NONCODI NG		
2483- 2484	cg39704218	359	GCTCAAGCGATC CTCCAACCCCGG C C T T C C C A A G TGCTGGGATTAC AGGCA	C	T				SILENT- NONCODI NG		

2485- 2486	cg39706539	180	CAAGCTCTGCTG GTCACCTCCAGTG G[G/A]GTCAACAT TTCAAGAAATGTT ACAAG	G	A				SILENT- NONCODI NG			
2487- 2488	cg39706539	224	TTACAAGCAGCT GGGCTTGGTGG CT[C/G]ATGCCCTA TAATCCCAGCAC TTTAAA	C	G				SILENT- NONCODI NG			
2489- 2490	cg39706617	52	CATATTCTTCAC CTAGCTTCCAAA A[C/T]CTATACTT CTCCTGGCTTTT CTCTG	C	T				SILENT- NONCODI NG			
2491- 2492	cg39707457	432	TCATTAAAGGAGG GAGCCCGCCAC GA[G/A]GATCTG GCTGCCCTCGGTT CTGCAGG	G	A				SILENT- NONCODI NG			
2493- 2494	cg39707457	444	GAGCCCGCCAC GAGGATCTGGCT GC[C/T]TCGGTTC TGCAGGCTGTCG CCACTC	C	T				SILENT- NONCODI NG			
2495- 2496	cg39707457	46	GCTCGCCGACG CCGCCGATGCC CTT[A/C]CCGGTG CAAAGGTGCGC GCGACCGT	A	C				SILENT- NONCODI NG			
2497- 2498	cg39707457	480	AGGCTGTCGCCA CTCAGTGCATTG C[C/T]GGCCTGG CATGTGGTCGCC CGATTG	C	T				SILENT- NONCODI NG			

2499- 2500	cg39707457	507	GCCTGGCATGTG GTGCCCCGATTG GTA/GGGTAAGG TCATCTTCCTTG GCGGTC	A	G				SILENT- NONCODI NG			
2501- 2502	cg39708746	71	AGCCAGGCATG GTGGCAGGTG CTG[C/T]AATCCC AGCTGCTCGGG AAGCTGAG	C	T				SILENT- NONCODI NG			
2503- 2504	cg39709129	349	GTTGGCAGCCAT TCATGGAGGGTG CT[C/T]ACCTGAA ATTGTTGCTCTT GGCCT	T	C				SILENT- NONCODI NG			
2505- 2506	cg39711126	50	GCTGCCTGGGA ACTCGAGCCAG GG[C/G]TTTC TCAGACTTATAT CAGCGCTAT	C	-				SILENT- NONCODI NG			
2507- 2508	cg39714236	263	GCTGACCGACAT TGCCCCATGGTG CT[C/G]CACTGTGT CTGGTCCTTTGG TGAGA	T	C				SILENT- NONCODI NG			
2509- 2510	cg39716704	408	CCTAATATCCA AGATTCCCTCTTT [G/T]ATGATTCC TTTATGTTTCAG GACT	G	T				SILENT- NONCODI NG			
2511- 2512	cg39721166	344	TTTCCCTTATCCT AAAGTATGTCCTT T/G]CATTCTTGT ACTGCACATCTG CTG	T	G				SILENT- NONCODI NG			
2513- 2514	cg39726191	354	TACTGAACAGCC CTTTGGAACTCT GTA/GATGATTG GGCCTCACAGAA GCTCC	A	G				SILENT- NONCODI NG			

2515- 2516	cg39731647	203	AGGTCCAGGCCT CGGCAGGCGAC CAJC/TCTGATT TCCTATGGACAA GCGCCC	C	T				SILENT- NONCODI NG		
2517- 2518	cg39731647	320	GATGAATGGATG AGCAAGGGGAA AG(A/gap)GAAGG GGAACACTTCAA AAATCCTC	A	-				SILENT- NONCODI NG		
2519- 2520	cg39731746	172	TCCACTTGGTGG TAGCCTGTGGTC TTT/C/GAGGCCAT GGAATGTCCAAG CCTGG	T	C				SILENT- NONCODI NG		
2521- 2522	cg39736402	215	GCCAGCTGGCC TCTGCGGGCAC GGG[G/gap]CCTT GCCCAGTGCATC CAGCTTCCA	G	-				SILENT- NONCODI NG		
2523- 2524	cg39736402	221	TGGCCTCTGCG GGCACGGGGCC TTG[C/gap]CCAG TGCATCCAGCTT CCAACGGGA	C	-				SILENT- NONCODI NG		
2525- 2526	cg39736402	223	GCCTCTGCGGG CACGGGGCCTT GCC[C/gap]AGTG CATCCAGCTTCC AACGGGACT	C	-				SILENT- NONCODI NG		
2527- 2528	cg39736402	261	TTCCAACGGGAC TAGTCCAGCGCC AIG[gap]CCCTGC CTGCCCCGAGCA CGGAATCT	G	-				SILENT- NONCODI NG		

2529- 2530	cg39736402	456	ATCTTCCTCCG TCCTTCCTGGCG C/C/GCTGGTTG CCACCTTGCCG TGCCTC	C	G				SILENT- NONCODI NG			
2531- 2532	cg40048937	487	AACACAAACACC TGGAAATCATG G(gap/TT)TTTTTT TAAAGGGGGCAA AGAAAG	-	T				SILENT- NONCODI NG			
2533- 2534	cg40048937	495	ACACCTGGAAAA TCATGGTTTTTT [T/gap]AAAGGGG GCAAAGAAAGAC ATTCA	T	-				SILENT- NONCODI NG			
2535- 2536	cg40048937	665	GGTATTACATT AGAAATTGGAAT T/C/TTACATTC AAGCAGAACACC TGTA	C	T				SILENT- NONCODI NG			
2537- 2538	cg40088791	468	CGGGCTCCGT AAGGCACAGCC GAG[A/G]GGGAG GTGGGGAGGCC CCAGTCCGA	A	G				SILENT- NONCODI NG			
2539- 2540	cg40088791	799	ATCCCAGCTACT CAGGAGGCTGA GGT/CJGGGAGG ATCACTTGAACC CCAGGAG	T	C				SILENT- NONCODI NG			
2541- 2542	cg40154721	297	ACAGTGAGCCAA GATTGTGCCACT G/C/TACTCCAGC CTGGGCGACAG AGTGAG	C	T				SILENT- NONCODI NG			

2543- 2544	cg40274847	299	TAAGGCTGGAAA GGAGGAGCTAG ATC/TJGGAGGA GAAACATCAGCA GGACTTG	C	T				SILENT- NONCODI NG			
2545- 2546	cg40274847	36	ACGTTGCCCAGG CTGGTCTCAAC A/GCJCTGGCTC AAACAATCCTCC CATCTT	G	C				SILENT- NONCODI NG			
2547- 2548	cg40296356	135	AGTTCTCCCCAA GGATGGCAAC GC/A/GJCCTGTG TGCCGGGCTCC GCGCAAGG	A	G				SILENT- NONCODI NG			
2549- 2550	cg40296356	149	GATGGCAACGCA CCTGTGTGCCG GG[C/gap]TCCGC GCAAGGGCTTTC CCTGTTTA	C	-				SILENT- NONCODI NG			
2551- 2552	cg40303588	354	CCTTGATTATGT GAGTAATGCGAG T/A/GJCCTGGTTG TTTCAGTTGAAG GTGCT	A	G				SILENT- NONCODI NG			
2553- 2554	cg40303588	392	AGTTGAAGGTGC TGTATTGACTTG C/C/TCTTTTCAT TCCTCTCCATGA GAGCC	C	T				SILENT- NONCODI NG			
2555- 2556	cg40307796	202	GCAGGAGAAGA CCTCCTTGTTCC CA/T/CJGGCTCAT GGCCACGTTGCT CCCATC	T	C				SILENT- NONCODI NG			
2557- 2558	cg40307796	259	CACCTGGTCTCAG GTCGCTGCCCTC CT/AJTTTCTCT TCTGGGAGTGG GGCTC	T	A				SILENT- NONCODI NG			

2559- 2560	cg40312834	332	AATCTTGGCAC CCGTTTCTCCGC A[G/gap]GAATGG CAGGAGATCCAG GGAAGGG	G	.				SILENT- NONCODI NG			
2561- 2562	cg40329454	68	CGCACGCGTTG GCCGGGCGCG CGG[T/G]GCTTG GCTGCGGTGCT CACACTCAT	T	G				SILENT- NONCODI NG			
2563- 2564	cg40341796	483	TAACATAAGCAG TGAAATGAGAC A[A/G]TGGAGTAT GGGAAGCAAAAA ATAAG	A	G				SILENT- NONCODI NG			
2565- 2566	cg40341796	495	TGAAATGAGAC AATGGAGTATGG G[A/G]AGCAAAAA ATAAGTCATTAG GCAGA	A	G				SILENT- NONCODI NG			
2567- 2568	cg40381397	303	CTTGAGTTGCT GGTAACAAACCT G[G/T]GCCTCCA CAATGGCAATGG GGGAGT	G	T				SILENT- NONCODI NG			
2569- 2570	cg40385017	72	AAACTTAAAGT ATAATAAAAAAAA [A/gap]TTTATATT AAATTAATCTGTA TGIG	A	.				SILENT- NONCODI NG			
2571- 2572	cg40389166	75	TGCTGGGACCAC AGGCGTGAGCC CCT[C/G]CACCC GGCCTGATTAC ATCATTT	T	C				SILENT- NONCODI NG			

2573- 2574	cg40389419	81	AAGGTTCAAAGT TTCAATAAATCC C[G/A]GAAACTA CATTCTAAAGG CTGTG	G	A				SILENT- NONCODI NG			
2575- 2576	cg40790872	390	TCTACTAAAAATA CAAAAATTAGCC[A/G]GGCATGGTG GCAGGCACCTGT AGTC	A	G				SILENT- NONCODI NG			
2577- 2578	cg40790872	406	AAATTAGCCAGG CATGGTGGCAG GC[A/G]CCTGTA GTCCCAGCTACT CGGGAGG	A	G				SILENT- NONCODI NG			
2579- 2580	cg40797606	440	TCCGGCCCGTGG GCGCCAGAAAGC GGT[C/G]GTGTA AATATGTGTGAA CAAGCGCT	T	C				SILENT- NONCODI NG			
2581- 2582	cg40797606	556	ACATGCTTTAAG ACTTGACTTCGG G[G/A]AAAAAAA AAAAAAAATTTT TTTT	G	A				SILENT- NONCODI NG			
2583- 2584	cg40885230	696	CCTGGGCCCTCCA GCTGCTGCAGAA G[G/A]ATGCCGC CGCCGCCCCCTG CCACCCC	G	A				SILENT- NONCODI NG			
2585- 2586	cg40927039	86	GCGTCTTCGGC ATCTTCTTTGGG G[C/T]CCTGGGC GGCCTCTTGCTG CTGGGG	C	T				SILENT- NONCODI NG			
2587- 2588	cg40932131	259	TGAAAGAAGCTT TTAACACCTGAA A[G/A]TCATCTCA AAATGGATATAT GGGTA	G	A				SILENT- NONCODI NG			

2589- 2590	cg40949022	569	TCAGAGACCAGC CCGGCCACATG G[C/T]GAAACCC CGTCCTCCACTAA AAATAC	C	T			SILENT- NONCODI NG			
2591- 2592	cg40949022	577	CAGCCCGGCCA ACATGGCGAAAC CC[C/T]GTCTCCA CTAAAAATACAA AAAATC	C	T			SILENT- NONCODI NG			
2593- 2594	cg40949022	583	GGCCAACATGG CGAAACCCCGTC TC[C/T]ACTAAAA ATACAAAAAATC AGCCAG	C	T			SILENT- NONCODI NG			
2595- 2596	cg40987225	413	CAACATGGCAAA ACCCCATCTCTA C[A/T]AAAAATAC AAAAAGATTAGC CAGGC	A	T			SILENT- NONCODI NG			
2597- 2598	cg40999240	399	TTCGCCATGTTG GCCAGGCTGGT CTT[C/G]ACCTCC TGAGCTCAAGAG ATCCAC	T	C			SILENT- NONCODI NG			
2599- 2600	cg41038983	473	CGCTTCCCCGCT CAGCGCACTCAG TTT[C/T]GCGGCTG GGAATGACCCCTC GCCGC	T	C			SILENT- NONCODI NG			
2601- 2602	cg41060726	128	CAATGGGCAAT ACACATTTTCTT G[G/A]TATTCTCC ACAAAGATAAAC TAATA	G	A			SILENT- NONCODI NG			
2603- 2604	cg41060726	206	CATCTCTTACCC TCTAAAAA A[A/gap]GGCAAT TATTTTAATTCCC TGTAAT	A	-			SILENT- NONCODI NG			

2605- 2606	cg41066315	407	AGGCCGCTTTCC CCTTCCTCTCGC C[C/gap]TGCGGC AGAGAGCGCAA CTTCCIGC	C	-			SILENT- NONCODI NG			
2607- 2608	cg41066315	522	CTCCTACTGCGG CGGTGGCGAGG CC[C/gap]TGCC GTGCCCTTCGAG CCGGCGCG	C	-			SILENT- NONCODI NG			
2609- 2610	cg41066315	527	ACTGCGGCGGT GGCGAGGCCCT GGC[C/gap]GTGC CCTTCGAGCCG GCGCGCCTGC	C	-			SILENT- NONCODI NG			
2611- 2612	cg41079413	357	CCTCTTCCCGCC TTTTCCGAGACT T[C/Γ]CTTAGACC TCATGATGTCTG GAATG	C	T			SILENT- NONCODI NG			
2613- 2614	cg41079413	383	CTTAGACCTCAT GATGCTGGAAT G[T/G]GACCTGG GAGATGCTGCAG CCTCCA	T	G			SILENT- NONCODI NG			
2615- 2616	cg41084544	198	ACAGGCATGCAC CACCATGCCCG GC[T/C]JAATTTG TATTTTGTAGTG AGACGG	T	C			SILENT- NONCODI NG			
2617- 2618	cg41084544	276	TGAACTCCCAA CGTCAGGTGATC C[G/A]CCTGCCTA GGCCTCCCAAAG TGCTG	G	A			SILENT- NONCODI NG			

2619- 2620	cg41084998	43	GGAGCTGGGAG TATCCCTCAAAG CC[AG]GGGCT GGGATGGGCATT AGCTTGT	A	G				SILENT- NONCODI NG		
2621- 2622	cg41085370	305	AAGGCTCTTAAA GCAACATTTAAA C[T/C]TTTTGGCG GCTGTCATTTCT GTGAG	T	C				SILENT- NONCODI NG		
2623- 2624	cg41085415	104	TTTTAAAGCTTTT TTGTAAGTCAGC[C/T]AGCAAGAAC ACAGGAAGAAAT ACTC	C	T				SILENT- NONCODI NG		
2625- 2626	cg41085637	295	TCCCGGGTGGG AAGAGGAACAGC CT[AC]TGTGGG CTTCCACGGAGG GCTGTGG	A	C				SILENT- NONCODI NG		
2627- 2628	cg41088106	272	CATATGACCTCC CTGCCCCGACCT C[T/G]CAGGTTG CTCCTTTCCCCA TCIGTA	T	G				SILENT- NONCODI NG		
2629- 2630	cg41090658	532	AAAGGCTGAAAC ACAGCATGTGAT G[C/T]GAGTCAA GGTAGTTGATGC CCAAC	C	T				SILENT- NONCODI NG		
2631- 2632	cg41362674	80	CAGGGTCATTTA TTTTGGCCAAAG G[AC]GGCCTCC AACGCCCCGAAA TGCTTC	A	C				SILENT- NONCODI NG		

2633- 2634	cg41389761	317	TGATGGTGTCTGT AGAACCCTCGAAGA A(Agap)CGGACC TGCAGTACAAC GACAGCA	A	.				SILENT- NONCODI NG		
2635- 2636	cg41389761	325	TCGTAGAACCAG AAGAAACGGACC T(Ggap)CGAGTA CAACGACAGCAT GATCGAT	G	.				SILENT- NONCODI NG		
2637- 2638	cg41394528	545	GATTTTCTTTA CTCAAGAATATA{ G/CJATCTAAAA AAAAAACACTT CTGC	G	C				SILENT- NONCODI NG		
2639- 2640	cg41394528	557	ACTCAAGAAATAT AGATCTAAAAA A(A/CJAAACACT TCTGCATCTCAA AAGCA	A	C				SILENT- NONCODI NG		
2641- 2642	cg41394528	558	CTCAAGAATATA GATCTAAAAA A(A/CJAAACACTT CTGCATCTCAA AGCAG	A	C				SILENT- NONCODI NG		
2643- 2644	cg41394528	596	ATCTCAAAAGCA GGCTCTACCTCC T(G/CJAGCTACAC ATATTGATCAGC ATTTT	G	C				SILENT- NONCODI NG		
2645- 2646	cg41567419	196	GGCTCAAGTAAT CTACCCACCTCA G(C/T)CTCCCAA GTGCTGGGATTA CAAGG	C	T				SILENT- NONCODI NG		

2647- 2648	cg41618657	561	GCTGTCCTATTT ACACTTACGTGT C/A/GJTGTTAAAA TAATCATTTTCTCT ATTA	A	G				SILENT- NONCODI NG		
2649- 2650	cg41622706	345	TTCCCTCTACCC ACAGAATGCCAA TIG/AJAGACCTCC CGACCATGACCA GTGT	G	A				SILENT- NONCODI NG		
2651- 2652	cg41628365	215	ATGGCTCACTGC AGCCTCAACCTC C/T/CJAGGCTCAA GCGATCCTCCTC TCAGC	T	C				SILENT- NONCODI NG		
2653- 2654	cg41628365	269	CCAAGTAGCTGG GACCACAGGCA CA/C/TJGCCACCA TGCCTGGCTAAT TTTTTA	C	T				SILENT- NONCODI NG		
2655- 2656	cg41640016	441	GCTGGGTGGGC GTGGAGGCAGG AGG[G/A]GCCCC AGCAAGGCCAG GGCAGGCAG	G	A				SILENT- NONCODI NG		
2657- 2658	cg41640016	457	GGCAGGAGGGG CCCCAGCAAGG CCA[G/C]GGCAG GCAGGAGGCTG CCTTCCCAT	G	C				SILENT- NONCODI NG		
2659- 2660	cg41643464	394	TTACACGGATAC TAAATGAGAAG A/A/GJTCGCACT TTTTGGTTTGGC CACTT	A	G				SILENT- NONCODI NG		

2661- 2662	cg41650847	254	CTCCCCACAGTC ATGGTGGCTGAA A[G/gap]CTGGTG TGCAACCTTGTT CCTCGAG	G	.				SILENT- NONCODI NG			
2663- 2664	cg41672460	513	GCAGCTCAGCTG GTGGCCGGGTG GC[C/gap]GGCCC GGCAACCCCA GTGAACCTG	C	.				SILENT- NONCODI NG			
2665- 2666	cg42036034	366	TGGCGCCCAGA AACTGCCGCTGC CG[C/A]TGACCTT GGCAGACTGC GCCCTCC	C	A				SILENT- NONCODI NG			
2667- 2668	cg42162412	463	GTGGTGAATCT CAGCTCACTGCA A[A/C]CTCTGCCT CCTGGGTTCAAG CCATT	A	C				SILENT- NONCODI NG			
2669- 2670	cg42162412	519	GCCTCAGCCTCC CAAGTAGCTGGG A[C/T]TACAGGCG CCGCCACCAC GCCCAG	C	T				SILENT- NONCODI NG			
2671- 2672	cg42176262	511	GGTGATCACTT GAGGTCAGGAG TT[C/T]GAGACCA ACCTGGCCCAACA TGGTGA	C	T				SILENT- NONCODI NG			
2673- 2674	cg42180672	198	GCCCCGGCTTTC CTTTGCTTTCCC G[T/C]TGGTTCAA GGTTTGAGCGCC TGCCG	T	C				SILENT- NONCODI NG			

2675- 2676	cg42186156	265	AACAAATACTTT CACCATTATATA A/C/TCTTTCAAA TTAAGGTTTGA GTAGA	C	T			SILENT- NONCODI NG		
2677- 2678	cg42282817	967	GGTGGGCAGCT CTTCATCCCTCT GAT/CJTTCAT CATATCTTCTCT TCCAG	T	C			SILENT- NONCODI NG		
2679- 2680	cg42283789	474	TGTCACCCAGAG AAGTGAACCTC A/G/CJCTTCCCA GCCAGTCTCTT CTTAT	G	C			SILENT- NONCODI NG		
2681- 2682	cg42283789	579	ATAGGTACTCTT TTGTGTCTGCTT T/G/AJTTCTGCTC AACACCATGTTT CTGAA	G	A			SILENT- NONCODI NG		
2683- 2684	cg42283789	623	TTCTGAAATCATT ACCATTGTTGTA T/CJGGTTCTCTA ACTCCATCATTT CCAT	T	C			SILENT- NONCODI NG		
2685- 2686	cg42308901	183	GGCGGGGCGG GTGGGGAGAGT GAG/CJTCGCG CCGCGGCTGGG GCGAGGCTA	C	T			SILENT- NONCODI NG		
2687- 2688	cg42313384	307	TCCTGGAGGACT ACGCCCTTCGTG T/G/JCGGGGCC TGCTGGACCTGT ATGAGG	G	T			SILENT- NONCODI NG		

2689- 2690	cg42322469	273	GAGCTACCGTGC CCGGCTTGAGGT GIC/TITTTTTAA CTAATACATTGT AGCAC	C	T				SILENT- NONCODI NG		
2691- 2692	cg42322469	439	GAGACAAGGTTT CACCATGTTGGC CIA/GGGCTGGT CTGACGCTCCTG ACTTCA	A	G				SILENT- NONCODI NG		
2693- 2694	cg423229503	531	TCACTCTCCAGA CCTTCCTAATTA AIC/TGCTCTCTC AGAATCGACCTT CTGTC	C	T				SILENT- NONCODI NG		
2695- 2696	cg42330545	252	CCGGCGGCCGC CTGACCCAGTCC ACIC/TTGCACCA GTGGGGTGTGG CATCAGT	C	T				SILENT- NONCODI NG		
2697- 2698	cg42330545	330	ACATTTCTGCCC CTAAGTTAGAGA AIC/TACACCTTT AGAGTGCGGATC TCATG	C	T				SILENT- NONCODI NG		
2699- 2700	cg42330545	345	AGTTAGAGAAC ACCTTTTAGAGT G/GA/CGATCTCA TGGGAGTGGCA GCTTGA	G	A				SILENT- NONCODI NG		
2701- 2702	cg42330545	355	CCACCTTTTAGA GTGGCGATCTCA TIG/AJGGAGTGG CAGCTTGACTCT GCAGGA	G	A				SILENT- NONCODI NG		
2703- 2704	cg42330545	401	CAGGAAATGTGG GTGCTATGAGTG CIA/GGAACAGA AACTCTTACCG TNC TGA	A	G				SILENT- NONCODI NG		

2705- 2706	cg423330545	498	GCTCTTTGAATT GAATAAAGGCAC CIG/AJCTGGATT CGAACCCAGGAT CTCCT	G	A				SILENT- NONCODI NG			
2707- 2708	cg423335352	258	GAAAGAACATC TCCAGAGGAAT G/C/GTGAATGA CCACGCCCGAG AGAACAG	C	G				SILENT- NONCODI NG			
2709- 2710	cg42340076	934	GGTTCTAGCTCC CTGTGTAGCTGT T/C/TCCAAAGTCT CTCTTCCTAACG TGGCT	C	T				SILENT- NONCODI NG			
2711- 2712	cg42340076	318	TGGTGCTGGCAC AGGCCCTTCCAG G/C/TJGGGAGGC TGGCTCTCAGGC TGGAGA	C	T				SILENT- NONCODI NG			
2713- 2714	cg42340076	691	AGCAGGAACAG GGCTCAGCACCA TG/C/TJCCGGCA CTCTTCATGCAT TACTGCG	C	T				SILENT- NONCODI NG			
2715- 2716	cg42340076	774	ACTAGCTAGCAA GGGGAAGGCTG GG[C/gap]CCAAG GAGATAAGGAAA CTGGGCCA	C	-				SILENT- NONCODI NG			
2717- 2718	cg42340076	809	TAAGGAACTGG GCCAGGGTCTC CC/A/GGCTTGA GCTTGGAGACG GGGTTTCA	A	G				SILENT- NONCODI NG			
2719- 2720	cg42340165	230	GATTTTATCTAA ATGAATAAATTTI C/A/TCTGTATTGT TAAACCATTTCT ACT	C	A				SILENT- NONCODI NG			

2721- 2722	cg42342525	613	TTCCGGGAAGG GATCACGGTGAT TGAGJGTGAAA GCCTCCATCGAC CCCGTC	A	G				SILENT- NONCODI NG		
2723- 2724	cg42343432	191	CTGGATGGCAAG TGCTACCCAGCA CAGJGCAGCCG TGAGGACCTTTC TTGGGC	A	G				SILENT- NONCODI NG		
2725- 2726	cg42344264	506	TACAGTTGACTT ACTTAAAGTGAT G[gap/A]JTATAATG CTGTTTCATGTA TTCAGA	-	A				SILENT- NONCODI NG		
2727- 2728	cg42344264	533	TTAATGCTGTTT CATGTATTTCAGA GTT/GJGTACAAAC CATCACAAATCAA TTTCA	T	G				SILENT- NONCODI NG		
2729- 2730	cg42344264	574	ATCAATTTCAGA GCATCCTCATAA GTC/JTGCACCCA AAAGAAACCCTG TACTCA	C	T				SILENT- NONCODI NG		
2731- 2732	cg42344264	598	GCGCACCCAAAA GAAACCCTGTAC TTC/JATTAGCAG TGAATCTCCATT TCCTC	C	T				SILENT- NONCODI NG		
2733- 2734	cg42344264	615	CCTGTACTCATT AGCAGTGAATCT CIC/JATTTCCTC GCAAACCTCCTC CCAGT	C	T				SILENT- NONCODI NG		
2735- 2736	cg42347810	473	TAAATGAATAC GTCTATTTATGC GTT/CJTAAAGAA TACCATGTAGTA GACGC	T	C				SILENT- NONCODI NG		

2737- 2738	cg42351001	324	AAGGGTCATCTG AAGTCGTGATTG G[G/gap]TCACTA ATAACACCAGGA CAAAGTT	G	-				SILENT- NONCODI NG		
2739- 2740	cg42356003	586	CGTAGTTACAAA TGCTTACTGATT T[G/A]CATATA TATTTTCATTGGA AGAC	G	A				SILENT- NONCODI NG		
2741- 2742	cg42356206	105	GAGGCGCAGGC AGAGCGCGCGG TAG[C/gap]TGGC CAGAGCAAGCAC GAGCAGCGG	C	-				SILENT- NONCODI NG		
2743- 2744	cg42369735	1118	TTCAGGTGACCA TGAAGGCACACG T[G/gap]CTACTT CTGGCCCGGGG GTGATATT	G	-				SILENT- NONCODI NG		
2745- 2746	cg42370741	367	AAAAGGCAATCT ACATCATCTGGA A[A/G]ATTGTAAC TTAGTAATTAATT AGGA	A	G				SILENT- NONCODI NG		
2747- 2748	cg42370741	374	AATCTACATCAT CTGGAATAATTGT A[A/C]CTTAGTAA TTAATTAGGATA ATTTC	A	C				SILENT- NONCODI NG		
2749- 2750	cg42381740	418	TATTCITGTGGG TGCCTGGAGGT GG[A/G]GTGAGG CCACCACCCCTG GGCTGTC	A	G				SILENT- NONCODI NG		

2751- 2752	cg42385141	58	TATTAAGAATTT CTAATTTGCATG[T/C]TTGTAGCCT GTTCTGGAGAGT TGGG	T	C				SILENT- NONCODI NG		
2753- 2754	cg42387697	966	GCAGGAAAGGC AGCCCAAGGAAT AG[C/T]AGGAGAT GTTGTTGGGTT TCACCA	C	T				SILENT- NONCODI NG		
2755- 2756	cg42387697	798	TGCTGAATCTGT GCTTTTGAATA GT[A/T]TGACTCA CAATGCTATTG CTGCA	T	A				SILENT- NONCODI NG		
2757- 2758	cg42387697	807	TGTGCTTTTGA ATAGTTTGACTC A[C/T]AATGCTAT TTGCTGCATGTG TATTG	C	T				SILENT- NONCODI NG		
2759- 2760	cg42392985	344	GAGAACCAAGCTG AAAAAGCTGTGG C[T/C]CGCATCCT GGTCCCGTGAC GACGG	T	C				SILENT- NONCODI NG		
2761- 2762	cg42458827	292	CACCCGTGGGC ACTGCCGGCTCT TC[T/C]GTCACAG TTCATCTTCATTG ACCTG	T	C				SILENT- NONCODI NG		
2763- 2764	cg42458827	300	GGCACTGCCGG CTCTTCTGTAC AG[T/C]TCATCTT CATTGACCTGCC TATGTT	T	C				SILENT- NONCODI NG		
2765- 2766	cg42458827	324	GTTTCATCTTCATT GACCTGCCTATG [T/C]TTCTTACCG CCCCCACAGCG GAACC	T	C				SILENT- NONCODI NG		

2767- 2768	cg42458827	332	TCATTGACCTGC CTATGTTTCTTAC [C/T]GCCCCCACC AGCGGAACCTTT TGCIG	C	T			SILENT- NONCODI NG			
2769- 2770	cg42458827	348	GTTTCTTACCGC CCCCACAGCGG AA[C/T]CTTTTGC TGAGAAATGATGA GGAGGC	C	T			SILENT- NONCODI NG			
2771- 2772	cg42458827	360	CCCCACAGCGG AACCTTTTGCTG AG[A/G]ATGATGA GGAGGCCCCACG ACGAAGG	A	G			SILENT- NONCODI NG			
2773- 2774	cg42458827	372	ACCTTTTGCTGA GAATGATGAGGA G[G/T]CCCCACGA CGAAGGCCCAGG CCCCGCGA	G	T			SILENT- NONCODI NG			
2775- 2776	cg42458827	420	CGAAGATCAGGC CTCCTTTGCGGA C[G/T]GTTTCATA GTCGTACTCGAA GGGAT	G	T			SILENT- NONCODI NG			
2777- 2778	cg42458827	432	CTCCTTTGCGGA CGGTTTCATAGT C[G/A]TACTCGAA GGGATTCTCTGT CCCCCT	G	A			SILENT- NONCODI NG			
2779- 2780	cg42460243	77	GAGTCCGAGACT GCTTGAGCGCTG C[G/gap]CACACC CCTCTCGTGGGC CCCCCACC	G	-			SILENT- NONCODI NG			

2781- 2782	cg42462239	1354	CACAGGAGAGA GCTGAAGGTGG GTGgap/G]CCCA GGCCAGGGTGT GAACTTTCTC	-	G				SILENT- NONCODI NG			
2783- 2784	cg42462775	247	GTGACTCCTTGT A TCATGAGAGCAG A[A]TTTTTAACA AGACAAGTATGA AAGGA	A	T				SILENT- NONCODI NG			
2785- 2786	cg42466107	84	AAATACCAACCG A GTCTGTAGTGTG T[A]G]CTCACCTA ATCACCTTCTGTT ATCGA	A	G				SILENT- NONCODI NG			
2787- 2788	cg42469263	232	AAATGTGGCACC C CAGAGGGAGTG GC[C/A]TAATAGC CAGTTACCAATA ATATAT	C	A				SILENT- NONCODI NG			
2789- 2790	cg42473468	411	CACAATCTCAGC C TCACTGCAACCT C[C/]ACCTCCCA GGTCAAGCGAT TCGCC	C	T				SILENT- NONCODI NG			
2791- 2792	cg42481310	541	GCTGGAATATA C AACATGGCATT T[C/]AGGTAAAG TTTCTTCCACTA GTGA	C	T				SILENT- NONCODI NG			
2793- 2794	cg42481963	328	GAGATCGTGCCA T CTGCACTCCAGC C[T/]GGGGGAC AAAGCAAGACTC CCTCTC	T	C				SILENT- NONCODI NG			

2795- 2796	cg42491212	300	GCCTCAGGAGC GGTGGCTGGATT TG[A/G]GAGAGA AAATTGGGTTTA GCATCAA	A	G				SILENT- NONCODI NG		
2797- 2798	cg42491212	345	CATCAAGGAGGT AACC CGCCCGTC C[C/Π]GGTACTTA CATCGTCGCCAC TCGCT	C	T				SILENT- NONCODI NG		
2799- 2800	cg42495105	123	TTTCACTGACGC CTAGGC TTGTCA T[G/A]CTGGCAG GTGAGAGTGTG TGGTTG	G	A				SILENT- NONCODI NG		
2801- 2802	cg42500135	780	AGCCCAACATCTG CCTCTGGCCCTC A[G/gap]GGGCGC TGGGAAAGGA AGGCCAAA	G	-				SILENT- NONCODI NG		
2803- 2804	cg42500135	926	CTCCTCAGCACG TGCTGGTGGGC C[A/G]GGCGTGC AGTGATGTGGC CAGGTC	A	G				SILENT- NONCODI NG		
2805- 2806	cg42500135	933	GCACGTGTCTGG TGGCCAGGCG TG[C/gap]AGTGA TGTGGGCCAGG TCCGCGGCC	C	-				SILENT- NONCODI NG		
2807- 2808	cg42500135	946	GGGCCAGGCGT GCAGTGATGTGG GC[C/G]AGGTCC GCGGCCCTGTCC AGCTTGA	C	G				SILENT- NONCODI NG		

2809- 2810	cg42501567	223	GCCTCAGTCCCC TCAGCGCCTTCT GTT/CJCTTCTGGC TGATTTCAGAGT CCCCG	T	C				SILENT- NONCODI NG		
2811- 2812	cg42510617	440	AGCCTAGGAGTT TGAGACCAGCCT ATG/AJACACATA GTGAGAAATCCA TCICA	G	A				SILENT- NONCODI NG		
2813- 2814	cg42513366	302	GTGGACGCTGTT CCTGCCTGAGAG TTC/TCTTTAGAG GAAGGCTGGGA ACACTG	C	T				SILENT- NONCODI NG		
2815- 2816	cg42513366	304	GGACGCTGTTCC TGCCTGAGAGTC TTC/TTTAGAGGA AGGCTGGGAAC ACTGTG	C	T				SILENT- NONCODI NG		
2817- 2818	cg42513366	443	TTTTTGGTAGA AAGTTTGCTTTT [G/T]TTTTTTTTT TTAAGACAAGG TCT	G	T				SILENT- NONCODI NG		
2819- 2820	cg42513366	454	AAAGTTTGCTTTT TGTTTTTTTTTTT /gap]TTAAGACAA GGTCTCATTCTG TCAC	T	-				SILENT- NONCODI NG		
2821- 2822	cg42513366	455	AAGTTTGCTTTT GTTTTTTTTTTT /gap]TAAGACAAG GTCTCATTCTGT CACC	T	-				SILENT- NONCODI NG		
2823- 2824	cg42513366	456	AGTTTGCTTTT GTTTTTTTTTTT T/gap]AAGACAAG GTCTCATTCTGT CACCC	T	-				SILENT- NONCODI NG		

2825- 2826	cg42513533	205	GCAGCCTCTCAG CTGCCACCATGG A[G/C]CACCTGG CGGCAGAACGC AGACCTC	G	C			SILENT- NONCODI NG		
2827- 2828	cg42513533	207	AGCCTCTCAGCT GCCACCATGGA GC[A/G]CCTGGC GGCAGAACGCA GACCTCTA	A	G			SILENT- NONCODI NG		
2829- 2830	cg42513533	221	CACCATGGAGCA CCTGGCGGCAG AA[C/A]GCAGAC CTCTAGCTCTCT TTGCCAG	C	A			SILENT- NONCODI NG		
2831- 2832	cg42513533	222	ACCATGGAGCAC CTGGCGGCAGA AC[G/C]CAGACC TCTAGCTCTCTT TGCCAGC	G	C			SILENT- NONCODI NG		
2833- 2834	cg42513533	243	GAACGCAGACCT CTAGCTCTCTTT G[C/A]CAGCCTC CTGGCTAGACCT GCGTTC	C	A			SILENT- NONCODI NG		
2835- 2836	cg42513533	266	TGCCAGCCTCCT GGCTAGACCTGC GT[C/T]CATTGCG CACCCCTGGCTGA CGTGC	T	C			SILENT- NONCODI NG		
2837- 2838	cg42513533	398	TTAGTCAAAGCC TGGAGAATAGTT A[C/T]ATCTCCTG GATGATCAGTTC AGAAA	C	T			SILENT- NONCODI NG		
2839- 2840	cg42513533	507	AGTGCAGAGATA TATCACAATGTC C[C/G]CTGTACAA AAAGCCTGGAAA TGATT	C	G			SILENT- NONCODI NG		

2841- 2842	cg42521007	439	AAGGTGGGTGG GTTGGTCCAGTA AAAGJTGACTGC ACCATCACACAA GCCAAG	A	G				SILENT- NONCODI NG			
2843- 2844	cg42527623	969	GAAGCAAACTCC CAAATGGGCAC AAGJAGGTAATA AAAAGCAGCTGA GAGAT	A	G				SILENT- NONCODI NG			
2845- 2846	cg42527623	723	AAACACTGGAAC ACCAGGTCTCTC AAGJATGCCCCG CGGAGGGGCC CCAGGGA	G	C				SILENT- NONCODI NG			
2847- 2848	cg42528323	392	CCCCAGAAAGCT GGGAATTGAGAG CAGJCAAGCATA TGGCTCACAAGG CCCCG	A	T				SILENT- NONCODI NG			
2849- 2850	cg42528323	400	ACCTGGGAATTG AGAGCACAAAGCA TACJTGCTCAG AAGCCCCCGCC CTGCCA	A	C				SILENT- NONCODI NG			
2851- 2852	cg42528323	401	CCTGGGAATTGA GAGCACAAAGCAT ATAGGCTCACA AGCCCCCGCCC TGCCAG	T	A				SILENT- NONCODI NG			
2853- 2854	cg42528323	407	AATTGAGAGCAC AAGCATATGGCT CAGJCAAGGCC CCGCCCTGCCA GCGGCC	A	T				SILENT- NONCODI NG			

2855- 2856	cg42528323	408	ATTGAGAGCACA AGCATATGGCTC A/C/T/AAGGCC CGCCCTGCCAG CGGCCCC	C	T				SILENT- NONCODI NG		
2857- 2858	cg42528323	443	CCCTGCCAGCG GCCCGCCCCA CCTT/gap]TCATT CATTGCTGGCTG CTAGGAGC	T	-				SILENT- NONCODI NG		
2859- 2860	cg42528323	444	CTGCCAGCGG CCCCGCCCCAC CTT/gap]CATT ATTGCTGGCTGC TAGGAGCT	T	-				SILENT- NONCODI NG		
2861- 2862	cg42528509	87	AGAAAAAGCTC CAGAGTTTCCTA TT/G]TTGGAGAA GCAGAACTGGTT GATTC	T	G				SILENT- NONCODI NG		
2863- 2864	cg42532779	545	TGTGAAACTTGC TTCTTTTTTTTTT T/gap]TTGAGACG GAGTCTCGCTCT GTCGC	T	-				SILENT- NONCODI NG		
2865- 2866	cg42532779	546	GTGAAACTTGCT TTCTTTTTTTTTT T/gap]TGAGACG GAGTCTCGCTCT GTCGCC	T	-				SILENT- NONCODI NG		
2867- 2868	cg42532779	547	TGAAACTTGCTT TCITTTTTTTTTT T/gap]GAGACGG AGTCTCGCTCTG TCGCC	T	-				SILENT- NONCODI NG		

2869- 2870	cg42537030	353	GGTGCCCTGC CCTTGCGGCT TCG/TJGGCG AGGCGCTAACA ACTACCG	G	T				SILENT- NONCODI NG		
2871- 2872	cg42537030	421	AGTTCGGGCC GGGTCATCGA GAIC/TJCCCCA GTACCCCAACCC GGCACTGC	C	T				SILENT- NONCODI NG		
2873- 2874	cg42539286	518	GGTGGCAGGT GGTCCTTAAAG GAIC/TJATCTGC TTAGAAATACG ATAAAT	C	T				SILENT- NONCODI NG		
2875- 2876	cg42542592	208	TAGAGAGGGGT TTCACCGTGTG GIC/TJGAGGCTG GTCCTAAACTGC CAACCT	C	T				SILENT- NONCODI NG		
2877- 2878	cg42543610	292	ATTCATCAATTC AACTTTCCCTG C/AJAGTAATAC TGGATGAAAT AACT	C	A				SILENT- NONCODI NG		
2879- 2880	cg42543610	416	AATAAACATAA ATTTCCCTTAATTT [G/gap]ATACTGT AAATGGAGTAAT TTGGTG	G	-				SILENT- NONCODI NG		
2881- 2882	cg42544183	650	CCTCCCAAAGTG CTGGGATTACAG GIC/TJGTGAGCTT CTGTGCCCCAGCC ATAAG	C	T				SILENT- NONCODI NG		
2883- 2884	cg42546822	253	GTATTCTGTGTT CCTAAGAAAAA A[gap/A]GAATTC TGAGCTTCACGA CCTTCT	-	A				SILENT- NONCODI NG		

2885- 2886	cg42547288	371	AAGACTTTTCAGA CCAGTCTGGCA AT/CJGTGGCGA GACCGTCTCTAC AAAAA	T	C				SILENT- NONCODI NG		
2887- 2888	cg42548835	511	GATTACAGGCGT GAGCCACTGIGC C/T/CJGTGCTTT TAATTTTTTAAAT GCCT	T	C				SILENT- NONCODI NG		
2889- 2890	cg42549000	403	CTCACGGAACGT CAGCAACGATCC CIG/CJATGTCATC AAGTTGCAAGAG ATTCC	G	C				SILENT- NONCODI NG		
2891- 2892	cg42560726	587	TCCCGCGGTGA GCCAGGTGTGG TGGIgap/CJTCAC GCCTGTAATCTC AGCACICIG	-	C				SILENT- NONCODI NG		
2893- 2894	cg42563045	447	GAACCAAAATAC AGGAAAAA A/AgapJTACAAC AGGTCGCACAA CATCCAG	A	-				SILENT- NONCODI NG		
2895- 2896	cg42563666	113	ATGATCTCATCA AAGAGATAACGG A/G/CJATCTTCCC ACGGGACCTGG GGAGGG	G	C				SILENT- NONCODI NG		
2897- 2898	cg42566605	352	GTCAAATAGGAT GGTGGCTGGGG CC/A/GJGGGCTC TGGGGACTCCTT CTGCCCC	A	G				SILENT- NONCODI NG		
2899- 2900	cg42647678	356	ACAACCCCTTAT CTTAACCCAGAC A/C/TJCCCTTCT ATTGATTCTAGG TCCTT	C	T				SILENT- NONCODI NG		

2901- 2902	cg42653839	337	ACTTTAAATTAAG ATAAGAGTATTT G/ATTATGGAGG ATTACTCTAAAG CCAA	G	A				SILENT- NONCODI NG			
2903- 2904	cg42655636	792	TTATTTTGTAGT TCAATGCTTTT C/GJTCCCGGAG GAAAGGGAGGA GCTCA	C	G				SILENT- NONCODI NG			
2905- 2906	cg42655636	798	TTGTAGTTTCAAT GCTTTCTTCCC C/GJGAGGAAAG GGAGGAGCTCA GGAGAA	C	G				SILENT- NONCODI NG			
2907- 2908	cg42655636	831	GGAGGAGCTC AGGAGAACAGTG TC/A/GJTCAAAT TTCCTGGTGGTT GTTTAA	A	G				SILENT- NONCODI NG			
2909- 2910	cg42655636	864	TTCTGGTGGTT GTTTAAATCACAG C/A/CJGCAGAGT AGGTCAGGAAAC TCTTCC	A	C				SILENT- NONCODI NG			
2911- 2912	cg42655636	867	CTGGTGGTGGTT TAATCACAGCAG C/A/CJGAGTAGG TCAGGAAACTCT TCCAGA	A	C				SILENT- NONCODI NG			
2913- 2914	cg42660192	184	GGAGAGCAGTTT CTCATAAAAGCT T[G/T]TGGATTCA ACTGTAAAAGTG GCAAT	G	T				SILENT- NONCODI NG			
2915- 2916	cg42660573	250	TCACATCTTGGC ACATTTAAGAGA C/A/TJGTCACCCC AGGACTCAAAA TAGGG	A	T				SILENT- NONCODI NG			

2917- 2918	cg42663908	424	TCAGCTGATATG AAATTATAAAATT [C/T]CACAAGTCT GAGTATTTGAAA CTTA	C	T				SILENT- NONCODI NG		
2919- 2920	cg42663908	425	CAGCTGATATGA AAATTATAAAATTC [C/T]JACAAGTCTG AGTATTTGAAAC TTAT	C	T				SILENT- NONCODI NG		
2921- 2922	cg42664168	291	TTGATCCCACCT AACACCAAATGG G[A/G]CTCCCAA TAGCGTTTGTG TTAT	A	G				SILENT- NONCODI NG		
2923- 2924	cg42667019	1413	CAGATAATTCTC AAGAAACGTGAA G[A/G]GCTCTTTA ATTAATATTAAAG TGAG	A	G				SILENT- NONCODI NG		
2925- 2926	cg42667523	402	CGGGTGCAGGG GGAGGAGAGAA CAG[A/G]GAAGT GCATGGTCTCAC CAGCTGGC	A	G				SILENT- NONCODI NG		
2927- 2928	cg42667523	460	GCAGCCCAGGA CCCTGCTGGGG CGA[G/A]CATTCC TTTTAGAAAAGA AAACCCA	G	A				SILENT- NONCODI NG		
2929- 2930	cg42667523	477	TGGGGCGAGCA TTCCTTTTAGAAA A[G/A]AAAAACCCA TCAGCAGGTATG AAGCC	G	A				SILENT- NONCODI NG		

2931- 2932	cg42667523	492	TTTTAGAAAAGA AAACCCATCAGC A[G/A]GTATGAAG CCCTCAGGGTCT GGTAT	G	A				SILENT- NONCODI NG		
2933- 2934	cg42667523	503	AAAACCCATCAG CAGGTATGAAGC C[C/TT]CAGGGTC TGGTATCAAAGG TGGGT	C	T				SILENT- NONCODI NG		
2935- 2936	cg42667523	535	TCTGGTATCAAA GGTGGTGGATT G[C/T]ACCTTGGC CTCTTATGTCATT AGGA	C	T				SILENT- NONCODI NG		
2937- 2938	cg42667523	545	AAGTGGGTGG ATTGCACCTTGG CC[T/C]CTTATGT CATTAGGAAAGG GGTTC	T	C—				SILENT- NONCODI NG		
2939- 2940	cg42667523	604	CCAGAGCCCAG GACAAATCCATG GA[C/T]AAATAAT GGGAGAGATGTG GTCAGGC	C	T				SILENT- NONCODI NG		
2941- 2942	cg42669434	155	CAAGCATAGCTT CCTAACTTTCAC A[G/A]CCATTACAG TAGATTTAGTGG ATGCC	G	A				SILENT- NONCODI NG		
2943- 2944	cg42669440	134	AAAATTTCATTGA GGGGGGGGCTC GC[A/G]TTGTACA AAGAAAATCAGA CCCACC	A	G				SILENT- NONCODI NG		
2945- 2946	cg42669876	286	CATGTCATGAGA ATATCAGGAACA C[A/T]CATTAAAC ATGAATTAGGTA CCTGC	A	T				SILENT- NONCODI NG		

2947- 2948	cg42669876	298	ATATCAGGAACA CACATTAAACAT GATATTAGGTA CCTGCCCTGTGG CAAGT	A	T				SILENT- NONCODI NG			
2949- 2950	cg42669876	373	GTCAGGCAACCC TAGGAAAAGCCC TATTAAGTGAAG GGGAAAAGAC ACACAC	A	T				SILENT- NONCODI NG			
2951- 2952	cg42669876	428	GTAACAGGAAT ACACACACAGGT AATCJACAAATG CTGCCAAGAG CCCAGA	A	C				SILENT- NONCODI NG			
2953- 2954	cg42670494	119	CCTGCTCCTTAA GTTTCAGTCCT CIGTCTCACCCCT GGAAGGAGACC TGAAAT	G	T				SILENT- NONCODI NG			
2955- 2956	cg42670494	141	CTCGCTCACCCCT GGAAGGAGACC TGATGATATCACA GGACAACGGCA GTGTGAC	A	G				SILENT- NONCODI NG			
2957- 2958	cg42670494	198	GTACAGGAGAG CAGAGCCTCCCA TTTgagCJCCAGG CACCCAGAGTTC CATTCCAG	.	C				SILENT- NONCODI NG			
2959- 2960	cg42670494	266	TCCTTCTTCTGG CACCATAATCTGT ATGATAGTTTGTCT GAACACCAAGCA ATTCT	G	A				SILENT- NONCODI NG			

2961- 2962	cg42670494	296	TGCTGAACACCA AGCAATTCTCCA A/C/AJACTAACAC ATTGTCTAACATT TGAA	C	A				SILENT- NONCODI NG		
2963- 2964	cg42670494	97	AGTGGGGTCTGT TATCAGAGCTCC T[G/T]TCCTCTAA GTTTCAGTCCT CGCTC	G	T				SILENT- NONCODI NG		
2965- 2966	cg42670545	349	GAATACATCTTA ATGTTCTCACCA T[A/G]CACACAAA AAAGGTAATTAT GTGAG	A	G				SILENT- NONCODI NG		
2967- 2968	cg42670658	193	AAAGAAAGTAAT TTGAATGGTTCT A[G/gap]TACTAG GGCCATTATTAA CTAGTAA	G	-				SILENT- NONCODI NG		
2969- 2970	cg42672418	61	TGGAACCGTTTC ATAGACTGAAGT G[T/C]GAACGTA GGAGGGGATGG ATATCAG	T	C				SILENT- NONCODI NG		
2971- 2972	cg42676483	106	GTTACGAAGGCA GCATTTTCTGCT GIC/TTCCTGGG AGAAGGCAGGC ACGGAGC	C	T				SILENT- NONCODI NG		
2973- 2974	cg42685163	341	TTACTATCCTCA AGGGTTTGTGAC T[A/C]AACTGGAA TTACTATTGTAAA GCAG	A	C				SILENT- NONCODI NG		
2975- 2976	cg42688225	329	ACTAGGAATGTC AGGTGATGGTTT G[A/G]CAATTATC ACACTGCCCTCTC TAAAA	A	G				SILENT- NONCODI NG		

2977- 2978	cg42695541	241	CGCTTTTCACAG GTTGGGGAGAT GG[G]A]CGCCTG GAGAAAGGGAAT CCAGTTA	G	A				SILENT- NONCODI NG			
2979- 2980	cg42698411	1163	CTCCACGACACAG GGTCTCTGGCC C[A/G]ATGTTGCA GAGCTCCAGCC CTAGAG	A	G				SILENT- NONCODI NG			
2981- 2982	cg42698411	925	CCACGGACCAC CCCCCTTCCCCA AC[C/]ACACTGG GGTGTCTGGGG TGAGGCT	C	T				SILENT- NONCODI NG			
2983- 2984	cg42704233	399	GGTAAGAGCCCT CTCTCCAGCCT CT[C/]GTCCCTCCC AGCCCTGGAGTC CTTGG	T	C				SILENT- NONCODI NG			
2985- 2986	cg42708153	305	CCGCCCGTTCTG AGCATGTCCCCC A[A/G]AACTCGG GGAGCGCAGGC AGGACAG	A	G				SILENT- NONCODI NG			
2987- 2988	cg42708452	273	ATGAGGTTGGAA CAGAAAGTTTAA A[A/]GCAAAAGA AGAAAGCTCTCC CCAGC	A	T				SILENT- NONCODI NG			
2989- 2990	cg42712591	369	TGACTGTGGGG CCACCCACAG GGA[C/]CCAGC GGCGAATCCCT GCTAGGAA	C	A				SILENT- NONCODI NG			

2991- 2992	cg42713200	128	TGACAGAGCTTT GGGGCCCGTGA TG[ap]/G ATTGC AGCTCCTGAGGT GGCCTGCT	-	G				SILENT- NONCODI NG			
2993- 2994	cg42714904	383	GCTGCCCCCG TGCCCCGGGGC CGC[C]/TCGCCC GCCCTTCTGGAC AGCCACTT	C	T				SILENT- NONCODI NG			
2995- 2996	cg42718881	517	CAGGGCTGCTG GACAACGGGCC AGA[C]/TCAGC CCCAGTGTGGAT CCAGAGGT	C	T				SILENT- NONCODI NG			
2997- 2998	cg42718881	618	CTGGTCTGCACT TCTGACCTGGGG C[T]/C CTGGCTGT GCGGTTCTGCTG AGCTC	T	C				SILENT- NONCODI NG			
2999- 3000	cg42718881	766	CAAATGAGCAAC TGGCTCATCAGT C[G/A]/GTGCAGG CTGACAGGTGCA GGAAAT	G	A				SILENT- NONCODI NG			
3001- 3002	cg42718881	845	GAATGCTTCCCA ACATGAGGGCAT C[T]/C CAGGCCA GCAGGCGGGGC CCAGAGA	T	C				SILENT- NONCODI NG			
3003- 3004	cg42718933	243	ATCTTATAAAGA AAAGCCCCATAA T[G/T]AAATTAGG CTCTGTGATACC CATCC	G	T				SILENT- NONCODI NG			

3005-3006	cg42719773	359	ATTTTCTCTCA AGTTGTAGCCAA C/AJATTTTGTC GTAAGTGAATTC AGGG	C	A				SILENT- NONCODI NG			
3007-3008	cg42719781	257	GGAGAATCCAGC AAAAGGAAAAAA A[gap/A]JGGACAG TTGAAGATGACT TACTGCT	-	A				SILENT- NONCODI NG			
3009-3010	cg42719781	271	AAAGGAAAAAAA GGACAGTTGAAG AT/CJGACTTACT GCTCCAAAAACC ATTTC	T	C				SILENT- NONCODI NG			
3011-3012	cg42719781	78	GTGCGGCAGGG CGCACGGGACC TGTC/GJCTGCA GCGGCTCTCTCA GGCCGTGG	C	G				SILENT- NONCODI NG			
3013-3014	cg42719906	74	CAGATGCAGAAA ATGCCITTTAAAG T/A/GJAGACTTAG CATCAGAGCAGC TCTTG	A	G				SILENT- NONCODI NG			
3015-3016	cg42722181	290	ATTTGATTATTAG TTCAATATACAT A/TJATTGAAACG TCATACTGTGCC ATAA	A	T				SILENT- NONCODI NG			
3017-3018	cg42722181	379	TATATTCAAAA GAAATGGGGACA G/GCJATTATCCT GATGTTTTACTC ATTCC	G	C				SILENT- NONCODI NG			
3019-3020	cg42722181	555	ATTGCCTAATGT CCATTATTAAACA G/A/TJAGCTGACC TCAAAAAAAAAG AGGAA	A	T				SILENT- NONCODI NG			

3021-3022	cg42724046	565	CCAGTGCAATGC AGTGAGGTAGG CA[G/A]GAGACT CCATCCTGGTCC ACCCGTG	G	A				SILENT- NONCODI NG		
3023-3024	cg42724046	628	AGAAGACTATGG TGGACCCCAATT C[C/A]CCCCITCC ATTCGATCCTGG CTCCT	C	A				SILENT- NONCODI NG		
3025-3026	cg42724046	633	ACTATGGTGGAC CCCAATCCCCC C[T/C]TCCATTG ATCCTGGCTCCT CCICT	T	C				SILENT- NONCODI NG		
3027-3028	cg42727359	456	TGAAGTTAAAC CAGGTACTGTGA G[C/T]GCTTACCT GATTTTGTAGTTCT CATG	C	T				SILENT- NONCODI NG		
3029-3030	cg42728523	312	AGATAGGGGAG CAGTCCCCGTG AG[T/C]TTGATGC CGCTGCCCAGG TCGAAGT	T	C				SILENT- NONCODI NG		
3031-3032	cg42729221	466	GGGCTGGACAT GAATGACTGAGC AG[G/gap]CTCAT CGCCCCITGTCC ACAGCTCC	G	-				SILENT- NONCODI NG		
3033-3034	cg42750426	308	AGGCTGAGGCA GAAGGATCGCTT GA[A/G]CCCCGG AGGTGGAGGTT GCAGTGAG	A	G				SILENT- NONCODI NG		
3035-3036	cg42751082	63	TGAGGTCTTCTC CAAGAAAAAAA A[gap/A]GAAAAA AAACAACATGG CTGCAAA	-	A				SILENT- NONCODI NG		

3037- 3038	cg42751082	73	TCCAAGAAAAA AAAGAAAAAA A[gap]/A]CAACAT GGCTGCAAGG AAAAACTG	-	A				SILENT- NONCODI NG		
3039- 3040	cg42833326	283	ATAGCCTTTTAA AATTTGTTTTGTG [A/G]TGATGTATT TTGACAACTTCC ATCT	A	G				SILENT- NONCODI NG		
3041- 3042	cg42833555	122	TAATGGTCACCA ATGAACATACAA A[G/A]CTTATTTA TTCCCCCTTATAC CCTCC	G	A				SILENT- NONCODI NG		
3043- 3044	cg42840564	449	CACITAAAAGTA CCCTTAACTTTT [C/T]TTCCAAAGT TACACAGTAGCC CCAA	C	T				SILENT- NONCODI NG		
3045- 3046	cg42846342	477	AAGGAAGCAAAC GGCTAAATTACC A[A/gap]CAACCG GGATACTTCTTG CTATCAA	A	-				SILENT- NONCODI NG		
3047- 3048	cg42846342	480	GAAGCAAACGG CTAAATTACCAA CA[A/gap]CCGGG ATACTTCTTGCT ATCAATGA	A	-				SILENT- NONCODI NG		
3049- 3050	cg42846342	557	CTGACTTTTTGG GGGTGTGGGG GGT[C]CACAAAC CCTCAGGAGAT CTGCTG	T	C				SILENT- NONCODI NG		

3051-3052	cg42846342	605	TGGATGCCACAA GCCCTCTCCTAG G[gap]/A/AAAAAA AGGAAACGCGT GCCCATAC	-	A				SILENT- NONCODI NG			
3053-3054	cg42863171	367	TACCTTTTCAGG TTTTTAAATGTCT [G/gap]ACAGGAA AAACAAAGATCA TTTTAT	G	-				SILENT- NONCODI NG			
3055-3056	cg42865804	386	ATTCAGATTCTG AATGTTCTAAAA A[C/G]CCCCAGC ATCATCTGTTTAA TTTCA	C	G				SILENT- NONCODI NG			
3057-3058	cg42866866	419	CTTGGGAATGCT CAGCCTCCCGAA G[G/gap]AGCAGG GCGGGATCCGC GTGGCCAG	G	-				SILENT- NONCODI NG			
3059-3060	cg42867960	289	TTGGCGCTGTC AGCGACCCAGTAT C[A/T]GCGCCCG GCTTGTCCTCCGC TGCCCG	A	T				SILENT- NONCODI NG			
3061-3062	cg42876829	554	AGAGGTCATGG GAAGCCAGGAG ATC[C/T]TTGTCC CATAGATGAGCA GTAGGAA	C	T				SILENT- NONCODI NG			
3063-3064	cg42883430	299	AGATGAGTAGGA CACGCGTCTGCA C[G/A]CTGGAGG CCCTGGGGGTT GACATGG	G	A				SILENT- NONCODI NG			

3065-3066	cg42883430	382	CCCTTCTGTTTT CTTGATTTTCAGT C/TTCACCTGGCC CAGGCCAAATCT TCAA	C	T				SILENT- NONCODI NG		
3067-3068	cg42883430	388	TGTTTTCTTGAT TTCAGTCTCACT G/gap]GCCCCAGG CCAAATCTTCAA GGTGT	G					SILENT- NONCODI NG		
3069-3070	cg42883430	98	TAAGAGACCACT CTAGATAAGCTA T/T/A]GAAAGTAT AAAAATCATTTTA CTTT	T	A				SILENT- NONCODI NG		
3071-3072	cg42884643	548	GGTAGCCCTTAAC CTGTGAATGAGA A/A/G]CCTTCAGA GGTGCTTGTGG AATTA	A	G				SILENT- NONCODI NG		
3073-3074	cg42884893	547	TATCAAGCTTCA GTGAGGACCCAG GC/A/C]GACCCC TGCCCTGCCAACG CCCTCTC	A	C				SILENT- NONCODI NG		
3075-3076	cg42884893	565	ACCAGGCAGAC CCCTGCCCTGCCA AC/G/C]CCCTCTC AGCTGGGCTTAA CTCTGG	G	C				SILENT- NONCODI NG		
3077-3078	cg42884893	731	GGTTTTTAAGAC CTTTGCCCCAGAC C/C/A]CTGCAACC AACTAGAACTG ACATC	C	A				SILENT- NONCODI NG		
3079-3080	cg42885383	428	TTTTATTATTTTG TAGAGATGGGT T/C]TTGCCCATGT TGCCCCAGGCTG GTCTC	T	C				SILENT- NONCODI NG		

3081-3082	cg42885676	188	CCTGCAATTGTA CTGGGGACTCCA C[G/A]AGTTCTTT TCTGGTGGGAG GACTAT	G	A				SILENT- NONCODI NG			
3083-3084	cg42892295	200	CTTAGTAGGACC ACCAACGATTAT T[T/C]TTTCTTT ACTAAATTATACA ATA	T	C				SILENT- NONCODI NG			
3085-3086	cg42893310	668	TGTTGGCACCTT CTGTGTCCTCTC T[C/T]ACCTTGCC TGTGAGCCTTCC AGTGG	C	T				SILENT- NONCODI NG			
3087-3088	cg42894278	197	TCAGTATTACTC GTGTTTTGTTTT [G/T]TTTTTGTTTT TTGTTTTCTTTT CC	G	T				SILENT- NONCODI NG			
3089-3090	cg42895269	350	GGAGAGCAGCC TGGGAGGCCCTG GCT[T/G]GGTC CCACGCGGGG AAGTAGGG	T	G				SILENT- NONCODI NG			
3091-3092	cg42896570	669	AAGTTTCCATT TCTTAAAGTAGG[A/gap]AAAAATGA ACAGTAATAATT ATGAT	A	-				SILENT- NONCODI NG			
3093-3094	cg42905189	270	TTACATTCTCTT AGTAATTATGGC[T/C]CAGCAAGCA TGCCACCAAAAT CATC	T	C				SILENT- NONCODI NG			
3095-3096	cg42906789	404	ACTACTGGATTA CATCCAATAGCA T[T/C]TACCTGGC CCGAGCAGGTA CTCTGT	T	C				SILENT- NONCODI NG			

3097- 3098	cg42909493	418	AGTGAGACATTG AGAATGAAAGCA C/T/C/ATTAATAA TTATCCAAGAAC AGCAG	T	C				SILENT- NONCODI NG			
3099- 3100	cg42912759	568	AGGGCTTATTT GAGGACAGAATC A/C/G/CCAGACA AAAGGGCCAGAA AGAGAG	C	G				SILENT- NONCODI NG			
3101- 3102	cg42912759	576	ATTTGAGGACAG AATCACCCAGAC A/A/G/AGGGCC AGAAAGAGAGTG CAGCTT	A	G				SILENT- NONCODI NG			
3103- 3104	cg42913480	437	GAGATCAAATTG TTACTGTGTCTG T/G/A/TAAGAAAG AGTAGACATAGG AGACT	G	A				SILENT- NONCODI NG			
3105- 3106	cg42913480	490	ATTTGTTATGTG CTAAGAAAAATT A/C/JTCTGCCTT GAGATTCTGTTA ATCT	A	C				SILENT- NONCODI NG			
3107- 3108	cg42917270	629	GCGTGCTGAAGA GAATTTGGAAAA A/A/C/JAAAAAAGA AATTAATAATCG TCTCT	A	C				SILENT- NONCODI NG			
3109- 3110	cg42918135	145	GAGGGATACGT GAGTCTTCTGGT GT/G/A/JATGTGCA GTCAAACCCACAG GAAAGG	G	A				SILENT- NONCODI NG			
3111- 3112	cg42918135	196	TTCCATTCTCTTA CCTAAGTCTCGT T/T/G/JGTCTAATA CACCTGCCAGCT ACTGA	T	G				SILENT- NONCODI NG			

3113- 3114	cg42918135	56	TTGACTCCTAAG GCCACACTGTTT C/C/TATCCCAT GATTCACAGAG GTGAT	C	T				SILENT- NONCODI NG			
3115- 3116	cg42919304	138	TACGCGTCAGAG CAGTGACTTTGA T/A/GJCGCAGTCA GGTTTTTCCATT AATAG	A	G				SILENT- NONCODI NG			
3117- 3118	cg42919304	285	GAAAGATAAAGA AGGGACCGGG CC/T/CJCTGAGG AAGGCAAAACAGA AAGGCAA	T	C				SILENT- NONCODI NG			
3119- 3120	cg42919821	225	ACGACGTGTTTG TGAATCTGGCAG A/G/CJAGTGAGAT CACCATCGCTCC ACTTG	G	C				SILENT- NONCODI NG			
3121- 3122	cg42920238	198	ATGAATCCAGTT TAATTTTAACTTT [G/T]TGGCTTGTC TAACACATTTTCA GTT	G	T				SILENT- NONCODI NG			
3123- 3124	cg42920238	205	CAGTTTAATTTTA ACTTTGTGGCTT[G/T]TCTAACACA TTTTCAGTTAAG AGTT	G	T				SILENT- NONCODI NG			
3125- 3126	cg42920603	362	TCGAGACCAGCC TGGCCAACATGG T/A/GJAAACCCCG TCTCTACTAAAA ATACA	A	G				SILENT- NONCODI NG			
3127- 3128	cg42920603	370	AGCCTGGCCCAAC ATGGTAAACCCC C/G/AJCTCTACT AAAAATACAAAA ATTAG	G	A				SILENT- NONCODI NG			

3129- 3130	cg42922107	699	CTCCTGCTGTG CACCTGGATCC T[A/gap]GCAGGC CACAGACCAGTA CCAGTCC	A	-				SILENT- NONCODI NG			
3131- 3132	cg42924228	279	TCTAAGCAATGT CCTCATTGGCAG G[G/A]GTGGAGT GGGGGAGTTTCT TAAAAA	G	A				SILENT- NONCODI NG			
3133- 3134	cg42924993	440	CAGGAGTTCGAG ACCAGCCTGGC CA[A/G]CATGGT GAAACCCCGTCT CTACTAA	A	G				SILENT- NONCODI NG			
3135- 3136	cg42925042	71	CCTCAGCAGCCA GCTCCCTTGAT A[C/A]ACAGTATA CACAGCCCAGC CAGCAC	C	A				SILENT- NONCODI NG			
3137- 3138	cg42925336	534	CGAAGAAGGGG TTGTCGTCCGCC TC[G/A]ATGCCAT AGTACTCCAGGG ACATTC	G	A				SILENT- NONCODI NG			
3139- 3140	cg42927064	230	GAGCTCTAAGAT CTCCTTTAGAGG G[C/T]ACAGTGA GGTGGGCTGTT GGGATGG	C	T				SILENT- NONCODI NG			
3141- 3142	cg42929433	224	CTCATTGGAAA AGGACACTGGG AT[G/C]AACACGT AAGCGTTGCAAG CACAGG	G	C				SILENT- NONCODI NG			

3143- 3144	cg429333706	307	GCGTGGGGCTG CCTATCACCCCTG CT[G/A]TCGTCG GCGCTGGGGCGG GCCCCACA	G	A				SILENT- NONCODI NG		
3145- 3146	cg42936190	139	TTTCACACTAAT GAAATGCCCTGAG AT[G/A]TTAAAGG TCTAAATGTAA ATTAA	T	G				SILENT- NONCODI NG		
3147- 3148	cg42936190	200	AAACAGATAAT ATATATGTACCC TIC/TJGGTTTGAA ATAGACTTTAAG CACTA	C	T				SILENT- NONCODI NG		
3149- 3150	cg42937265	1099	GACAATGATTTT ATCAGGCTAAAG GT[G/G]GAAATCAG CTCAGTGACACA GAGTG	T	G				SILENT- NONCODI NG		
3151- 3152	cg42940691	328	GGAGGAAGGAA GCAGTGTGTTGA TT[G/T]ATACCTT AGCCCCAAGCTCC TTATTT	G	T				SILENT- NONCODI NG		
3153- 3154	cg42942726	558	GTCACCTTCATTG TCTCACCCAGGC C[G/C]GAGACCA CAATTTCCCTGG AAGGAC	G	C				SILENT- NONCODI NG		
3155- 3156	cg43008771	419	GGGATTAGAAG TTAGCATTTGTT GT[C/G]AGTGATTT TCAAACCTTAGT GTGCC	T	C				SILENT- NONCODI NG		
3157- 3158	cg43013298	556	AGGATTTACAGGA AAACCATGGTTA T[A/gap]AAAAATGA TCAATCTTGAA AAGTAT	A	-				SILENT- NONCODI NG		

3159- 3160	cg43013298	560	TTTCAGGAAAC CATGGTTATAAA A[A/gap]TGATCA ATCTTGAAAAAG TATGTAC	A	-				SILENT- NONCODI NG		
3161- 3162	cg43021539	95	CCTGAGTGTTC GATCCAGGCTCT G[C/gap]CCAGAG CTGGATGTAAAT TTATGAC	C	-				SILENT- NONCODI NG		
3163- 3164	cg43021539	97	TGAGTGTTCAGA TCCAGGCTCTGC C[C/gap]AGAGCT GGATGTAAATTT ATGACCT	C	-				SILENT- NONCODI NG		
3165- 3166	cg43028648	405	TCITGCTTCAGT AGGCAACCGA CG[G/TT]GTGCTT CATCCACCTCCT AGGCCG	G	T				SILENT- NONCODI NG		
3167- 3168	cg43040591	352	TCCGGCTTTGCT CCAAATGCCAGC A[C/TT]TTTCAGTC GGGGGTAGAGC TGACAC	C	T				SILENT- NONCODI NG		
3169- 3170	cg43042003	655	GTGTAATAACTG GGCCCGTGTCTT CIA/GJCCTGAAAA CTGGGGGTCAC ACGGCC	A	G				SILENT- NONCODI NG		
3171- 3172	cg43042003	713	AAGAACTCTGAT GTGATAAACACC A[C/TT]AGAGCAG CATCACATTTTC CTATCG	C	T				SILENT- NONCODI NG		
3173- 3174	cg43045398	1195	TTGATGTATTCA CAGAGCTTCCAA A[C/TT]ATTTCTT CACAGCAACAGC CGCTG	C	T				SILENT- NONCODI NG		

3175- 3176	cg43045398	664	TTTCTCCACAGT TCCACATCTTGA G/A/GC/CAAGTTTC AGCAGTTTTTAC TGCCA	A	G				SILENT- NONCODI NG			
3177- 3178	cg43047493	120	GATGGCGACTG CGGGAATCGA GTTT/C/TCATGC TGGGGCGAAAG GACCGTCC	T	C				SILENT- NONCODI NG			
3179- 3180	cg43051491	287	TACTGAATCAGT GTATGAAAATA T/C/TCCAAACAG ACAAAGCAGAAC ATGGA	C	T				SILENT- NONCODI NG			
3181- 3182	cg43054909	412	GTTTTCATTGTG ATAATAGGTAGC A/G/A/AATGATGA GCATCCCTATCA CTTAC	G	A				SILENT- NONCODI NG			
3183- 3184	cg43063075	179	TGAGCATAGCAG TCGACTTTTTTTT T/gap/ATATTTTC CTTCACAGTCTG GCATT	T	-				SILENT- NONCODI NG			
3185- 3186	cg43063683	325	AGTGTCACCAA AGCTGAGCACCA G/C/T/CATCTGCC CTAGCTGTGTGC ACAGG	C	T				SILENT- NONCODI NG			
3187- 3188	cg43064195	495	GCCTGTGGTCCC AGCTACTCGGGA G/A/G/CTGAGGC AGGAGAATCGCT TGAACC	A	G				SILENT- NONCODI NG			
3189- 3190	cg43064195	529	GGAGAATCGCTT GAACCCAGGAG G/C/A/G/GAGGTT GCAGTGAGCCAA GATCATG	A	G				SILENT- NONCODI NG			

3191- 3192	cg43064195	553	CAGAGGTTGCAG TGAGCCAAGATC ATT/C]GCCACTGC ACTCCAGCCTGG GTGAC	T	C			SILENT- NONCODI NG		
3193- 3194	cg43064233	628	CAACCAGAGCCA GTGGACTTCAGT ATT/C]GGGTCCG TTTCATTGGCAG ACCCTC	T	C			SILENT- NONCODI NG		
3195- 3196	cg43066356	603	TGGACTTGGAGC AGAAGAGTCCCT C/C]gap]AGGGCT GAAGATTGGACA CAGAAAA	C	.			SILENT- NONCODI NG		
3197- 3198	cg43066356	728	ACAATTCACAGA AACTGGAATTGG G/A/G]TGGTGAG ATTTAGTTTCAG CCGCCG	A	G			SILENT- NONCODI NG		
3199- 3200	cg43069434	337	TGAGACCTCCAG TCCCAGGGGCG GG[C/]TTCATGC GGTCCACAGCT GTTGGC	C	T			SILENT- NONCODI NG		
3201- 3202	cg43069949	313	TCACITGTGCAC ACACACACACAC A/gap/C]GGTCAC GGAGCTGGACG TGCGGATG	.	C			SILENT- NONCODI NG		
3203- 3204	cg43073473	408	CTCACTTATAATT CCAAATTCATGT[T/gap]GTGTTAGC TCAATATTTTCA AATA	T	.			SILENT- NONCODI NG		

3205-3206	cg43073473	561	TATCTGCACCAT GATGATATGACA CIG/AJCCCATACC CCCCATTTTACA TTTTG	G	A				SILENT- NONCODI NG			
3207-3208	cg43073473	572	TGATGATATGAC ACGCCCATACCC CIC/TJCATTTTAC ATTTGTGAGAA GTGCA	C	T				SILENT- NONCODI NG			
3209-3210	cg43073924	502	TAGGCACAAAGA GACCGAGTGGC TCIG/AJGGTGGC TTCACAGGAGGC AGTTAGA	G	A				SILENT- NONCODI NG			
3211-3212	cg43076876	746	TCTAATGGCTTC CCATGACCACAC AIC/gapJAGGAGT GGGGAACCTTA CTTGTA	C	-				SILENT- NONCODI NG			
3213-3214	cg43076876	800	ATCGGTTTCTT CCAAATCAGCGA CIG/AJGGAGTAA CATTTTATTCTT ATCAC	G	A				SILENT- NONCODI NG			
3215-3216	cg43077574	138	GCCTCCCAGAGT GCTAGGATTACA GIG/AJTATGAGC CACCATGCCCG GCCCTAG	G	A				SILENT- NONCODI NG			
3217-3218	cg43082358	259	TATTTAAACCCA ATTCTGTTTTT[g ap/TJACAGAATA AAATTCCTCTGTT CTT	-	T				SILENT- NONCODI NG			
3219-3220	cg43085612	139	CTGGGATCACAG GATCCCGCCCC CAT/CJGCTCAGC TAATGTTTGTATT TTTAG	T	C				SILENT- NONCODI NG			

3221- 3222	cg43085612	162	CATGCTCAGCTA ATGTTTGATTTT [T/C]AGTAGAGAT GGGGTTTCACCA TGT	T	C				SILENT- NONCODI NG		
3223- 3224	cg43085612	165	GCTCAGCTAATG TTTGATTTTAG [T/C]AGAGATGG GGTTTCACCATG TTGCT	T	C				SILENT- NONCODI NG		
3225- 3226	cg43090728	384	CAGAATCGCTGG GCTTTAACCACA C[A/gap]TGAGAG TCTGGTCCCTG TGAGACT	A	-				SILENT- NONCODI NG		
3227- 3228	cg43091174	679	GGTGTCTTCAGG CTGAGTTTACTT GT[C]AGGAGTG GCAGGATTGCTC TTCAAT	T	C				SILENT- NONCODI NG		
3229- 3230	cg43094867	1016	TTCTCTCCAGCG GCAGCGGAAAA CG[G/A]GCAATG GGTGGATTGCG GTCCAGAT	G	A				SILENT- NONCODI NG		
3231- 3232	cg43094867	1149	GGGGACAAAAAC CAGAGGCCCGGG GA[A/gap]GGCGC CGGTGGGAGGC AAGGCACGG	A	-				SILENT- NONCODI NG		
3233- 3234	cg43094867	423	GGGGAAACTTC AAATTATTTAAAT [A/T]ATGAGAGGC GAAAAACATTGC TAAA	A	T				SILENT- NONCODI NG		

3235- 3236	cg43095751	244	CAATAAAAAAGA ATGCACTGCCAG TAAACAGCAACA TGGATAATTCTC AAATG	A	T				SILENT- NONCODI NG		
3237- 3238	cg43095751	256	ATGCACTGCCAG TACAGCAACATG GAAATTAATTCTC AAATGCATTATG CCAGT	A	G				SILENT- NONCODI NG		
3239- 3240	cg43095751	489	GCATTGTCAAG ACTCAGTGCTAT AICATGCTGAAA GGGCAGGTTTAA CTATA	C	T				SILENT- NONCODI NG		
3241- 3242	cg43096831	389	TCCCTATGTTGC CCAGGCTGGTCT CAGAACTCCTG GGCTCAAGCGAT CCTCC	A	G				SILENT- NONCODI NG		
3243- 3244	cg43099151	1358	TCGCCGTATGGA GGTGAACCTCTG AAGAAACCTCT TCATAGCCCAT TTCAI	G	A				SILENT- NONCODI NG		
3245- 3246	cg43099552	2432	ATATTGGATTA CCAAATAACACT TTCTGTAGATG CACTGATACCGA AGTT	T	C				SILENT- NONCODI NG		
3247- 3248	cg43105272	396	GGCCAACATGG CGAAACCCCATC TCCTCACTAAAA ATAAAAAATAAAA AATAG	T	C				SILENT- NONCODI NG		
3249- 3250	cg43106767	235	GAAATAGCCAGG CGTGGTGGCTCA CAGCTCTGTGAT CTAGCACTTTG GGAGG	A	G				SILENT- NONCODI NG		

3251- 3252	cg43107247	354	TGCCCAGGCTG GTCTTGAACCTCC TG/AGJCCTCAAG CAATCCTCCTGC CTCGGC	A	G				SILENT- NONCODI NG		
3253- 3254	cg43107247	367	CTTGAACCTCCTG ACCTCAAGCAAT C/C/TTCCTGCCT CGGCCTCCCAAA ATGCT	C	T				SILENT- NONCODI NG		
3255- 3256	cg43111395	703	AGCACCCAGGG GGATGGTGTAA AC/C/TATGAGAA ACCACCCCAAT ATCCAA	C	T				SILENT- NONCODI NG		
3257- 3258	cg43111948	421	GGCGTGGAGAC ATGGAACATGGA TA[G/gap]GGCAG CGGCCTCCTTGC CCCTGATG	G	-				SILENT- NONCODI NG		
3259- 3260	cg43111993	281	AAGACGGAAGCA GTCACCTGGTCCT T/C/TCCCTCGTC CCACCCCGCAG CACCTC	C	T				SILENT- NONCODI NG		
3261- 3262	cg43114589	695	CAACATGGTGAA ACCCCGCCTCTA C/T/C/AAAAATAC AAAAATCAGCTG GGCAT	T	C				SILENT- NONCODI NG		
3263- 3264	cg43117303	272	TGTGCAGCCGAT GGTGAGGGACT GG[G/gap]CGCCC TCGCCTGCCCCC GGGGTTGT	G	-				SILENT- NONCODI NG		

3265- 3266	cg43117554	348	GGTGGCTGTTCC CGTCCTTCCCTG G(G)TCGGTGCA GGCTGTGGAGC ACGAGGA	G	T				SILENT- NONCODI NG			
3267- 3268	cg43117554	504	CCAGAAGAATGC AGTTCTGAACAA A(C)TTGAAACT GCAATTGGAGCA GTGGA	C	T				SILENT- NONCODI NG			
3269- 3270	cg43118191	1227	CCTTCCCTGAAG GCCATCCTGTGC G(G)gap]CCAGGG CCCCGCAGACC CCTCCACA	G	-				SILENT- NONCODI NG			
3271- 3272	cg43120277	308	ATATTGATTAGG TTTTAAAGCAAC T(G)C]ATCACTTG CTGACAGCTCAG CCACG	G	C				SILENT- NONCODI NG			
3273- 3274	cg43124193	478	CATTTCAACATA CAAGTCCTTCACI G(C)AGTGGGTCT GCCTTAGTGTTT TTGC	G	C				SILENT- NONCODI NG			
3275- 3276	cg43126118	389	TCTCAGCCTCCC GAGTAGCTGGG AC(C)T]ACAGTG CCGGCCACCAC ACCCGGC	C	T				SILENT- NONCODI NG			
3277- 3278	cg43129484	292	TCCAGAGAGAAA AAGAATGGGAAT C(A)G]AATTGACC TCAGACTATACG TGAGA	A	G				SILENT- NONCODI NG			

3279-3280	cg43129603	543	TTTGGGAGGCCA AGGCAGGAGGA TC[G/A]CTTGAGC CCAGGAGTTTAA GACCAG	G	A				SILENT- NONCODI NG		
3281-3282	cg43134281	223	CAAAAGACCACC ACTCAGTATTTG T[G/C]TACCCCTGC AGCCAAACACCAC CTCCT	G	C				SILENT- NONCODI NG		
3283-3284	cg43134281	230	CCACCACCTCAGT ATTTGTGTACCC T[G/T]CAGCCCAAC ACCACCTCCTGG GCTTC	G	T				SILENT- NONCODI NG		
3285-3286	cg43136191	54	TACACAAGTGAT CAATTTGTCACA AT/CJATGACAAG TTATTGATAACAA GTAT	T	C				SILENT- NONCODI NG		
3287-3288	cg43136321	217	TGGTTTGACCAG GTGTGACGTTTA C[G/A]TAGTGCAC GAGAAAGGCTG GCCACC	G	A				SILENT- NONCODI NG		
3289-3290	cg43136321	256	AGGCTGGCCAC CCCACCCAAATT CT[G/T]ATTATGC AAATGGACTTTC CACTTG	G	T				SILENT- NONCODI NG		
3291-3292	cg43138399	570	ATGTTTCCCATTA CAGCACTCATTG[A/gap]AAAAATA ATTAGGAGGCCAA TCCTT	A	-				SILENT- NONCODI NG		
3293-3294	cg43139520	75	CCTGCTTTGCTA TTGTCCGCTTTG C[G/gap]CCCCGG AAGCAGGTCCT AGCTCAG	G	-				SILENT- NONCODI NG		

3295-3296	cg43144367	966	GAAGGGAAGGT CTTAAAGATAA AA[G/gap]GGGG GTTGCTACCCCA GTCTCAGG	G	-				SILENT- NONCODI NG			
3297-3298	cg43144435	446	ATAAGATGTTAT GGCCAGACGCG GA[G/gap]CTCAC GCCTTTAATCTC AGCACTTT	G	-				SILENT- NONCODI NG			
3299-3300	cg43144658	333	ACCCCCCAAAA AAAAGGAAAAA A[A/gap]TCTAGAT CCAACAGTGGAA AATTCT	A	-				SILENT- NONCODI NG			
3301-3302	cg43144658	554	GGGGAGTTAGC CTGGGACCAATG GA[G/A]GAGAAG TACGAACCCCTGG GAAAAAG	G	A				SILENT- NONCODI NG			
3303-3304	cg43144705	282	TCCGAAGTGTG GGATTGCGGC GT[A/G]AGTCACC ATGCCAGCCAA GAAAGC	A	G				SILENT- NONCODI NG			
3305-3306	cg43144729	31	CTGATCATCTG CCGCTGACTGTG G[C/T]CTCTAGAG AATCCACCAGCT CTGCT	C	T				SILENT- NONCODI NG			
3307-3308	cg43145001	269	ACTTGAAGGCAC TTCATTTTTTTTTT gap/TJAAGATACA CTCTTAGGAGTT TACTT	-	T				SILENT- NONCODI NG			
3309-3310	cg43145001	269	ACTTGAAGGCAC TTCATTTTTTTTTT gap/TJAAGATACA CTCTTAGGAGTT TACTT	-	T				SILENT- NONCODI NG			

3311-3312	cg43145724	259	ATAACAGTCACC CACTACAGACAT T[C/gap]TTTTCCC CTGTGGGATGTC ATACTG	C	-				SILENT- NONCODI NG			
3313-3314	cg43146633	1005	CAAGTGATCTTT CCACAACATTAA A[A/gap]CCACAT TTTGCTCCTCAG ACACCTC	A	-				SILENT- NONCODI NG			
3315-3316	cg43146633	1024	ATTAAACCCACA TTTTGCTCCTCA G[A/G]CACCTCTT TGCACTCTAGAT CTTTT	A	G				SILENT- NONCODI NG			
3317-3318	cg43148723	281	AAAAAACGACAA TTGGCTGCAGAA A[A/gap]GCTGGT TTGGGAAGGGG TGCCCTGTT	A	-				SILENT- NONCODI NG			
3319-3320	cg43148723	373	CGGCCCTGGCT CCCCCTGGGGCC TCT[C/gap]TGCT CTGAGGGAGGA AAGGCAACAG	C	-				SILENT- NONCODI NG			
3321-3322	cg43155030	172	GAGGGTCAGGA GTTGAGAGCCAG CC[T/C]GGCCAA CATGGTGAACCC CCCCGTC	T	C				SILENT- NONCODI NG			
3323-3324	cg43242324	133	GTGAGTGCGTGT GCGTGGTGTGT GC[G/A]TCTGTAT GTGTATGCATGT GGGTAT	G	A				SILENT- NONCODI NG			
3325-3326	cg43242324	137	GTGCGTGTGCGT GGTGTGTGCGTC T[G/A]TATGTGTA TGCATGTGGGTA TG TAG	G	A				SILENT- NONCODI NG			

3327- 3328	cg43242324	257	CGTGTGTGCGTGT TTGTGTGTGTGT GTT/gap]GCATGC ACATTTGAAGTG ACCTCAG	T				SILENT- NONCODI NG			
3329- 3330	cg43247175	731	TGAAAGAGAAGG CCAGCTTTCTCC C/GA]CCTGTGG AAAGCCAGACC TGAGTG	G	A			SILENT- NONCODI NG			
3331- 3332	cg43247846	19	NAATCATGATC CGCCCGTT/C]CT CGGCCTCTCAA GTGCTGGGATT	T	C			SILENT- NONCODI NG			
3333- 3334	cg43247846	222	TGTGAACCTGGAC TGAACGAGACAA G/GA]TGTGCTCT GGGCTGCGGG GTCAGC	G	A			SILENT- NONCODI NG			
3335- 3336	cg43250188	128	CTCTGCCCTGGAG AAAAAGCCCTG C/A]C]TGCCTTGT GAAGGTTTATGA AGATT	A	C			SILENT- NONCODI NG			
3337- 3338	cg43250188	137	GAGAAAAAGGCC CTGCATGCCCTTG T/GA]AAGGTTTA TGAAGATTGGGA TTGTT	G	T			SILENT- NONCODI NG			
3339- 3340	cg43250188	161	TGAAGGTTTATG AAGATTGGGATT GTT/C]TCAAAGT AAATGACATTCT TGAGC	T	C			SILENT- NONCODI NG			
3341- 3342	cg43250188	186	TTTCAAAGTAAAT GACATTCTTGAG[C/T]TATATGGCA TACTGTCTGTGG ATCC	C	T			SILENT- NONCODI NG			

3343- 3344	cg43250188	200	ACATTCCTTGAGC TATATGGCATAC TIG/CJCTCTGTGGA TCCTGTGCTGAG TATAC	G	C				SILENT- NONCODI NG			
3345- 3346	cg43250188	209	AGCTATATGGCA TACTGTCTGTGG A/T/CJCTGTGCT GAGTATACTGAA TAATG	T	C				SILENT- NONCODI NG			
3347- 3348	cg43250188	213	ATATGGCATACT GTCTGTGGATCC TIG/AJTGCTGAGT ATACTGAATAAT GATGA	G	A				SILENT- NONCODI NG			
3349- 3350	cg43250188	221	TACTGTCTGTGG ATCCTGTGCTGA GT/CJATACTGAA TAATGATGAAAG GGATG	T	C				SILENT- NONCODI NG			
3351- 3352	cg43250188	236	CTGTGCTGAGTA TACTGAATAATG A/T/AJGAAAGGGA TGCCTCTGCACT GCTGG	T	A				SILENT- NONCODI NG			
3353- 3354	cg43250188	263	AAAGGGATGCCT CTGCACTGCTGG A/T/CJCCGATGGA GTGCACAGACAC AGCAG	T	C				SILENT- NONCODI NG			
3355- 3356	cg43250188	272	CCTCTGCACATGC TGGATCCGATGG A/G/AJTGACACAGA CACAGCAGAGG AGCAGA	G	A				SILENT- NONCODI NG			
3357- 3358	cg43250188	278	CACTGCTGGATC CGATGGAGTGCA C/A/GJGACACAG CAGAGGAGCAG AGAGTAC	A	G				SILENT- NONCODI NG			

3359-3360	cg43250188	284	TGGATCCGATGG AGTGCACAGACA C[A/G]GCAGAGG AGCAGAGAGTAC ACAGTC	A	G				SILENT- NONCODI NG			
3361-3362	cg43250188	290	CGATGGAGTGCA CAGACACAGCAG A[G/A]GAGCAGA GAGTACACAGTC CTCCTG	G	A				SILENT- NONCODI NG			
3363-3364	cg43250188	302	CAGACACAGCAG AGGAGCAGAGA GT[A/G]CACAGTC CTCCTGCTTCAT TAGTGC	A	G				SILENT- NONCODI NG			
3365-3366	cg43250708	404	AGATCTTCCGAT TCAGTCCTGGTT C[A/G]GCTCTGAG AATTGCAATTCT AACAT	A	G				SILENT- NONCODI NG			
3367-3368	cg43252277	1189	GGGAGAGGAGT AGGCCAAAAAAA AA[A/gap]AAGTC TTGATTCTCTGAA TGTGCTT	A	-				SILENT- NONCODI NG			
3369-3370	cg43252277	1190	GGAGAGGAGTA GGCCAAAAAAA AA[A/gap]AGTCTT GATTCTCTGAATG TGCCTTA	A	-				SILENT- NONCODI NG			
3371-3372	cg43252277	1191	GAGAGGAGTAG GCCAAAAAAA AA[A/gap]GTCTT GATTCTCTGAATG TGCCTTAT	A	-				SILENT- NONCODI NG			

3373- 3374	cg43253001	642	CTCTGTCTCGGG GAAGCCGGGG TG(Gap)CAGAT CCAGCTGGAAGT GAACTGAC	G	-				SILENT- NONCODI NG			
3375- 3376	cg43253077	179	TAAATTAAAGC AGATTCTTTTT T(Gap)AAATCTGC AACTTTGTCTAC AACGT	T	-				SILENT- NONCODI NG			
3377- 3378	cg43253093	752	TTACCGCATCTT CTTTGCTGACTT T(GA)GTAACCG GGTGCCAGAGA GGAGCG	G	A				SILENT- NONCODI NG			
3379- 3380	cg43253436	60	AGCAAGTACTCT ATGTTGGCTGTT C(C)GCAGTGA ATGACTGGTTAA TAAA	C	T				SILENT- NONCODI NG			
3381- 3382	cg43253873	550	TGTGTGCTTCC TCTCTCCAAGCA C(A)GCAGCACT GGGAGAGTCTTG TCTCCA	A	G				SILENT- NONCODI NG			
3383- 3384	cg43257902	536	AAGGCTACTATA AAAATATTGCAA A(A)GCAATAAA AACACAATATCG TACAA	A	C				SILENT- NONCODI NG			
3385- 3386	cg43258630	503	GTGTCAAGAGCC AAGGGCAAAAA G(GA)AGGAGAA GCTGGAGTCG GCATAAT	G	A				SILENT- NONCODI NG			

3387- 3388	cg43259564	649	AAACATTAAATT CTTAAAAAAA A/gap/AGGCATG CCACATGTCACC CTTTAA	A	-				SILENT- NONCODI NG			
3389- 3390	cg43259564	650	AAACATTAAATTC TTAAAAAAA A/gap/AGGCATG CACATGTCACCC TTTAAG	A	-				SILENT- NONCODI NG			
3391- 3392	cg43259814	241	TAATGAAAAACAA AATCAAGAAATGA T[C/T]CACTGGTA CTGCAGGTTACA GAGAA	C	T				SILENT- NONCODI NG			
3393- 3394	cg43259814	344	AAATACCTTAG AAAAATCAAACA G[C/A]ACCTGCAA CACATGCTTATA TAAAG	C	A				SILENT- NONCODI NG			
3395- 3396	cg43260502	297	TGTGCGGTGGG AGCGAGCTGGG CGG[C/gap]GTGC GCTCCCGAGG ACTGGCCTGA	C	-				SILENT- NONCODI NG			
3397- 3398	cg43261866	212	ATGTTGCCCAGG CTGGTCTCAAAC TT[C]CTGGGCTC AAGTGATCCTCT CACCT	T	C				SILENT- NONCODI NG			
3399- 3400	cg43261866	232	AACTTCTGGGC TCAAGTGATCCT CT[C]CACCTCAG CCTCCCATAGTG CTGGG	T	C				SILENT- NONCODI NG			

3401- 3402	cg43262113	605	CCGCACTGAGCAC GCAGCAGCAGC AG[C/gap]AGATG GAGCGGGAGGA GTGAGGGGC	C	-				SILENT- NONCODI NG			
3403- 3404	cg43263775	1439	TATTAAGTTGTT GTAAGCTACTAC A[C/T]TATTCTTC AGGTATGGCTGC GGGGT	C	T				SILENT- NONCODI NG			
3405- 3406	cg43263775	1843	TTCAGGTTTGG CTGCGGAACCC CC[T/A]GGCCAA GGCAAAGATCCA GCACCAT	T	A				SILENT- NONCODI NG			
3407- 3408	cg43264142	952	CTATTTGCGTGG ATTTTTTTTTTTT T/gap]AAGGAAAA ATACGTTTGGAA AATAA	T	-				SILENT- NONCODI NG			
3409- 3410	cg43265542	461	TATTGCAGACAT ATTTTGTGAGATG T[gap/A]AAAAAAA AAAAATTTAAAGTT AAATG	-	A				SILENT- NONCODI NG			
3411- 3412	cg43267277	259	CAAGTAGCTGAG ACCACAGGTGTG C[A/G]CCACCAT GCCTGGCTAATT TTTTTA	A	G				SILENT- NONCODI NG			
3413- 3414	cg43267337	370	ATACACACACAC ACACACACACAC AT[gap]AAAGAA AAAAAAGAAAT TATAAGA	T	-				SILENT- NONCODI NG			

3415-3416	cg43267337	374	ACACACACACAC ACACACACATAA A[G/gap]AAAAAA AAGAAAATTATA AGAAGTT	G	-				SILENT- NONCODI NG		
3417-3418	cg43267337	383	CACACACACACA TAAAGAAAAAA A[G/gap]AAAAATTA TAAGAAAGTTAAT ATTGAC	G	-				SILENT- NONCODI NG		
3419-3420	cg43267337	459	AGTATTAGTCA TTAACATTTTGCT [A/T]TTTCATCA TGTAATAATTAA TTT	A	T				SILENT- NONCODI NG		
3421-3422	cg43267337	542	AGTACATACATG TTTAGCTACTAA A[G/A]AAAAAGTA ATCAGAAAGCAAA TTCAA	G	A				SILENT- NONCODI NG		
3423-3424	cg43268162	1163	CCCAGTGACTC ATACTTATTTGTC [T/C]GCAAAAGTTA CAAAAGAAAGATC CCCA	T	C				SILENT- NONCODI NG		
3425-3426	cg43268348	939	CTTTTGTITTTGT TCACTGCTGTGT[C/T]TAAATAATG CCTGGCTCAAT ATT	C	T				SILENT- NONCODI NG		
3427-3428	cg43268348	974	GCCTGGCTCAAA TATTGTGTAAT G[A/G]GTAAATAT GCTGACITTTGCT GAAGT	A	G				SILENT- NONCODI NG		
3429-3430	cg43268348	1075	CACITTAATGAAA CAGTAAAAAAA A[A/gap]ATAGGT TTGAAACACATA ATCCTTC	A	-				SILENT- NONCODI NG		

3431-3432	cg43268348	1076	ACTTAATGAAAC AGTAAAAA A[A/gap]TAGGTTT GAAACACATAAT CCTTCG	A	-				SILENT- NONCODI NG			
3433-3434	cg43268348	1078	TAAATGAAACAG TAAAAA [A/gap]GGTTTGA AACACATAATCC TTCGTT	A	-				SILENT- NONCODI NG			
3435-3436	cg43268348	1372	TTTGAATAATTGA CTTTTGAATTCA T/CjAAAAACCTT CCCTTATTATC ATCC	T	C				SILENT- NONCODI NG			
3437-3438	cg43268348	929	GCAAGAAATGCCT TTTTGTTTGTTC [A/C]CTGCTGTGT CTAAAAATAATGC CTGG	A	C				SILENT- NONCODI NG			
3439-3440	cg43268590	1209	CTCAAACTCCCG ACCTCAGGTGAT C[G/C]GACCGCC GCGGCTCTCCCA AAGTGCT	G	C				SILENT- NONCODI NG			
3441-3442	cg43270809	363	CACITGGCCCCC AAACCCAGCCTC G[C/T]GAGCTGT GCCCTCTGAGAG TGACA	C	T				SILENT- NONCODI NG			
3443-3444	cg43271020	161	TGCCCAGCTAAT TTTTTGATTTTT T/gap]AGTAGAGA TGGAGTTTCACC GTGTT	T	-				SILENT- NONCODI NG			
3445-3446	cg43271689	1698	CTTTTCTTTT ACAAAACCTTCA A/G]TTTCACATTT TAGTGACACTG TGG	A	G				SILENT- NONCODI NG			

3447-3448	cg43271689	1716	ACCTTCAATTTC ACATTTTAGTGT A/C/TACTGTGGT TTCCAGAGAAAT ATATG	C	T				SILENT- NONCODI NG		
3449-3450	cg43271689	1731	TTTATGTTACA CTGTGGTTTCCA G/A/GGAAATATA TGGATCTCCTAT ATTCT	A	G				SILENT- NONCODI NG		
3451-3452	cg43272452	889	CGGTCTCCAGC GGGCAGGGTAT CCC/C/A/CCCC TACCCGGGGGA ATAGCAAGC	C	A				SILENT- NONCODI NG		
3453-3454	cg43273280	464	CAATCTTTTAAG GGGCAGAGGAA AT/G/A/JAGGAAGA AAAGAAAAAGGAA TTACAG	G	A				SILENT- NONCODI NG		
3455-3456	cg43273935	112	CAC TGCCATACT CCAGCCACTGCT T/G/A/JATCACCTC CAGCTGCAGAGA GCTCA	G	A				SILENT- NONCODI NG		
3457-3458	cg43274254	747	GTAATTAACAATT CTTTCACACTTA[A/T]AACTTTATGG GAAAAGTATTGC AAA	A	T				SILENT- NONCODI NG		
3459-3460	cg43274931	1104	TCATAAGAAATA CAAAGCTAGTTT T/C/T]GGAGCAG GTGTAATTCAGG CACTGT	C	T				SILENT- NONCODI NG		
3461-3462	cg43275466	178	CTGAAATAGAAC GCACACCCCGTAC T/G/A/JCTTTACTT CATTAGATTCTT ACTC	G	A				SILENT- NONCODI NG		

3463- 3464	cg43275466	242	CTACTCTCCCAT CTTAAAAATGAT C/C/TGAGTAGTC CTTTCCGCCTC GTCCC	C	T			SILENT- NONCODI NG			
3465- 3466	cg43275493	881	GTATCCGCCGGT ATTCCAGGTAAC G/gap/C/TGTCCG ACAAAGTCCTCA GTAATGA	-	C			SILENT- NONCODI NG			
3467- 3468	cg43276309	199	ACAGTAGACAGA AGTTGGGCAAAA G/G/C/CTGATTG AGGAAGTTTTGG GCTTC	G	C			SILENT- NONCODI NG			
3469- 3470	cg43276309	385	AGTGCCATGAG GCAAGAGCTGG GC/C/TJGGAAAA AGCCCTGGGA GGCAAGA	C	T			SILENT- NONCODI NG			
3471- 3472	cg43276309	389	GCCATGAGGCAA GAGCTGGGCCT GG[A/gap]AAAAG CCCCTGGGAGG CAAGAGCAG	A	-			SILENT- NONCODI NG			
3473- 3474	cg43276309	455	TTCCTCAAGTCAA AGCTGGGCCTGT T/C/GATGCCACC GGGAAGCAGAA GGTGGG	C	G			SILENT- NONCODI NG			
3475- 3476	cg43277914	370	AAATGAGGACAC ACACACACACAC A/C/gap/ATGCAT GCATATGCACAC ACACAGA	C	-			SILENT- NONCODI NG			

3477- 3478	cg43279568	622	CCACTGCACTCC ATCCAGCCTGGG C(A/G)ACAGAGC GAGACTCCATCT CAAAA	A	G				SILENT- NONCODI NG		
3479- 3480	cg43280385	352	TTCCTTTAGAAAT TCTTATTGGTTCT C/GJTCCCTGCA GCGACAACCCGG CTGCC	C	G				SILENT- NONCODI NG		
3481- 3482	cg43280932	63	TAGTCCCAGCTA CTCAGGAGACTG A(A/G)GCAGGAG GATCAGTTGAGC CCAGGA	A	G				SILENT- NONCODI NG		
3483- 3484	cg43281897	249	ATTTCATATGCC ACTGAGAAAGAGG T(G/A)TCAGTATA CAGAACATAGGA AGAAG	G	A				SILENT- NONCODI NG		
3485- 3486	cg43281897	280	ATACAGAACATA GGAAGAAAGAAAA A(A/C)GCATGAGA ACATCTGCTTAG TTAGA	A	C				SILENT- NONCODI NG		
3487- 3488	cg43284148	1244	AACAGCAACAAT TACAAATTTATTT [C/T]AACAAAGCC ACACCCAATAGG AGGC	C	T				SILENT- NONCODI NG		
3489- 3490	cg43284565	100	TCGAGACCAGCC TGGGCAACATGA T(A/G)AAACCCAT CTCTACTAAAG TACAA	A	G				SILENT- NONCODI NG		
3491- 3492	cg43284565	119	CATGATAAAACC CATCTCTACTAA A(A/G)GTACAAAA GTAGCCAGGCG CGGTGG	A	G				SILENT- NONCODI NG		

3493-3494	cg43284565	150	AAAGTAGCCAGG CGCGGTGGCG AC[G/A]CCTGTG GTCCTAGCTATT CGGGAGC	G	A			SILENT- NONCODI NG			
3495-3496	cg43284565	156	GCCAGGCGCGG TGGCGCACGCC TGT[G/A]GTCCTA GCTATTCGGGAG CCTGAGG	G	A			SILENT- NONCODI NG			
3497-3498	cg43284565	157	CCAGGCGCGGT GGCGCACGCCT GTG[G/A]TCCTAG CTATTCGGGAGC CTGAGGC	G	A			SILENT- NONCODI NG			
3499-3500	cg43284565	183	TCCTAGCTATT GGGAGCCTGAG GC[A/G]GGAGAA TCACATGAACCC AGGAGGC	A	G			SILENT- NONCODI NG			
3501-3502	cg43284565	93	CAGGAGTTCGAG ACCAGCCTGGG CA[A/G]CATGATA AAACCCATCTCT ACTAAA	A	G			SILENT- NONCODI NG			
3503-3504	cg43285946	205	GGGAAGAAGAG GACTGGACATGT TT[G/T]GGCCCT GTTCCCGGTCTT TGGTAA	G	T			SILENT- NONCODI NG			
3505-3506	cg43285946	335	GCTTCAGATGAC GAAAATGCCACA T[C/gap]AGATTAA ATGAGAAAAAAA CCTTTC	C	-			SILENT- NONCODI NG			

3507- 3508	cg43286741	931	TGTTTCAGGTGAG AAAACATAATGG A[T/gap]TTTTTTT TTTTCCCTCTGGA GCTGCC	T	-				SILENT- NONCODI NG			
3509- 3510	cg43291195	398	TTGATGTTTGAT GGTTGGTTGGTT [A/G]TTTGATTCA TTGTTGGGGTT TGGA	A	G				SILENT- NONCODI NG			
3511- 3512	cg43292021	221	TGAAATTAACGC GTATGCTGCTAC A[G/A]GACCCC GCATTTAAAGCT GGGCT	G	A				SILENT- NONCODI NG			
3513- 3514	cg43293043	184	GGCCCCCATACC CTCAGAGATGGA G[G/A]GTGACCA GGTAAATACAAG GGACTG	G	A				SILENT- NONCODI NG			
3515- 3516	cg43293043	277	AAGGAGCAGCA GTGGGCTGGCC TGG[G/A]GGTCC GAACATGATCCC CTGCGGAG	G	A				SILENT- NONCODI NG			
3517- 3518	cg43293043	408	TGCAGGGTGCA GAGGGAACAG GGC[G/A]CGGTG AGTCACAGGGC CAGAGCCCC	G	A				SILENT- NONCODI NG			
3519- 3520	cg43293043	430	GGCGCGGTGAG TCACAGGGCCA GAG[C/gap]CCCA GGCAGTGGCTG GGCCAGGACA	C	-				SILENT- NONCODI NG			

3521- 3522	cg43296511	200	CCAAGGTCACAC TGTTGGAAGGAAA A[C/gap]AAATTCA TAACAAATAGATG TTAACA	C	-				SILENT- NONCODI NG			
3523- 3524	cg43296511	223	AACAAATTCATA ACAATAGATGTT A[A/T]CATTTGTT AGGCCTGAAGAC ATTTT	A	T				SILENT- NONCODI NG			
3525- 3526	cg43297399	153	AGGTGTAATATT GCTAAGTCGGAT T[C/A]GCATATGA GGTGCAGCATCA AGTCT	C	A				SILENT- NONCODI NG			
3527- 3528	cg43297399	63	TACATTTGGTTAT CATGAGACATGC [A/G]AACTCCTCC AATTTAATGAG AACA	A	G				SILENT- NONCODI NG			
3529- 3530	cg43299091	685	CTGAGCTGGCCT GAGAGGGAATG GG[C/T]AGTGCA CCAAAGTCAGCC CTGCC	C	T				SILENT- NONCODI NG			
3531- 3532	cg43299091	730	CTGCCCTAATAG TCTGCCCTCAGCC C[C/gap]TGAGGT CTGGAAGGCTG CCTGGTTC	C	-				SILENT- NONCODI NG			
3533- 3534	cg43299326	1133	CTCATGAGACTT ATTCACATATCAT G[G/A]GAACAGT ATGGGGGAAACT GCCCC	G	A				SILENT- NONCODI NG			
3535- 3536	cg43300082	563	CTCCAGCCCCCA CTGCCTCTGGGA C[T/C]GGCTCTC GACGCACCTGAA GGCTGA	T	C				SILENT- NONCODI NG			

3537- 3538	cg43300240	405	ATTGAGGCACCT CCACAGCAGGCT G[C/T]GGACAAAA AAAGGAAAAAAG GCCCA	C	T				SILENT- NONCODI NG			
3539- 3540	cg43300347	1116	AAACAGGACAA AATGGCTCTTG C[T/gap]TTTTTTT TTTAATTAACTTT CCITT	T	-				SILENT- NONCODI NG			
3541- 3542	cg43300765	448	TGTAACATATACA GAGCGATTTTT TT[gap]ATACAA TATTACAACGAT TAAAAA	T	-				SILENT- NONCODI NG			
3543- 3544	cg43301130	348	GGGGCTCGAC GTGGCTGATACC CC[T/gap]AATAG CCCTGTTTATCA CATCCCCCT	T	-				SILENT- NONCODI NG			
3545- 3546	cg43303307	729	TCGGGACCTGT CCGTAAGGGA CC[A/G]TTGGGG GCTGGCCTGGC GGTGATCT	A	G				SILENT- NONCODI NG			
3547- 3548	cg43304430	297	CCCCCAGCCAG GGCCTGGTGGG AGG[G/A]GTTGG TCACCATTCCT GCCGIGTT	G	A				SILENT- NONCODI NG			
3549- 3550	cg43304430	386	GGGAGGTCAGG CCACCGCCCCC ACT[A/G]CAGTCT GAATCATCCACG TTCCCGC	A	G				SILENT- NONCODI NG			

3551- 3552	cg43304574	592	TGCTCACACCTG GGCAGGCCCGG CG[G/gap]CAGCA ATGGCAGCTCTC CTGTACAG	G	-				SILENT- NONCODI NG			
3553- 3554	cg43304574	665	AAGTCAAAGCTA ACCGAGGCTGT GC[C/gap]TTCCG AGACCCCGGG ATGGCCCT	C	-				SILENT- NONCODI NG			
3555- 3556	cg43304574	698	ACCCCGGGAT GGCCCTGGGA GGC[C/gap]AAGG AGTCGGGGACT GGGTACC	C	-				SILENT- NONCODI NG			
3557- 3558	cg43304744	137	TGCAGAGAGATC TGAGCTTCGCTG T[C/A]TCCCGGTC GGACGCTCGCA GCTGCG	C	A				SILENT- NONCODI NG			
3559- 3560	cg43305900	1660	GAACCTTGCACA TGAAATGTGTTG G[A/G]AGAAAAG CTGAGTGTGGG AGAGAA	A	G				SILENT- NONCODI NG			
3561- 3562	cg43307969	452	CCTCTCTCGCTC AGCGGCCAAGG TG[A/G]GCGTCT CCACCACAATCT CCTGGAT	G	A				SILENT- NONCODI NG			
3563- 3564	cg43307969	571	CTTGCCGGATCA CAAACCTGGGA G[C/T]CTGTTTCA AAATTTCTCAGC AGTCA	C	T				SILENT- NONCODI NG			

3565-3566	cg43311814	351	TAGTAGTTAATTT TGCCCTTCTCCAT G/AJAGAGACAT CCTGATTAACCTC CTTA	G	A				SILENT- NONCODI NG		
3567-3568	cg43312162	811	GCACCAATTTTC AATTTGTACATA [A/gap]TGCACAT CTCTTAACACTT ACATTT	A	-				SILENT- NONCODI NG		
3569-3570	cg43312305	198	TGCTAGTCCAG GTTGATGTTAAT G/G/CJAACCTTGAA GGGGCAGACAC AGGAGA	G	C				SILENT- NONCODI NG		
3571-3572	cg43312687	121	GCCAGGGAGAG AAATAATTGATTT TTT/GJCTCTCTGT CAAGGTTTCTGG CAGCC	T	G				SILENT- NONCODI NG		
3573-3574	cg43312687	497	TCTGGCTCTGCC AGATGGTAAAGG C/GAJTGCTTTAG TGTGTAGACAAT ATGGG	G	A				SILENT- NONCODI NG		
3575-3576	cg43312687	572	GGATTTCTTAGA ACACAGGCTAAC C/A/GIAAACTACG CTTAGGCTTTGC GTGTT	A	G				SILENT- NONCODI NG		
3577-3578	cg43313505	379	TTGTTCAGGAGC AGATCACTTGA A/GAJCCTCTGAG CTCTTCAAAGAA TTCCA	G	A				SILENT- NONCODI NG		
3579-3580	cg43315440	726	GCTGCCAGCCCT TACCATGCAACA A/C/TJACTGCGCT AAGTGCATCGAA CCACA	C	T				SILENT- NONCODI NG		

3581-3582	cg43315796	982	AGCTGTACCCAT CCAGCTCAAACC G[A/gap]AAAAA AAATCATTTGA CTGTAA	A	-				SILENT- NONCODI NG			
3583-3584	cg43316687	338	AGAGCATTCTAA ATGTTTCACACC CT[C]CATTTGAT TGACAACAGGAA CTCCT	T C					SILENT- NONCODI NG			
3585-3586	cg43318220	880	GCATCGCCTGTC GGATCATCTATC G[G/gap]TCAGAC GAGCACCAACCT CCCATCC	G	-				SILENT- NONCODI NG			
3587-3588	cg43318445	606	TAGCATTGCTAG TTCAAAGAGCTT A[C/T]GCATTTC ACTTTTGATAGA CACCG	C	T				SILENT- NONCODI NG			
3589-3590	cg43318557	304	GGGGATCACCTT GAGGTCAGGAG TT[C/T]GAGACCA GCCTGGCCAACA TAGTGA	C	T				SILENT- NONCODI NG			
3591-3592	cg43318557	358	CTGTCTCTACT AAAAATACAAA A[A/gap]TTAGCC AGACATGGTGGC AGTGCC	A	-				SILENT- NONCODI NG			
3593-3594	cg43319575	757	CGGATGACCTGA GGTCGGGGCCTG GG[C/gap]CTGTC CCTTTGTGCATG CGGCGGIGA	C	-				SILENT- NONCODI NG			

3595-3596	cg43321121	312	GAAAATGGCTGT GGCTTAGCTTTT C/A/TGCTGATGC AGGGTAATAAGC TTTCT	A	T				SILENT- NONCODI NG		
3597-3598	cg43322119	918	GCATTGACTGCA GTGAGAAGGCA GGT/C/GCCTCC ATGGCTCACTGC CCCTTGG	T	C				SILENT- NONCODI NG		
3599-3600	cg43322827	461	AATATTATAAGT TAACACTCTTGC C/TACTTACTCAT CAGATTATATTT TT	C	T				SILENT- NONCODI NG		
3601-3602	cg43322827	665	TTGAGCATGGGA AGGAGCACTGCA T/GA/TAGGAGCT AAGAAAAAGTAC ACACT	G	A				SILENT- NONCODI NG		
3603-3604	cg43323576	576	TTATTGAGGCTG TGTTTTGAAGCA T/GA/CCATTGAT AGTTGAACATA ACATT	G	A				SILENT- NONCODI NG		
3605-3606	cg43323676	282	TCITTAGATGGA AAAGGCGTTGGT G/T/C/GGTGTGG ATTGAGCTTCC CGAAAC	T	C				SILENT- NONCODI NG		
3607-3608	cg43323860	1075	GGCCAACATGGT AAAACCCGTGCT C/T/C/JACTAAAA ATACAAAAATTA GCTGG	T	C				SILENT- NONCODI NG		
3609-3610	cg43324124	761	ACAAATCCATGG CAATAGAAAGAT T/A/TATGCTATT CTCTGATGATCT TAAAG	A	T				SILENT- NONCODI NG		

3611- 3612	cg43325035	373	GAATTCCTTGC TAGAAGGCTTTT TT[<i>gap</i>]CCTCAAA GATTCCTTTTAG GCTTAC	T	-			SILENT- NONCODI NG			
3613- 3614	cg43325035	410	CCTTTAGGCTT ACTTTGATGTC A[G]A[GATCTCCA ATTATAAATGTA GTCCTC	G	A			SILENT- NONCODI NG			
3615- 3616	cg43325862	2558	CCATCTGGTCAT CGGGGATCTCAC C[G]A[CTGAAGC GGTCACCTTAGTG CCTTCA	G	A			SILENT- NONCODI NG			
3617- 3618	cg43326835	631	GAGGTCATCAAC TCACCAAGAAAA G[<i>gap</i>]/AJAGGGGC TTATTTGCTACC CAGCAGC	-	A			SILENT- NONCODI NG			
3619- 3620	cg43327292	381	CTGAGTAGCTGG GACTACAGGCAC A[C]TACCACCAC ACCTGGCTAATT TTTGT	C	T			SILENT- NONCODI NG			
3621- 3622	cg43327899	477	ATCACCTCAATT GGACTGGATGTT A[A]GICAAAACAG ATGAAGTTAAAA ATGAA	A	G			SILENT- NONCODI NG			
3623- 3624	cg43328701	853	TAAACACAGAACC AAGTGATGAAGG G[A]CIGTAGGTT GGCCTGTGGTG CACGTG	A	C			SILENT- NONCODI NG			
3625- 3626	cg43330024	112	ACACATTACCCA CATCTCAGTCAA A[A]GIGAAAAAGG GTGGCCTGGCC CAGCCCC	A	G			SILENT- NONCODI NG			

3627- 3628	cg43330024	196	AAAGGTCCACG CGTGACCCACA GT/C CCGTGGC ACCTTCCTCTGG TGCACC	T	C				SILENT- NONCODI NG		
3629- 3630	cg43330024	387	TCCGGGCCCTTG GAAGTTTCTTCC TA/C T TCTGACG CAGGCTGGGAAT TCTAGA	C	T				SILENT- NONCODI NG		
3631- 3632	cg43330373	848	GCGCCACTCGTC CGGGTCCCGGT TC/T C CCGCCG CCAACGCCTCGC AGGGGA	T	C				SILENT- NONCODI NG		
3633- 3634	cg43330373	850	GCCACTCGTCCG GGTCCCGTTCT C/C T GCCGCCA ACGCCTCGCAG GGGATA	C	T				SILENT- NONCODI NG		
3635- 3636	cg43331856	196	GAAAAGAGAAAC CTGGAAATGCTC C/A G GACATTCC AGAACCAAGATTG CGGCC	A	G				SILENT- NONCODI NG		
3637- 3638	cg43332827	266	GTGAAGGAAAT CCTTAATAGATT A/C T ATTTTGGT TGTTCAAGAAAG TCTGT	C	T				SILENT- NONCODI NG		
3639- 3640	cg43333186	143	GAGCAGCCTTCC TCTGAAATGCT T/A T GTTTTGGA TCCTCCTTTAAC AAGTA	A	T				SILENT- NONCODI NG		

3641- 3642	cg43333186	191	GTACAACTTTTC TTTTCAACAAG T[A/G]CAACCAA CATGCAGTCTGG TCGGC	A	G				SILENT- NONCODI NG		
3643- 3644	cg43333186	257	GGCGCTTCTCCA AAGCTAGACTGG A[A/G]CATAACAA ACCCAGTCGACA GAAGT	A	G				SILENT- NONCODI NG		
3645- 3646	cg43333186	293	CCAGTCGACAGA AGTCATTGTTGC A[G/T]GGAGGGG CTCGTTTCCTTA TGATTG	G	T				SILENT- NONCODI NG		
3647- 3648	cg43333186	309	ATTGTTGCAGGG AGGGGCTCGTTT C[C/T]TTATGATT GTGTGGATAGGT TTAGT	C	T				SILENT- NONCODI NG		
3649- 3650	cg43333186	368	ATGCTTGAGCTG TAAGTAGAGTTG T[T/C]AAGGATAC ATCTGCTCGCTC TTCTG	T	C				SILENT- NONCODI NG		
3651- 3652	cg43333186	392	TTAAGGATACAT CTGCTCGCTCTT C[T/A]GTGATGTA TGTCCTTGGTTT TCCTT	T	A				SILENT- NONCODI NG		
3653- 3654	cg43333186	452	CACAGTCTTCCA GGTCCATAAGCT T[C/T]ACCTGAGA TTTAGACAAGCC TGGAG	C	T				SILENT- NONCODI NG		
3655- 3656	cg43335897	100	TTGATGGGGATT GCATTGAATCTG T[A/T]GATTGCTT TTGGTAAATGG CCATT	A	T				SILENT- NONCODI NG		

3657- 3658	cg43335897	104	TGGGGATTGCAT TGAATCTGTAGA TTC/CJGCTTTTGG TAAATGGCCAT TTTTA	T	C				SILENT- NONCODI NG			
3659- 3660	cg43335897	113	CATTGAATCTGT AGATTGCTTTTG GTTC/JAAAATGGC CATTTTACTATA TTAA	T	C				SILENT- NONCODI NG			
3661- 3662	cg43335897	26	CCTAGGTTTTTTT GTTATTCCAAAT A/GJAATTTGCAA ATTGCTCTGTCT AACT	A	G				SILENT- NONCODI NG			
3663- 3664	cg43335897	29	AGTTTTTTTTGTT ATTCCAAATAAA T/CJTTGCAAAT GCTCTGTCTAAC TCTT	T	C				SILENT- NONCODI NG			
3665- 3666	cg43335897	35	TTTTGTTATTCGA AATAAATTTGCA A/GJATTGCTCTG TCTAACTCTTTG AAGA	A	G				SILENT- NONCODI NG			
3667- 3668	cg43335897	47	AAATAAATTTGC AAATTGCTCTGT CIT/CJAACTCTTT GAAGAATTGAAT TGGAA	T	C				SILENT- NONCODI NG			
3669- 3670	cg43335897	52	AATTGCAAAT GCTCTGTCTAAC TTC/TJTTTGAAGA ATTGAATTGGAA TTTTG	C	T				SILENT- NONCODI NG			
3671- 3672	cg43335897	71	CTAACTCTTTGA AGAATTGAATTG G/A/TJATTTTGAT GGGGATTGCATT GAATC	A	T				SILENT- NONCODI NG			

3673- 3674	cg43335897	78	TTTGAAGAATTG AATTGGAATTTT G A/G TGGGGAT TGCATTGAATCT GTAGAT	A	G				SILENT- NONCODI NG		
3675- 3676	cg43335897	93	TGGAATTTTGAT GGGGAATTGCATT G A/G ATCTGTAG ATTGCTTTTGGT AAAAAT	A	G				SILENT- NONCODI NG		
3677- 3678	cg43336005	426	CAGGGGGCCTG AGCGGGACAGG CCT G gap GCCA CAGCCCCATGTCC TTGGCCCTTC	G	-				SILENT- NONCODI NG		
3679- 3680	cg43336005	427	AGGGGGCCTGA GCGGGACAGGC CTG G gap CCAC AGCCCATGTCCT TGGCCCTTC	G	-				SILENT- NONCODI NG		
3681- 3682	cg43336714	906	GCCTCAGATGGC TCCCCAAGGTCA TT C CATATCTC GGTTTGAGCTCA TATCT	T	C				SILENT- NONCODI NG		
3683- 3684	cg43336760	462	TGGTGACAGTCA GGCCTGGGAGG AG C gap CCACA AACTGGAGCACA GAGACATG	C	-				SILENT- NONCODI NG		
3685- 3686	cg43336794	118	CTATAACATCT CTTTATATCCAG AT C GTTTTCCA AATCACAAAGGAC TCAAA	T	C				SILENT- NONCODI NG		

3687- 3688	cg43336815	855	TTACTAAACCTG AAATCCGTCGTA T[A]gapTTCTGTTT TTACACTTGTAAAT CTTGA	A	-				SILENT- NONCODI NG			
3689- 3690	cg43336925	560	TTTGGAAAACAA ACTGTTTCTTGTT [C/T]ACTAGATAG AATCTGTATTGT AGTA	C	T				SILENT- NONCODI NG			
3691- 3692	cg43336925	657	TATTACTCAATAA TATATGTATGGT C/TACAGGTTCC TGGAGTTGTTTT ATT	C	T				SILENT- NONCODI NG			
3693- 3694	cg43337702	243	AATCTTTTGTAG AGACAAGGTCTC [A/C]CCATGTTGC CCAGGCTGGTCT TGAA	A	C				SILENT- NONCODI NG			
3695- 3696	cg43338533	108	AATGCAGATCCT TAAATTTTCACAC [A/G]AATGAGATA ATTATAGTACAT GTAG	A	G				SILENT- NONCODI NG			
3697- 3698	cg43916985	485	CCGACGGGGCG GCCGAGCCAGC TTG[C/T]TCACAC TCTCGCATGACC TGGTAGG	C	T				SILENT- NONCODI NG			
3699- 3700	cg43917183	450	CTCCATCTCTA TCTTTTGTCCCT C[G/A]ACATTGTC TGCTTTGATCCT TATGC	G	A				SILENT- NONCODI NG			
3701- 3702	cg43917418	122	ATTCACATCAGT TATCCGCTCTGCT T[T/G]TTCTTGAG AGCTTGTGGAAG GIGTT	T	G				SILENT- NONCODI NG			

3703-3704	cg43917418	129	TCAGTTATCCGT CTGCTTTTCTT G[A/G]GAGCTTG TGGAAGGTGTTA ACGTGG	A	G				SILENT- NONCODI NG		
3705-3706	cg43917418	135	ATCCGTCTGCTT TTTCTTGAGAGC TT[C]GTGGAAG GTGTTAACGTGG CTGGGA	T	C				SILENT- NONCODI NG		
3707-3708	cg43917418	204	GCATGAATGTTA AGTCAGGAAGG CC[A/G]GCGATC ACCTTGATAGCT TCITTCAC	A	G				SILENT- NONCODI NG		
3709-3710	cg43917418	225	GGCCAGCGGATC ACCTTGATAGCT TC[T/C]TCACTTA GGTGCCTCTCTC TTTTCG	T	C				SILENT- NONCODI NG		
3711-3712	cg43917418	240	TGATAGCTTCTT CACTTAGGTGCT CT[C]CTCTTTT CGGTTTCCTACT GGTAG	T	C				SILENT- NONCODI NG		
3713-3714	cg43917443	671	ACACAACAGTGC TTTTTTTTTTTTT T[gap]TTAATCCC CCACACAAAGCTT TTCCA	T	-				SILENT- NONCODI NG		
3715-3716	cg43917544	1201	AAGATCTGTTTA GAAAATACCTTT G[A/gap]AAAAACG AGGGTAACCTTTA AAAAATG	A	-				SILENT- NONCODI NG		
3717-3718	cg43917746	779	ACATGAGGTGCC CACAGACAATGG CTT[C]GCCAGCG AGTAAAGGGAAA GAAACC	T	C				SILENT- NONCODI NG		

3719- 3720	cg43917764	452	CAGGGAACAATT CAAGGCTGGAG AG(A/gap)AAAAG GCCACCTTTGAC CCAGCAGA	A	-				SILENT- NONCODI NG			
3721- 3722	cg43918187	362	TGCTTGTGCTCC TCTTGGTTGGCT A(G/A)AGTAGGC ATCACACTGGGG AGCGTG	G	A				SILENT- NONCODI NG			
3723- 3724	cg43918199	323	TAATGTACACTT CCTTAAAAATCT A(G/C)TTTTGCCA CTTATATACATT AATA	G	C				SILENT- NONCODI NG			
3725- 3726	cg43918326	124	GCCAAGGCCCA AGAAAGTTGATT AC(A/G)CCTGGG GAGAAAGAAAT AAACAA	A	G				SILENT- NONCODI NG			
3727- 3728	cg43918370	620	TTGGGGCTACTG CTTGTCCTCGTG G(G/T)GGTCACC AGGAAAGCCTGC CTCCTC	G	T				SILENT- NONCODI NG			
3729- 3730	cg43918591	652	CCCGATGGACTA GGCCCAAGGCC TG(G/A)TTGACAG ACGGCCCCGTGG GGCCCCGG	G	A				SILENT- NONCODI NG			
3731- 3732	cg43918620	968	AGTTCAGTCGTC TCTGTCTTGGAG G(G/gap)CACTGT CGGCCCCCTCA GGTTGAAG	G	-				SILENT- NONCODI NG			

3733- 3734	cg43918620	267	CTTCATGTAAAC AGTTCTAGATGG A[AG]GACCCAG ATGGCACTCCTC CCGGGG	A	G				SILENT- NONCODI NG		
3735- 3736	cg43918725	521	GGTGGGGCGGG GGATCAGGGATT TG[C/T]CTTTGAG AGTCTTCCTAAA GGACCT	C	T				SILENT- NONCODI NG		
3737- 3738	cg43918725	597	CTAGGCTAGTT AGTATCTCAGTG GT[C/G]AGGCTA CCAAATGCCCTTC GCAGTG	T	C				SILENT- NONCODI NG		
3739- 3740	cg43919050	1208	TTCTTTACATA GTTTCCTACCTG CT[gap]GCCAGT TACCCCGGCCCTC CGGAGCT	T	-				SILENT- NONCODI NG		
3741- 3742	cg43919189	331	TGCAGTCTCCA GTTGCCCCAGCAG C[AG]GTGGGAC GCTCAGTGGCAC ACAGTG	A	G				SILENT- NONCODI NG		
3743- 3744	cg43919189	340	CCAGTTGCCCAG CAGCAGTGGGA CG[C/T]TCAGTG GCACACAGTGG GTCTCTGT	C	T				SILENT- NONCODI NG		
3745- 3746	cg43919529	535	TCAGCCTCCTGA GTAGCTGGGATT ATT[AGGCGCA CACCACCACACC CGGCTA	T	C				SILENT- NONCODI NG		
3747- 3748	cg43919529	578	CCCGGCTAATTT TTTTGTATTTTTT[T[gap]TTTATAGTAG AGACAGGGTTTC GCCAT	T	-				SILENT- NONCODI NG		

3749-3750	cg43919529	579	CCGGCTAATTTT TTTGATTTTTTTT T/gapJTTAGTAGA GACAGGGTTTCG CCATG	T	-				SILENT- NONCODI NG			
3751-3752	cg43919529	580	CGGCTAATTTT TTGATTTTTTTT T/gapJTTAGTAGA ACAGGGTTTCGC CATGT	T	-				SILENT- NONCODI NG			
3753-3754	cg43919529	591	TTTGATTTTTTT TTTAGTAGAGAC A/GJGGTTTCGC CATGTTGCCAG GCTG	A	G				SILENT- NONCODI NG			
3755-3756	cg43919529	600	TTTTTTTAGTAGA GACAGGGTTTCG [C/T]CATGTTGGC CAGGCTGGTCTT GAAC	C	T				SILENT- NONCODI NG			
3757-3758	cg43919529	621	TTGCCATGTTG GCCAGGCTGGT CTT/CJGAACTCC TGACCTCAGGTG ATCCAC	T	C				SILENT- NONCODI NG			
3759-3760	cg43919655	1270	CTTTGCCGCTT TGTTCCACCATT G[C/A]TTTGATTA AAATCTGGATCT TTTTT	C	A				SILENT- NONCODI NG			
3761-3762	cg43919705	1391	ATAAACTGAAGG ACAGGGATGGTT T[C/A]TTTCTTTC TTCTTTTTTCTT TCCA	C	A				SILENT- NONCODI NG			
3763-3764	cg43919707	411	CTCTTCTGATTA GTAAGAAAAAA A[A/gap]ATGATA GGCCTGGAGA ATTCAAGG	A	-				SILENT- NONCODI NG			

3765- 3766	cg43919707	412	TCCTCTGATTAG TAAGAAAAAAA A[A/gap]TGATAG GGCCTGGAGAAT TCAAGGA	A	-			SILENT- NONCODI NG			
3767- 3768	cg43919798	679	GGCGCCAGGGG TCCCAATCCTG GA[G/A]CCCCAC TGGCTTCGAGG GCTGGGGG	G	A			SILENT- NONCODI NG			
3769- 3770	cg43919798	831	ACCCTGAAGGG GAGGGAGGAAA ATG[G/A]ATAAT GAGAGAGGGAG GGAACAGT	G	A			SILENT- NONCODI NG			
3771- 3772	cg43919880	540	ACTCTGGCAAT ATAAATACATGC A[G/C]AGAAGTTT CTGACAGTTTAA ATTG	G	C			SILENT- NONCODI NG			
3773- 3774	cg43919880	621	TTAAAAATACAC ATACGTGAAACT A[C/T]GGTGAACA TGTTATGGGTTT GTCCC	C	T			SILENT- NONCODI NG			
3775- 3776	cg43920332	721	AGTGACTATCAT CTTCTGAATTC A[A/G]GACCCATA TATCCGACAGT TTCAG	A	G			SILENT- NONCODI NG			
3777- 3778	cg43920449	330	AAGTACTTCATTT CAACACAGAAGA [A/G]ATGAACAG GTGAGGGATGC CTCICA	A	G			SILENT- NONCODI NG			

3779-3780	cg43920465	1016	AATATTTTGTCC AGAAACATACAG C/TCTTATCAGC TAATTCATAAAA GAGC	C	T				SILENT- NONCODI NG			
3781-3782	cg43920465	1043	TTATCAGCTAATT CATAAAAGAGCT A/gap]TTTTACAA AGGTACATCTGG ATAAT	A	-				SILENT- NONCODI NG			
3783-3784	cg43920465	1056	CATAAAGAGCT ATTTACAAAGG T[A/G]CATCTGGA TAATTAGAACAA TAAAG	A	G				SILENT- NONCODI NG			
3785-3786	cg43920465	1073	ACAAAGGTACAT CTGGATAATTAG A[A/G]CAATAAAG TCTTTTAGGCAT TTCAA	A	G				SILENT- NONCODI NG			
3787-3788	cg43920465	1133	AGTAAAATACA TGATTATTAATAA [A/G]GTTTTTTTA AAGATAGTTCCA GATA	A	G				SILENT- NONCODI NG			
3789-3790	cg43920465	1136	AAAATACATGAT TATTAATAAAGTT [gap/C]TTTTTAAA GATAGTTCAGAG TATT	-	C				SILENT- NONCODI NG			
3791-3792	cg43920465	1158	AGTTTTTTTAAAG ATAGTTCAGATT A/TTTTTTTTAAA GCAATTTCTGTT AAA	A	T				SILENT- NONCODI NG			
3793-3794	cg43920465	4857	AACCTGCAGTCA CCTCCAGGACAT G[C/A]GGCTCTAA CTTTATCTGAG TGCIT	C	A				SILENT- NONCODI NG			

3795-3796	cg43920465	938	CCTTTAAGCTTA TTTAATATTTGAA [A/T]TCTTATTTTC TATTTTCCCCAGA CCC	A	T				SILENT- NONCODI NG		
3797-3798	cg43920465	978	TCCCCAGACCCC AGAAAAACAGAAA GTT/gapTTTTTAGA TGACCAATATTTT GTCC	T	-				SILENT- NONCODI NG		
3799-3800	cg43920465	982	CAGACCCAGAA AACAGAAAGTTT TIT/gapJAGATGA CCAATATTTTGT CCAGAA	T	-				SILENT- NONCODI NG		
3801-3802	cg43920498	844	AGAGCCAGGCC ATCTACCTGGAG TC[A/T]AAGGACA ACCAGAAACTGA GCTGCG	A	T				SILENT- NONCODI NG		
3803-3804	cg43920498	946	GCACCAAGATGA GGATCTACCTGG G[C/T]CAGCTTCA GCGCGGGCTCT TCGTGA	C	T				SILENT- NONCODI NG		
3805-3806	cg43920546	886	CATCACAATGAA ATCCTAGAAAA A[C/gap]AAAAAA CAAAAAACCCCTC AAAGGAA	C	-				SILENT- NONCODI NG		
3807-3808	cg43920546	893	ATGAAATCCTAG AAAAAACAAAA A[C/gap]AAAAAA CCCTCAAAGGAA AAACAG	C	-				SILENT- NONCODI NG		
3809-3810	cg43920616	1827	GGTGTCCAGCC CTAAGGCTCATA TTG/AJACATTAA AGACAAGACACT TTTCA	G	A				SILENT- NONCODI NG		

3811-3812	cg43920738	1007	ACTGCAGCCGGT C CAGGGATCTCCC C[C/gap]AGCAAC AGCTCCACACG ATGAGAA	C	-				SILENT- NONCODI NG			
3813-3814	cg43920883	453	TAAATTTACCC ATTTTTTAAAA [gap/A]GAGCTAA AAGTTACTCAAT AGCACA	-	A				SILENT- NONCODI NG			
3815-3816	cg43920919	242	GGTTTAAATTC CATATGCAACTA TT[C]CCCATATG TACTATGTACAA GTGAT	T	C				SILENT- NONCODI NG			
3817-3818	cg43920959	475	GCAATGAGCTAT C GATCATGCCACT G[C/T]ACTCCAGC CTGGGCCACAG AGTGAG	C	T				SILENT- NONCODI NG			
3819-3820	cg43921044	247	AGCTTCCAAACC AGCGCCATTTC A[gap/G]GGACAT CGACACAGCAG CCAAGTTC	-	G				SILENT- NONCODI NG			
3821-3822	cg43921050	870	ACTTAAAGATGA AACAGTTAAGCC A[A/T]TTTTTTTT TTGAAGAATGTA GATC	A	T				SILENT- NONCODI NG			
3823-3824	cg43921103	505	TGTTTATCCAT GATCAGTACAGA C[C/A]AAATGCAT ATTCACCGTATG AAAGT	C	A				SILENT- NONCODI NG			

3825- 3826	cg43921103	577	AGTTGGCCAAC ACTGAGGCACCA G[C/gap]GTCGTG GTGTAGAGTGG GTTCTCAT	C	-				SILENT- NONCODI NG			
3827- 3828	cg43921103	733	GGGAGTCTCTGC CTTAGTCTGTGG C[G/gap]CCCCCA GGCCCCGGTTC CCACCTCA	G	-				SILENT- NONCODI NG			
3829- 3830	cg43921332	227	TAAAGTGCTGTT TAGATTTAGTAG A[G/T]TCCCATAT TTACTTACTGCT ACCTA	G	T				SILENT- NONCODI NG			
3831- 3832	cg43921332	400	CCTGAGTATTAA CTAGTGGACGTA G[G/A]AAAAAAA ATTCCCTACCTA GG	G	A				SILENT- NONCODI NG			
3833- 3834	cg43921594	460	CCCGCCGCCCT CTCGCTCTCGCA GC[A/G]ACAAGG GAAGAGCCGGA GGAAAGAG	A	G				SILENT- NONCODI NG			
3835- 3836	cg43921594	464	CCGCCCTCTCGC TCTCGCAGCAAC A[A/G]GGGAAGA GCCGGAGGAAA GAGGCGT	A	G				SILENT- NONCODI NG			
3837- 3838	cg43921594	473	CGCTCTCGCAGC AACAAGGGAAGA G[C/A]CGGAGGA AAGAGGCGTCCA CGCCGC	C	A				SILENT- NONCODI NG			

3839- 3840	cg43921596	408	TGGGGTCAGCTC GTTACTCAACTC C[A/G]GTTGACAT TTGGAGTATAGG CACCA	A	G			SILENT- NONCODI NG		
3841- 3842	cg43921645	1361	CCCAAGAACTGT TGCCAGAGATGG A[G/A]GAAAGGG GAAGAGGCCTG GAAGGAC	G	A			SILENT- NONCODI NG		
3843- 3844	cg43921651	399	AAGGAAATTACA CTATATGTTCAA A[A/G]AATGTAAT AATGCTTTTGA AAATG	A	G			SILENT- NONCODI NG		
3845- 3846	cg43921722	829	TCCCCTCCCTTG GCAAAGAGACAT G[A/G]TGCACAC ATGACTGGAAGG GACTCA	A	G			SILENT- NONCODI NG		
3847- 3848	cg43922038	540	TCATACACACAA TGCTACCAATGG A[C/T]TAAACCA GAATCCCTGCT CTGTA	C	T			SILENT- NONCODI NG		
3849- 3850	cg43922038	731	TCCCCTTGTAAG GGTTTAAAAAA A[A/gap]CCCCAA GGGTATTTAAAG CAACAG	A	-			SILENT- NONCODI NG		
3851- 3852	cg43922038	753	AAACCCCAAGG GTATTTAAAGCA A[A/gap]CAGCAG AAACCAGAAAGCT TCTGACC	A	-			SILENT- NONCODI NG		

3853-3854	cg43922074	165	GGGTGGAAGG CACTCGGGAGT GGC[CT]GCTGC CAACAGCAACAG ACTGCCCCA	C	T				SILENT- NONCODI NG		
3855-3856	cg43922313	732	TGTTTGAAGA TGGCTTGAGCTC A[A/G]CAGATTGT CCATGGAATGC AGAAA	A	G				SILENT- NONCODI NG		
3857-3858	cg43922333	604	GGAGCAGTGCA GTTTCACGGGAG GA[A/G]GGCAGA GCTCCTTGCGA TATCIGT	A	G				SILENT- NONCODI NG		
3859-3860	cg43922353	249	AATGGCAAGTAA AACAAAGTAAGG C[T/gap]TTTTTT TCTCCTTTTCCC CTTTT	T	-				SILENT- NONCODI NG		
3861-3862	cg43922353	644	CCCAATGTATT ACTGGAAAAAAA A[A/gap]GAAAAA AATGCCCTTTACT AATTCT	A	-				SILENT- NONCODI NG		
3863-3864	cg43922409	1499	AAACAAAAACA AAAACCCCCCAA T[G/A]AACAAAA CAAAACCCCTCAA AACAA	G	A				SILENT- NONCODI NG		
3865-3866	cg43923026	1399	TATTCTTAAATT ATAGGTACACCA[A/G]TAGCTGGTG CTGGGGAAGGA TGTTT	A	G				SILENT- NONCODI NG		

3867- 3868	cg43923299	418	CTGGGTGGACCT AAGGTTCCCTCC C[G/A]CCCCATTG TGCGGACACTTG GAGCC	G	A				SILENT- NONCODI NG			
3869- 3870	cg43923357	576	CCCACCCACAGT AAAAAGACAAAT T[C/T]TAAAAATT AAAAAAAAGCGC ATAAT	C	T				SILENT- NONCODI NG			
3871- 3872	cg43923357	653	CCCCTCCCCATT TTGCTTTTAAAC [T/gap]TTTTTTTT TTTAAGTTTGTGAT TTTT	T	-				SILENT- NONCODI NG			
3873- 3874	cg43923357	664	TTTGCTTTTAAA CTTTTTTTTTTT /gap]AAGTTTTGA TTTTTTTTTTAAT CCT	T	-				SILENT- NONCODI NG			
3875- 3876	cg43923357	683	TTTTTTAAGTTT TGATTTTTTTTTTT /gap]AATCCTGAA AAGTAGACAGTA AAAC	T	-				SILENT- NONCODI NG			
3877- 3878	cg43923648	252	GAAAGGCCAAAG AAACAAAAAAA A[A/gap]CCTTTTC ATTAAGCATTTTC ATCTTC	A	-				SILENT- NONCODI NG			
3879- 3880	cg43923681	736	CCAAATGCAGAC CAGTGCACCTCT GT[C/G]TAGTTTC CGACTAGTCACC TGGTA	T	C				SILENT- NONCODI NG			
3881- 3882	cg43923691	258	AGTAAAGAAGC TAGCTACATGAT AT[C/A]TACTTGG TTTAACCATATTT TGTC	T	C				SILENT- NONCODI NG			

3883-3884	cg43923691	340	ACAGTTTGATGT TAAAGTATTTGA C[A/C]GTTTTCTC AAAAGCCCAACAG TTTTG	A	C				SILENT- NONCODI NG		
3885-3886	cg43923801	1266	GTTCATAGACTC CTTCTTTTGGAG G[T/C]TTTTCTAA TTTGCACCATGG TACCA	T	C				SILENT- NONCODI NG		
3887-3888	cg43923884	1574	GCCCATTAGGGC GTTGAAGGCGTG CT[A/G]GGGGCTG CTGCTGCTGGTG GTGATG	T	A				SILENT- NONCODI NG		
3889-3890	cg43923910	794	GTTTGTAGCAT CTCAAATCCATC T[G/A]CACTGAAG CTTCTCTTCGAG AGTCT	G	A				SILENT- NONCODI NG		
3891-3892	cg43924053	198	CTTTCGGAGCCC ACTGTGGACATG G[T/G]GGGGGCC AGCCTGTGCTGC TAAACA	T	G				SILENT- NONCODI NG		
3893-3894	cg43924063	238	TGAAAATTAGTG ACTGGTTAAGGT G[T/C]GCCCACTGT ACATATCATCATT TTCT	T	C				SILENT- NONCODI NG		
3895-3896	cg43924180	201	CATACTGCTGCT GCAGCAGCGGG TG[C/gap]GACAC GCGCTCCACCTG CGGGGAAG	C					SILENT- NONCODI NG		

3897-3898	cg43924188	973	AATCACATTTTAA TACTTTTTTTTTT /gapTGGACTCTC TCAACTGTTGTT TGCT	T	-				SILENT- NONCODI NG			
3899-3900	cg43924212	457	TAAATTTTGAATA TTAACAAATAGCA A/GAAGAAAAAC AAACTCAAAAAT GACC	A	G				SILENT- NONCODI NG			
3901-3902	cg43924289	3649	TTACATCTTTATT TAAATTTTTTTTT /gapAACATCTTA TGTTTACAGGCT TCCCT	T	-				SILENT- NONCODI NG			
3903-3904	cg43924289	3784	CAAGACAACATT TATTAACCTGTTA G/A/GJACACTTGC TTTATGTTTGTGT GTAC	A	G				SILENT- NONCODI NG			
3905-3906	cg43924289	3898	TAAAGGTGCTGC AGTTAAAAAAA A/A/gapCAACCT TTTCTTTCAATAT GGCATG	A	-				SILENT- NONCODI NG			
3907-3908	cg43924384	2621	GACTCAATCTCG TCACGGGCAGTAA C/G/A/GTTGCAG GTATTTTCGTCA TGTAGG	G	A				SILENT- NONCODI NG			
3909-3910	cg43924384	2686	CTTCTTACACTC CACACATTCTTT CT/CJTAAAGGTG CAGGCATCTGG GCAGGT	T	C				SILENT- NONCODI NG			
3911-3912	cg43924384	2801	CACTTGCCGCG GCCGCTGCACA GCA/G/AJCCCAT GCTGGACATGCA GGTGICA	G	A				SILENT- NONCODI NG			

3913- 3914	cg43924511	2123	GACCGTTGGTGT TGGCATCTTCTG G(A/C)AAAAAGAG CAAAGGAATGGT TACCC	A	C				SILENT- NONCODI NG		
3915- 3916	cg43924511	2746	TGTCATGTGGCT ACCTGTAACCTG A(A/gap)GGTGGC TACAAAGATGAC TGTTGGAC	A	-				SILENT- NONCODI NG		
3917- 3918	cg43924620	375	AAC TAGGAAAA AGGTTTTTGTG G(gap/T)TTTTTT TTTTTAAATCAT AGTAG	-	T				SILENT- NONCODI NG		
3919- 3920	cg43924620	386	AAAGGTTTTTGT TGGTTTTTTTTT [T/gap]TTAAATCA TAGTAGTACTAG AGTCA	T	-				SILENT- NONCODI NG		
3921- 3922	cg43924620	387	AAGGTTTTTGT GGTTTTTTTTTT [T/gap]TAAATCAT AGTAGTACTAGA GTCAA	T	-				SILENT- NONCODI NG		
3923- 3924	cg43924620	388	AGTTTTTGTG GTTTTTTTTTTT[T/gap]AAATCATA GTAGTACTAGAG TCAA	T	-				SILENT- NONCODI NG		
3925- 3926	cg43924948	555	CCAGGTCAACTG CCCCATGGCTCA C(C/A)CACCCAG GCCGCCCTCCGG AGTCCCTG	C	A				SILENT- NONCODI NG		
3927- 3928	cg43924952	314	AATTGCCTCTAG GGTCCTCCTGG GA(G/A)AGGGAC TGGGGGCCTTT GGCAGAG	G	A				SILENT- NONCODI NG		

3929-3930	cg43924952	444	GCCAGCATTTGG GGCTGTTGCTTA A[G/A]ACAATTC TGAGACTAATGG GTAAG	G	A			SILENT- NONCODI NG			
3931-3932	cg43925029	1537	TCCAATAGAGAA AACCTTCTCAAA AT[C/C]CAGCACAA ATGCACATTTGC TTATA	T	C			SILENT- NONCODI NG			
3933-3934	cg43925029	1717	AGTTTCTCGGAA GAGATGGCAGAT G[C/T]CAGACTG GAGACGGAAGA CTGCCTG	C	T			SILENT- NONCODI NG			
3935-3936	cg43925033	833	GGTCTGTATTAT CCTTGGATGACA A[C/T]GGTGTCT GTGACACTATCT AGGGT	C	T			SILENT- NONCODI NG			
3937-3938	cg43925139	108	ATAATAGTTACAT CTCATACTTCAA C[T/T]ATTAGACA GAGAGAACATTA AAG	C	T			SILENT- NONCODI NG			
3939-3940	cg43925204	227	GAAAGCAAGAAA GAAAGAAAAAAA A[A/gap]CATCTTT ACAAACAAAGTA AAAGAA	A	-			SILENT- NONCODI NG			
3941-3942	cg43925287	242	TGTAGGAGGCA GGGGAAGCTGG CGG[T/G]GGTGG GGTTATGAAGCT GTGATGTC	T	G			SILENT- NONCODI NG			
3943-3944	cg43925287	245	AGGAGGCAGGG GAAGCTGGCGG TGG[T/G]GGGT TATGAAGCTGTG ATGTCAGT	T	G			SILENT- NONCODI NG			

3945-3946	cg43925322	332	TTATGATGGTTA GACTTTGAGCAA CA/GJCTGGGATT CTTCTCTGGGTC CTATG	A	G				SILENT- NONCODI NG		
3947-3948	cg43925322	786	GCTCAAGAGTGG CATGGTTCCAAT T/A/CJTGTATTAA CCCTCAAAGAGG TCCCC	A	C				SILENT- NONCODI NG		
3949-3950	cg43925523	330	AAAATCAGTAGC CTTTCTGCTACC C/T/CJTAGGGTG TTAAAGCAGTGA GTTGT	T	C				SILENT- NONCODI NG		
3951-3952	cg43925523	357	TAGGGTGTTAAA GCAGTGAGTTGT GT/CJTGGGGGT TATTTTCAACCC AGGGT	T	C				SILENT- NONCODI NG		
3953-3954	cg43925525	2043	TCCACACCTGTG ATTGTTCCATGG A/C/AJCTGTGTTT CGTTCTTCAATT CAATG	C	A				SILENT- NONCODI NG		
3955-3956	cg43925674	777	AAAACTCCTCC AGAGTCACCAAT C/T/GJGTCCTTTGT TAGTATCAACCT CATTG	T	G				SILENT- NONCODI NG		
3957-3958	cg43925785	1412	ACATCTTATAATT CAGATCTGCATT C/TJGGTAACAGG AGAATTGAGAGT TTTG	C	T				SILENT- NONCODI NG		
3959-3960	cg43925785	338	TTGTTATAGACA AAAAATAAAGCA T/T/CJCTGTAAC TTCTAAAAGCAT ACACA	T	C				SILENT- NONCODI NG		

3961- 3962	cg43926022	934	AAAAATCCACCT ACACACACAGTC TTC/GTCTTTATC TAAGTGGATTCA AGATG	C	G				SILENT- NONCODI NG		
3963- 3964	cg43926066	1080	CCAGGTGGCTG GCCATCCTCTTC TA[G/gap]GGGCT CCAGGGCGCCC TGCACCTGGC	G	-				SILENT- NONCODI NG		
3965- 3966	cg43926066	433	GTGGCTGCCCC CCGGAGACATGT GT[C/A]AGAGAG GCACGGGTCAG GTGACCCA	C	A				SILENT- NONCODI NG		
3967- 3968	cg43926186	732	CCCCGGGCAC TGGGGAACAGAA AG[G/gap]AATGA GACCCCAACAG GCAGAAAGCC	G	-				SILENT- NONCODI NG		
3969- 3970	cg43926292	1050	AAGATAAACCTT TAAGTCTGAGTA T[G/T]CCTGTAAT TACAGAAGAAGA AGAGA	G	T				SILENT- NONCODI NG		
3971- 3972	cg43926292	1074	TGCCTGTAATTA CAGAAGAAGAAG A[G/A]AATGAAAG TTTGAGTGAAC AGAGT	G	A				SILENT- NONCODI NG		
3973- 3974	cg43926326	464	GGCAACTTGTGT TCCATGTGTCAA G[C/T]CTACTTCC AAGCAGAAAATG AAGAA	C	T				SILENT- NONCODI NG		

3975- 3976	cg43926397	1970	TATTATAAACTG CAACAAATCCTC[C/T]ACCCTCCGA TGGTCAACGACG CTTT	C	T			SILENT- NONCODI NG		
3977- 3978	cg43926442	1067	TTGTGCCAAACG TGCCTCCTTGTT TG/C]TGGGTAA GTGAATCTGACA GAGGTT	G	C			SILENT- NONCODI NG		
3979- 3980	cg43926481	234	ACGTCTTTCAGCA GCGCTTTTCTGGA G[C/gap]TTCGCG AAGTCGGAATAG CGCCGTT	C	-			SILENT- NONCODI NG		
3981- 3982	cg43926489	507	GCCAGTACTGCT GAAGCTCCCGC GT[G/A]GTCATGC TGGAGTTGGAGC TCAGGC	G	A			SILENT- NONCODI NG		
3983- 3984	cg43926603	212	TTATTGTACTAT AAGAAAAAAA[A/gap]TCCTAAAA AGTCCATACAGA TTGGA	A	-			SILENT- NONCODI NG		
3985- 3986	cg43926788	1563	TCCTGGACACT GCCACTCTCCCC A/T]TGGCACC GCTTCTCAGCCA CAAAC	T	C			SILENT- NONCODI NG		
3987- 3988	cg43926788	1813	CTTTATGGGACT TAAGTTTTTTTTT[T/gap]CTCCTCTC CATCTCTAGGAT GTCGT	T	-			SILENT- NONCODI NG		
3989- 3990	cg43926828	1799	TACTAAATGAGT TACCCATTTTTT [T/gap]GTTTCATC CTGAGAACATGC TAACAG	T	-			SILENT- NONCODI NG		

3991- 3992	cg43926935	1337	CTGTAGAGGTAC ACAAAAAGAAAA A(gap/A)JGGAAAA ATAACTACTAGA AAAAAGT	-	A				SILENT- NONCODI NG			
3993- 3994	cg43926973	681	TTTGTAGCTTCAAA GTTGAAAAACAG A/GJTGGTACTA ACAGTCCTTCTA GAGA	A	G				SILENT- NONCODI NG			
3995- 3996	cg43927077	1748	TGTTCTTAGTGC ACACGCGTGAAG G/A/GJCCTGGTAT CGGCTTTAGCAC AATCC	A	G				SILENT- NONCODI NG			
3997- 3998	cg43927077	619	TGGCCAAAACCA GGTCCTTTCTCA G/G/JACAGGGT TGGGCAGATGG ACACATT	G	T				SILENT- NONCODI NG			
3999- 4000	cg43928057	509	TGGTCTGGAGA AAGTTCTCCCTT T/C/GJTTCATCTA CCTTAATTTTCA GTCCA	C	G				SILENT- NONCODI NG			
4001- 4002	cg43928063	414	GTTTGGCATTCA AACAGGACTTC A/C/TJGTTTCAGT GGACAGCTGGG GAAAGG	C	T				SILENT- NONCODI NG			
4003- 4004	cg43928063	524	CTCTCGAGTCTT ACTTAACCTAAA A/G/AJACAAACTG GGTCAACTTGGT AAATG	G	A				SILENT- NONCODI NG			
4005- 4006	cg43928177	471	CAGTCAGTGTGA TCAGTTTTTCTG C/G/AJGTGTGAAT AATTTATCAAAAT AAGT	G	A				SILENT- NONCODI NG			

4007- 4008	cg43928213	80	CTCTTATAGTGC AACCATGGCAGA C/T/CJATTCAACA GTGCCTCCCCCC TCCTC	T	C				SILENT- NONCODI NG			
4009- 4010	cg43928396	427	TTTTAGACCATA TAGGGTAACTTC[C/T]TGATGTTGC CATGGCATTGT AAAC	C	T				SILENT- NONCODI NG			
4011- 4012	cg43928430	462	GTTTCTTGGTTG CTGCTTTATCTTT [G/A]CCATAGTTA TGCTTGATCAGG TATT	G	A				SILENT- NONCODI NG			
4013- 4014	cg43928432	344	TGTTGAGGCAGA AGTCAATCTTAG G/A/GTGTGGTCT GTACATATCTGC AGATA	A	G				SILENT- NONCODI NG			
4015- 4016	cg43928785	140	GGAAGAGTCCTG CGTTTTACTGCG T/C/T]AATTTGTG GAGGCTCCTGCT TCACA	C	T				SILENT- NONCODI NG			
4017- 4018	cg43928902	261	TCCTGGCCTCAA GGAATCCTCCTG C/T/C]TTGGCCTC CCAAAGTGCTGG GATTA	T	C				SILENT- NONCODI NG			
4019- 4020	cg43929221	2190	CTTCTAATAATTT CTGTTATAAATT[T/G]CCAGCAATT TAATGAAAAATCT AATG	T	G				SILENT- NONCODI NG			
4021- 4022	cg43929415	3896	ATGGTAGAATTA CTAGTTCAGAAT T[G/A]GCATAGAT TCTGGTGTTAAA ATAGA	G	A				SILENT- NONCODI NG			

4023-4024	cg43929656	217	GGAAGAGGAGG AAGGCGACGGC AAC[AG]GTGAC CAGCTCATGGGC TTCGAGAG	A	G				SILENT- NONCODI NG		
4025-4026	cg43929652	1023	TTTATTGCAGCC CAGTTCAGCCA GT[AG]TTTGCCA ACTTGTACAACA GAAGT	T	A				SILENT- NONCODI NG		
4027-4028	cg43929652	1037	TTCCAGCCAGTG TTTGCCAACTTG T[gap]/TACAACA GAAGTCCAGCAA TAGGTGG	-	T				SILENT- NONCODI NG		
4029-4030	cg43929652	1131	CCTGAAATAAGT GAAGTTACTAGC T[GA]CTAAATAA ATGTCACACTCAA AGCAG	G	A				SILENT- NONCODI NG		
4031-4032	cg43929652	1141	GTGAAGTTACTA GCTGCTAAATAA AT[C]GTCACACTCA AAAGCAGTCTCT TGGCT	T	C				SILENT- NONCODI NG		
4033-4034	cg43929652	1158	TAAATAAATGTC ACTCAAAAAGCAG TIC/TTCCTTGGCT TTTTCTTACACA GCGGG	C	T				SILENT- NONCODI NG		
4035-4036	cg43929652	1191	TTTTCTTACACA GCGGGCAACTTT T[C]CTTTTAAAT TCTCCATTTCTAT CTT	T	C				SILENT- NONCODI NG		
4037-4038	cg43929652	1212	CTTTCTTTTAAA TTCCTCATTTCTT A/GTCTTCCCTC CATTCCTTCGCA GCAT	A	G				SILENT- NONCODI NG		

4039-4040	cg43929652	1239	CTTCCCTCCATT CTTTGCGAGCAT C/A/TACATTAGC AGGTGAGTCTCC ATTAG	A	T				SILENT- NONCODI NG		
4041-4042	cg43929652	1245	TCCATTCTTTTCG CAGCATCAACAT T/A/TGCGAGGTGA GTCTCCATTAGG GTCTG	A	T				SILENT- NONCODI NG		
4043-4044	cg43929652	1266	CATTAGCAGGTG AGTCTCCATTAG G/G/A/TCTGCCA GCATAGAAATGA CACTAA	G	A				SILENT- NONCODI NG		
4045-4046	cg43929652	887	TCCGGATCATGT TGTGCTATGTAC A/G/A/GTCTTTAC AATTCTTCTGA AGTT	G	A				SILENT- NONCODI NG		
4047-4048	cg43929880	980	ACATCGAAGATT TGTTTATAATAG G/A/gap/AAAAAA AAAGCTACCCAC TGTCATG	A	-				SILENT- NONCODI NG		
4049-4050	cg43929880	989	ATTTGTTTATAAT AGGAAAAAAA A/gap/GCTACCCA CTGTCATGCGCT GGAA	A	-				SILENT- NONCODI NG		
4051-4052	cg43929880	758	CATCCTCAGCGG CCCCTCTGCAGG G/C/TAGAGTCTC GCTCTCACTCTC CCAGC	C	T				SILENT- NONCODI NG		
4053-4054	cg43929880	910	ACTCCACCTTGC ATAAGTGCTTGA G/G/A/TACACACA ACCAGATACGTA GATCA	G	A				SILENT- NONCODI NG		

4055- 4056	cg43930022	1265	GCCATTGAGGAC CTAATTGAACAA T[C/T]GCTACCAT TCCTTCCACTTTT AGGC	C	T				SILENT- NONCODI NG			
4057- 4058	cg43930314	1636	CCCAGAGCATC TGCGGCCTTCAG G[C/gap]GCACCC CCCGGTTGGAGT CCTGCAG	C	-				SILENT- NONCODI NG			
4059- 4060	cg43930314	2332	GATCACAGCCTG ACAAATGGCCAT CT[A]CCAGCTGC TCATCTGGGGTC CCAAG	T	A				SILENT- NONCODI NG			
4061- 4062	cg43930342	604	CAGGGCTCAGTT GGGACCCAGTGT GG[A/G]GAAAGA CAGGAAAGTGA AAAGCTT	A	G				SILENT- NONCODI NG			
4063- 4064	cg43930456	741	CTGGGTGCACAC TGGACGCTTAGA C[G/A]TGAACATC TTTCTCAGCTCA TCACC	G	A				SILENT- NONCODI NG			
4065- 4066	cg43930460	445	TAAAGGTTTAA GAAAAAAGGGAG G[G/A]GCTTTCTT ACAAGCTTTTTT ACAAG	G	A				SILENT- NONCODI NG			
4067- 4068	cg43930652	141	TGACATACAAGT ACAAGAAGAGCA A[A/T]TTGTGCTC AAAATACTTTATT CTTA	A	T				SILENT- NONCODI NG			
4069- 4070	cg43930652	198	TGGACATGTGAT GAGCACATGTCT A[G/T]TATTGCAG CAAGGAAATCAC ATCAG	G	T				SILENT- NONCODI NG			

4071- 4072	cg43930874	244	CAACCCAAATTA ACAGTATTATTAA [C/A]TTCCTACCC CAAGCTGGCTCT CCCC	C	A				SILENT- NONCODI NG		
4073- 4074	cg43930919	585	ACATGGCTAGAC ACAGAGCCCCG GA[G/T]GGCAAA GGAAATTTGGAG GCCCTT	G	T				SILENT- NONCODI NG		
4075- 4076	cg43931240	714	GGAGGGAGGAA ACACCAGTAAGA CA[C/T]GAAAGG GCAATAGTGAG TCAGAAAT	C	T				SILENT- NONCODI NG		
4077- 4078	cg43931447	639	TTTAAACCTAGG TTTGGTATTTCC [T/C]GGGGTGAT GGTGACTTTTGA AAATT	T	C				SILENT- NONCODI NG		
4079- 4080	cg43931447	670	GATGGTGACTTT GGAAATTTGGGC C[G/A]GGGCGGA AGTGAAGGCTGC AACATT	G	A				SILENT- NONCODI NG		
4081- 4082	cg43931671	336	CAAAAAGGAAAA ACAAACAAAAA A[A/gap]CAGTAA TTCTGAACACAT GAAGAGT	A	-				SILENT- NONCODI NG		
4083- 4084	cg43931755	966	ACTTGAAAAATA AAAGATTTTTTTT [T/gap]CCAAAGG AATGCTGCACCC ATTTCAT	T	-				SILENT- NONCODI NG		
4085- 4086	cg43932129	1914	TGACTCTTCCAA ATCCCCACATGT T[igap]/AJAAAAAAA CCTGTTGGTACA GGCTCA	-	A				SILENT- NONCODI NG		

4087- 4088	cg43932330	614	GTAAACATTC TAAATGTTGA A/CJTAATTTAA TGTAATACTGT TAAAC	A	C			SILENT- NONCODI NG			
4089- 4090	cg43932388	1359	TATGTATTCAGG GGTTCAGATAAG G/A/TCTGGAG CAACCCCAAAAT TAGACG	A	T			SILENT- NONCODI NG			
4091- 4092	cg43932459	1540	GTAGCAGGGCC CGGGTGGAGG GTC/A/GJGGCAC CGACCTCATCAG GGCCACGA	A	G			SILENT- NONCODI NG			
4093- 4094	cg43932618	433	AAAACACATTG GCAGATGCCGTC G/A/GJCAAGTACT GCATTGGTGTGC CACCC	A	G			SILENT- NONCODI NG			
4095- 4096	cg43932761	420	AGTTACGATCA CTGTCAGTTTCC C/T/AJGGAGTACT TAATCCGTTTCC TTTCT	T	A			SILENT- NONCODI NG			
4097- 4098	cg43932964	957	ACTTCTCACACA TAGTAAGTGGGA A/A/CJAGAAAGTG CTTTGAAAGTTC CTCCC	A	C			SILENT- NONCODI NG			
4099- 4100	cg43932964	1817	GCTTCAGTTGGT CGAAGACAGAG GTT/GJ/CAGGTAA GGATGACTGATA GGAAAT	T	G			SILENT- NONCODI NG			

4101- 4102	cg439333034	997	CTGTACTGTTAA AATTTTACCCTT [G/C]TTTAGTCTC TCTACTTTGACT AAGC	G	C				SILENT- NONCODI NG		
4103- 4104	cg43933066	598	ATAATTCCTCAAT TAATTTTATTG[T/C]TCTTACAATA TTTGTAAGATGA GTG	T	C				SILENT- NONCODI NG		
4105- 4106	cg43933072	558	AGCGCCAAGTTT CCTTTCAACCAG T[G/gap]GGGCCT GCAGCCTCGAA GTCCTCTC	G	-				SILENT- NONCODI NG		
4107- 4108	cg43933072	561	GCCAAGTTTGCT TTCAACCAGTGG G[G/gap]CCTGCA GCCTCGAAGTCT CCTCCTC	G	-				SILENT- NONCODI NG		
4109- 4110	cg43933106	662	CAAGTGTGGCG GTACCGCTGAGG AGT[A]GAGGCT GTTGTCCAGGA ACGCTGA	T	A				SILENT- NONCODI NG		
4111- 4112	cg43933106	722	AGACGGTCATCA GTGCAGACGCA GC[G/A]GACGCT GCTGAGGATGG CTCAGTGG	G	A				SILENT- NONCODI NG		
4113- 4114	cg43933114	226	AAGGATGGCTCC CTTCCTTCAACC CT[A]TGATAAGG GGAGGGAAGAA AAAAGA	T	A				SILENT- NONCODI NG		
4115- 4116	cg43933365	827	CATCTCCGCTC TAGAAGGGCTG GG[A/G]AGCTCG CGGCCGGGTT CCACCTGG	A	G				SILENT- NONCODI NG		

4117- 4118	cg439333482	411	TTGAGCTCTTTT CTGAGATCATCA C/TTCACCCCGAC GGAGACTTGTGA CGAC	C	T				SILENT- NONCODI NG		
4119- 4120	cg439333539	722	CATTCTTGTGA GCCCCAGTTTG A/T/CJTCTGTAC CGAGGGGCCAG TACTTG	T	C				SILENT- NONCODI NG		
4121- 4122	cg439333539	736	CCCCAGTTTGAT CTTTGTACCGAG G/G/C/GCCAGTA CTTGAACAGCT TTGGGA	G	C				SILENT- NONCODI NG		
4123- 4124	cg439333539	747	TCCTTGATCCGA GGGGCCAGTAC TTG/TAAACAGC TTTGGGATCAAA TCCTTC	G	T				SILENT- NONCODI NG		
4125- 4126	cg439333539	766	GTACTTGAAACA GCTTTGGGATCA A/A/GJTCCTTCTC TGTGAGCCAGAA GTCAG	A	G				SILENT- NONCODI NG		
4127- 4128	cg439333539	775	ACAGCTTTGGGA TCAAATCCTTCT C/T/AJGTGAGCCA GAAGTCAGCCAT GCGCA	T	A				SILENT- NONCODI NG		
4129- 4130	cg439333539	796	TCCTGTGAGCC AGAAGTCAGCCA T/G/AJCGCATGG CTCGTTCGTTAG TGCTCTC	G	A				SILENT- NONCODI NG		
4131- 4132	cg439333539	814	CAGCCATGCGCA TGGCTCGTTCGT T/A/GJGTGTCTCC CAGCTTCCCAT GTCGA	A	G				SILENT- NONCODI NG		

4133- 4134	cg439333539	829	CTCGTTCGTTAG TGTCCTCCAGCT TCTCTCCATAGTC GATGAGCTTCTC CGCGT	C	T				SILENT- NONCODI NG			
4135- 4136	cg439333745	307	TCAAACCTCTGA CCTCAGGTAATC TIGAJCCCGCT CGGCCTCCCAAA AGTGCT	G	A				SILENT- NONCODI NG			
4137- 4138	cg439333777	10926	AAGATTACGGGG AGCAGAAGTCTA CJAJTCCATCAG CACAGCAAAGCG CCTGG	A	G				SILENT- NONCODI NG			
4139- 4140	cg439333777	11083	TGCCATTTTCCA AGCAGAGCCCCA CGJAJTGAGGA AGCACTTTCTCC GGAATG	G	A				SILENT- NONCODI NG			
4141- 4142	cg439333908	681	ATTGTAATAGAT CTGATTATATGA GJAJGTGTGAAAG TCAATATGGGTA ATT	G	A				SILENT- NONCODI NG			
4143- 4144	cg439333964	965	AAAGCTTTTCAA CCTAAATGTGGG Ggap/AJAAAAAA CAGGTAAGGCAT TATTTT	-	A				SILENT- NONCODI NG			
4145- 4146	cg43934149	391	TATGTTATCTATT CAGTTTTGAAAA CAJATTCATTAAAG ATTTAAATGCAA AT	C	A				SILENT- NONCODI NG			
4147- 4148	cg43934157	2035	TAAACCATTTATTC TATAAGACATAA GJAJGGAAGGTAA ATAATGGCCAC AAAA	G	A				SILENT- NONCODI NG			

4149- 4150	cg43934300	473	CCAGGATAGTTA ACTTGAATTTTCAT [C/A]AGTGTCCAC AGTCAGAGTATT AAAG	C	A				SILENT- NONCODI NG		
4151- 4152	cg43934316	3195	CATTACAAAAC AATTCTGGTACT A[C/G]AGACCAG TGGTGTCAGAAT AGGCCT	C	G				SILENT- NONCODI NG		
4153- 4154	cg43934316	3203	AAACAATTCTGG TACTACAGACCA GT[C/G]GGTGCA GAATAGGCTTAG TGCCCTC	T	C				SILENT- NONCODI NG		
4155- 4156	cg43934316	3214	GTACTACAGACC AGTGGTGTCCAGA AT[C/G]AGGCTTAG TGCCTCCTTGTT TGCTG	T	C				SILENT- NONCODI NG		
4157- 4158	cg43934316	3308	TCAGAGTTTCATT TTATGCAGGGCC AT[G/T]CTCAGTC CTCAATGTACTC CCACA	T	G				SILENT- NONCODI NG		
4159- 4160	cg43934316	3309	CAGAGTTTCATT TATGCAGGGCCA TT[G/T]CTCAGTCC TCAATGTACTCC CACAG	T	G				SILENT- NONCODI NG		
4161- 4162	cg43934316	908	ACTGCAATACCC TCAGGCAGTATG C[C/T]AACATTGA AATAGAAAGCAT CTCTA	C	T				SILENT- NONCODI NG		
4163- 4164	cg43934439	1151	GGATGATGCAG GTATGGAGTTGC AG[C/T]CCCCACA GCAGACATTGCT GCTGCT	C	T				SILENT- NONCODI NG		

4165- 4166	cg43934462	1189	GGATCTGTGAC CCGCTTGTGAC TGAJGTGGCA GATTCAGTCTC TACCGC	G	A				SILENT- NONCODI NG		
4167- 4168	cg43934499	1096	TGTGTCTTCCTG TGTTCTCAAGAT TIGTJAGAAATCCC AGATGATCACGC GATT	G	T				SILENT- NONCODI NG		
4169- 4170	cg43934499	1111	TCTCAAGATTGA GAATCCCAGATG ATTCJACGCGAT TTCAGACCTATC CATGT	T	C				SILENT- NONCODI NG		
4171- 4172	cg43934499	1132	ATGATCACGCGA TTTCAGACCTAT CIC/TJATGTACAA TTACATAGAGAT GCGAG	C	T				SILENT- NONCODI NG		
4173- 4174	cg43934499	1159	TGTACAATTACA TAGAGATCCGAG C/A/GJCATGTCAA CTCAAGCTGGTT CATT	A	G				SILENT- NONCODI NG		
4175- 4176	cg43934499	1167	TACATAGAGATG CGAGCACATGTC A/A/TCTCAAGCT GGTTCATTTTC AGAAG	A	T				SILENT- NONCODI NG		
4177- 4178	cg43934499	1249	CATCGACCTTTA TCCCTCTCTATA C/A/JATGGTCAC TTTTCCAGAATA AGAT	A	C				SILENT- NONCODI NG		
4179- 4180	cg43934665	299	CCCGGGTTCGA GCGATTTTCCTG CC/T/CJAGCCTC CCAAGTAGGGG GACTACA	T	C				SILENT- NONCODI NG		

4181- 4182	cg43934665	321	GCCTCAGCCTCC CAAGTAGGGG ACTTCJACAGCA CCCACCACCACG CCCGGC	T	C				SILENT- NONCODI NG		
4183- 4184	cg43935007	151	GTGGAGATTGTA GAATAACTATCA TTTGJAGCAAAGG CAGAAAGTATTC ATTTC	T	G				SILENT- NONCODI NG		
4185- 4186	cg43935063	465	GGCACCAGGAA GTCCACACCATA TGIC/GJAGTATTG GGGCTGTAGGT CTCCGAG	C	G				SILENT- NONCODI NG		
4187- 4188	cg43935145	1828	CCTCCATCACCA CGAACATGTGGT A[G/gap]GCCCGG CCGGGCCCCCG CTCCAAGA	G	-				SILENT- NONCODI NG		
4189- 4190	cg43935384	284	TTGCAGATTTTT CTTCTAAAAAA A[A/gap]CTATAAT TCTCTCACAGAT CACATA	A	-				SILENT- NONCODI NG		
4191- 4192	cg43935526	480	TTTTTTTCCAAAA TCACTGTTGGGG TTGJGGGGGATC CCAGTCTCGGGA CTGTG	T	G				SILENT- NONCODI NG		
4193- 4194	cg43935836	547	TGGCCTTGGCCA GACACAAACCA G[A/G]GACTGCC ATGACAGACAGA GCAGAA	A	G				SILENT- NONCODI NG		

4195- 4196	cg43935861	345	TGGCAGAGAAAA AGGCCACCGAT GC/T/GGAAGCC GACGTAGCTTCT CTGAACA	T	G				SILENT- NONCODI NG		
4197- 4198	cg43935933	876	ATGATGACACTG TGCCTGCCAAGG C/C/T/AGTTTGCT TTCTTCAACTCT AGGC	C	T				SILENT- NONCODI NG		
4199- 4200	cg43936041	779	GTGAAAAGCAG ATCTGTGGATGT C/A/G/JAGCCGAA GATCACTCCGTT TATGGA	A	G				SILENT- NONCODI NG		
4201- 4202	cg43936051	648	TGTTACCAGCTT TACATACTGTTT T/G/A/CCATTGT GAGGGGTGCAA CCAGAA	G	A				SILENT- NONCODI NG		
4203- 4204	cg43936117	223	GGAGGGCGAGC AGAAAAACGGAA AA/C/T/JACGGAAC GCCACAGAAAGTA TGATCC	C	T				SILENT- NONCODI NG		
4205- 4206	cg43936154	674	GGATGCCGTGA GGGGATGTGAT GTC[C/gap]TCAG TGCTCTCTGATGA CACAGTTGC	C	-				SILENT- NONCODI NG		
4207- 4208	cg43936249	556	CCACGATCCCTT TCACTCATTGGT G/A/G/GCACACC AGATTAGGTACA AGAATC	A	G				SILENT- NONCODI NG		
4209- 4210	cg43936432	647	TATGCTGCCTGA AATGGCCTATGC C/T/C/JCTAAAT TCCTTTCACCTT GTCAC	T	C				SILENT- NONCODI NG		

4211- 4212	cg43936887	327	TCTGTTGTCCCT TCAGTCAGGTCA C/T/C/GTTCAAAT AGCTCTCTAGAC AGGCT	T	C				SILENT- NONCODI NG		
4213- 4214	cg43936887	378	CTTCCTTATCATT CTACTTAAATAA G/A/C/C/C/C/AATC ACTCTGTGTCCC TTTA	G	A				SILENT- NONCODI NG		
4215- 4216	cg43936887	439	TCTTCCTGCTAT TTCATACTACCT G/A/gap/AAAAAA TACTTGAAC TTC CTAGAAC	A	-				SILENT- NONCODI NG		
4217- 4218	cg43936887	445	TGCTATTTCATA CTACCTGAAAAA A/A/gap/TACTTGA ACTTCCTAGAAC ATAAGC	A	-				SILENT- NONCODI NG		
4219- 4220	cg43936905	30	AGTTTTC TGCC GCTGGCAGGGC TG[C/gap]GGGA CCGCCAGCTGCT GCAGTGCG	C	-				SILENT- NONCODI NG		
4221- 4222	cg43937728	490	GGCTTTGTACAG GTGAGCTACTTC T/C/TACAGGAGT CGGATCCACAT CTGCA	C	T				SILENT- NONCODI NG		
4223- 4224	cg43937732	1147	GTTGCCCCACAG GGGAAGGGGCG CC[C/T]GGGCGC GGCCGCCGGAG GCATTGG	C	T				SILENT- NONCODI NG		

4225- 4226	cg43937732	1402	TATTTTGGGATT ACCCAATTTTTT [gap]/TTCTACTAT TCTCAGATATCT ATCAA	-	T				SILENT- NONCODI NG			
4227- 4228	cg43937732	566	CTTAAGGCACAG ATCACTCATGCT A/TCTGTTTG GTTAGGAATGC CTTA	T	C				SILENT- NONCODI NG			
4229- 4230	cg43937732	631	CTGGGTGGCC AGGTGTTCTTG CC/C/TTCATTCC GGTAAACCCAAA ACCTTC	C	T				SILENT- NONCODI NG			
4231- 4232	cg43937732	776	GGGCTTCTCCC AATATGTCCCC TT/C/CTTTGATT TGCAAATCGATA AAAGC	T	C				SILENT- NONCODI NG			
4233- 4234	cg43938515	150	AGATGGGGGT GATTCAGCATC AC/C/A/CACCCCTC CTATATGGCCAG GCCTCC	C	A				SILENT- NONCODI NG			
4235- 4236	cg43938812	604	CACTGACAGTGC CCCCGTGTCGTG C/A/GTGTATTCT GCGCATTTTCCT GTGCT	A	G				SILENT- NONCODI NG			
4237- 4238	cg43938812	930	CTGCCTCTGTGC CTGCCTGTACTG C/C/T/GATGCTCC AGTGGATAACTC AGCAT	C	T				SILENT- NONCODI NG			
4239- 4240	cg43939553	1192	AAGAACCACAA GTGTCCAGAGG GA/T/gap]TTCTA GGTGATCTCTCT CTTAACCC	T	-				SILENT- NONCODI NG			

4241- 4242	cg43939553	1194	GAACCCACAAGT GTCCAGAGGGAT TTT/gap]CTAGGT GATCTCTCTCTT AACCCCT	T	-				SILENT- NONCODI NG		
4243- 4244	cg43939553	617	AAAAGAAGAAGA AACTCAAAATTC CTT/CATCTGCGT GCTAATTTGAAA AGAAC	T	C				SILENT- NONCODI NG		
4245- 4246	cg43939553	793	ATCAAGAGCAAA GGGAACAGCAG GC[C/gap]TAACA GCAGGGTTGGG AAGGCAAAA	C	-				SILENT- NONCODI NG		
4247- 4248	cg43939553	913	TAGCAGGCATT ATAAGTCCCCAC C[C/gap]TCACCA ATGCATCGGG GTGGTCCC	C	-				SILENT- NONCODI NG		
4249- 4250	cg43940188	278	GCTGCTGGCCAA GGCGGAGCGCG TG[A/G]GCTCGC ACGCCAACGCC GCCCAAGA	A	G				SILENT- NONCODI NG		
4251- 4252	cg43940467	1539	AGTACATAAATA AATACTAAAAAA A[A/gap]TTAAAT CCTTGTTCTTATT TTGTA	A	-				SILENT- NONCODI NG		
4253- 4254	cg43941368	1021	GGCAGAATCCTG CTATTCCTCAAGA A[C/G]CCTCGTAA TGGCAAAACTCC CCAAA	C	G				SILENT- NONCODI NG		

4255- 4256	cg43941368	1027	ATCCTGCTATTC. CCAAGAACCCCTC GTT/CJAATGGCAA AACTCCCCAAAT GACAC	T	C				SILENT- NONCODI NG		
4257- 4258	cg43941368	1038	CCCAAGAACCCCT CGTAATGGCAA A/C/TJTCCCCAAA TGACACCCAGGA CCACA	C	T				SILENT- NONCODI NG		
4259- 4260	cg43941368	1066	CCCAAATGACAC CCAGGACCACA GC/A/GJATGATCT GTCGGAACCCAGT AGATCA	A	G				SILENT- NONCODI NG		
4261- 4262	cg43941470	380	AGAGCTGCTGTA GTCTCTGCTTGG C/C/TJCTTTGCT CAGCTTCACCAT GGCGA	C	T				SILENT- NONCODI NG		
4263- 4264	cg43941536	346	TTCTCTGCTAGCT CTGAAAAAACAGG A/A/gap/CAGGCA TTGAACAGGGCC TTGACCA	A	-				SILENT- NONCODI NG		
4265- 4266	cg43941567	1109	CCTCCCGCCTCG GCCTCCCAAAGT G/C/TJGGGATTA CAGGCGTGAGC CACCGC	C	T				SILENT- NONCODI NG		
4267- 4268	cg43942501	694	CCTTTCTCTAGG CGGCTCTCTGGC T/C/TJGACTTCA TCAGCCAGTGGC TGCIT	C	T				SILENT- NONCODI NG		
4269- 4270	cg43942588	1753	ATGAAATCATGG AGCAGAAGTCCA G/G/TJAGAGTTCA ATACGATTCTA AATCC	G	T				SILENT- NONCODI NG		

4271- 4272	cg43942890	915	TTGCTCACTCCG AGGTGGAATAAG G[G/A]GACGTTA GTAGTCACATAT GTACT	G	A				SILENT- NONCODI NG			
4273- 4274	cg43943086	162	TCTAGCTATTTTC AAGACAGACTTA[A/gap]TCAATACT GTGTTTGCTTTC CAATT	A	-				SILENT- NONCODI NG			
4275- 4276	cg43943163	651	TGGTTCTCGGCC TCCTGTTTCTGC A[C/T]ATGGCGC CGCAGGGTGTC CCGTTGC	C	T				SILENT- NONCODI NG			
4277- 4278	cg43943237	1056	CATCTTGAGAAG AACTAACTTCT G[C/T]CTTTAATT TGCATATAAGTA TCATA	C	T				SILENT- NONCODI NG			
4279- 4280	cg43943237	120	CTTAACGTGTAC CACTATAGTCAA G[C/T]CCAGTACC TCAGTGACTTCA CAGAT	C	T				SILENT- NONCODI NG			
4281- 4282	cg43943237	245	AACITTAAGTTC CTATGACATAGT A[C/T]GGTGTTAG TATGGTGATAG CTGTA	C	T				SILENT- NONCODI NG			
4283- 4284	cg43943237	584	GGAGTTTGTCTA CTAGGTTTTTTTT [T/gap]GTTTTTTG TTTTTTTTTACAA ATCA	T	-				SILENT- NONCODI NG			
4285- 4286	cg43943787	1063	AAAGTCCGAAAT CACTGATCTTGG C[G/A]TAATGTTG GGTAACTAGCAA CACAT	G	A				SILENT- NONCODI NG			

4287- 4288	cg43944032	672	TGACAGAAAGCTC ATTAAACCAAG TIGCJCCCCAAC CTCCTGAAACAT CGTTA	G	C				SILENT- NONCODI NG		
4289- 4290	cg43944291	1232	CCACTTCTGAAC GGCCGAAGGTG CC[C/T]CATTCCA GACCTGCCCATTT TGATGG	C	T				SILENT- NONCODI NG		
4291- 4292	cg43944291	1409	ATATTCTTCACA GGCTGTGGAATT [C/T]CTAGCTAA ACATTCTAGTTT CTCC	C	T				SILENT- NONCODI NG		
4293- 4294	cg43944291	319	TAAAAAATACATT CATACAGAAATA[T/A]ACAATCTTG CAAAAAACAATT TCA	T	A				SILENT- NONCODI NG		
4295- 4296	cg43944291	427	AGGTGCTTCCA AAAAA A[A/gap]GAAATTT CACTAATAGAAA TTTTT	A	-				SILENT- NONCODI NG		
4297- 4298	cg43944310	554	GGTATTAACTG GGAATAAGGGA GA[C/A]ACAAACC ATTCTCTCCCG CACTCC	C	A				SILENT- NONCODI NG		
4299- 4300	cg43944408	1484	TGTTGTAGTC ATGGTAGATGGT C[G/A]GTCTGGA ATTCCTAGAGGA AGAGGA	G	A				SILENT- NONCODI NG		
4301- 4302	cg43944408	752	AGCCGGCATCTC TTAACTTTTTTTT[T/gap]CCCCCA GTAAATTGGTAT GCAATA	T	-				SILENT- NONCODI NG		

4303-4304	cg43944446	1244	ACTGGGACCAAT CCAGTGGGCAG CG[C/gap]CCTCC CCAGGGTACATT CCAGAACA	C	-				SILENT- NONCODI NG			
4305-4306	cg43944446	911	ATCGGTTATTAT CCCTCATTTTTT [gap/T]GTAGGAA ATAAGTTTGCTT GTTTCT	-	T				SILENT- NONCODI NG			
4307-4308	cg43945296	266	GGGCAGTGGG AACCGCCACCG GG[C/gap]CGCT GTAGCGGGCCTT AAAGGATGG	C	-				SILENT- NONCODI NG			
4309-4310	cg43945296	267	GGGCAGTGGGA ACCGCCACCGG GG[C/gap]GCTG TAGCGGGCCTTA AAGGATGGG	C	-				SILENT- NONCODI NG			
4311-4312	cg43945296	299	GCGGGCCTTAAA GGATGGGAAAC CT[T/gap]GATCA CAGATGCCCCCC GCCGGCCT	T	-				SILENT- NONCODI NG			
4313-4314	cg43945296	68	CTCCCCGAGCG CAGGCCCTCTC TC[T/C]TTGCCCT ATTATTTTGA ACATA	T	C				SILENT- NONCODI NG			
4315-4316	cg43946435	719	GGCTGCTGGT CCCAACCAGCTG GT[G/gap]CCTGT GGCTGGATGTGT TCAGTGTG	G	-				SILENT- NONCODI NG			

4317- 4318	cg43946684	1039	AAAACAACAATA AAATTCTCTTTGA [A/C]GGGAACCA AAGACAATGATG TGTTCT	A	C				SILENT- NONCODI NG		
4319- 4320	cg43946814	47	CCCAGGAAGGT GGCGCCCGCT CCC[C/A]AGCCT GCTACAGGGAAC CCGGGACT	C	A				SILENT- NONCODI NG		
4321- 4322	cg43947005	142	AACTGTACAAGC AATTAAACATG AT/AJATGTAGCA AGTGTATCAGG AGTTT	T	A				SILENT- NONCODI NG		
4323- 4324	cg43947375	1978	GGCGATCTCCAC ATCCTGCCGGTG G[C/gap]ATTTAG GGTGACTCCTT CACACAT	C	-				SILENT- NONCODI NG		
4325- 4326	cg43947477	1116	ACAAATTTGGCT TTAATAAAAAA [A/gap]AACAGTT CAAAAGGACAAT AACACG	A	-				SILENT- NONCODI NG		
4327- 4328	cg43947477	1117	CAAATTTGGCTT TAATAAAAAA [A/gap]ACAGTTC AAAAGGACAATA ACACGG	A	-				SILENT- NONCODI NG		
4329- 4330	cg43947477	1118	AAATTTGGCTTT AATAAAAAA A[A/gap]CAGTTC AAAAGGACAATA ACACGGG	A	-				SILENT- NONCODI NG		
4331- 4332	cg43947477	1187	TGTGCAGTTTCC TGATCATAATCA C[A/gap]TGCTC CTGCCITTTTACA GGGAATG	A	-				SILENT- NONCODI NG		

4333- 4334	cg43947477	1695	CCCATCTCCTA TGGAATGGTTT C/A/GGGGGTCC AGCAATGTCACT GCAGGT	A	G			SILENT- NONCODI NG		
4335- 4336	cg43947477	1898	GGGAGACTCTGT TGTAGGCAGCTG T/G/C/GGAGAAG GCTAGGGTTGGA GGTACA	G	C			SILENT- NONCODI NG		
4337- 4338	cg43947638	822	AGATTTGAGTGT GCGAGGAAAAA T/A/gap)AAAAAG AGAAACTTGAAG ACTTCTT	A	-			SILENT- NONCODI NG		
4339- 4340	cg43947646	1478	CTCTCACATCC TCTATATCTGT G/C/T/GACTTGAA AGCTGTTTGAGA ACTTC	C	T			SILENT- NONCODI NG		
4341- 4342	cg43947743	385	ACACTTTTGGGA AGCCTGGGACC AT[G/gap]GCTCT GCCAGGAATCTG TGACATCT	G	-			SILENT- NONCODI NG		
4343- 4344	cg43947977	1885	GAGCAGGACCT CCATTAGAAATA TT[G/A]AATTTGA TTCACAAATCTC CATTGG	G	A			SILENT- NONCODI NG		
4345- 4346	cg43947977	2045	CAAGCGACCGAT CCCGTTGGCGG CA[G/gap]CGATG CGAGCGATGAG CTGGATGGC	G	-			SILENT- NONCODI NG		

4347- 4348	cg43948105	487	GCCTCCTACTCC CCAGCACAGGT GC(Agap)GGAGG AACTCTGGAAGC ACTGCTCT	A	-				SILENT- NONCODI NG			
4349- 4350	cg43948257	310	GCGGCTCATGC CTATAATCCCAG CA(T/C)TTTGGGA GGCCAAAGCAG GAGGATC	T	C				SILENT- NONCODI NG			
4351- 4352	cg43948257	430	AAATTAGCCAGG TGTGGTGGCCTG T(G/A)CCTGTAGT CCCAGCTATTTG GGAGG	G	A				SILENT- NONCODI NG			
4353- 4354	cg43948280	555	ACAAATGTCCAT CACAGAGTTTTTC C(T/gap)TTTTTTT TTTTTGAGACAG AGTCTT	T	-				SILENT- NONCODI NG			
4355- 4356	cg43948730	1441	GCTCACGGTTGG AGGCCACGCGC TC(G/A)TACAGCT CTGCCGCTTTGG GGAACA	G	A				SILENT- NONCODI NG			
4357- 4358	cg43948766	901	AGTGGTGACACT GCTTGTGTTAGT A(C/T)GCCGGGT TGC GTTGC GTGC GGTCIC	C	T				SILENT- NONCODI NG			
4359- 4360	cg43948766	986	TCTAGCTGCAGC TGCATCTGCAGT T(G/A)TTGTAAC GAGAAGGGGAA GGGCCA	G	A				SILENT- NONCODI NG			

4361- 4362	cg43949166	968	CTTCAAAATGGTG CAGTTGTTTAAA T[G/A]TGAAGAAG ATGCTGCCCCAGG CAGTA	G	A				SILENT- NONCODI NG			
4363- 4364	cg43949166	922	AAAACAAAGATG TGAAGACATGGT A[G/A]ATGTGCCA AGGTTAAAGATG CTTCA	G	A				SILENT- NONCODI NG			
4365- 4366	cg43949166	939	ACATGGTAGATG TGCGAAGGTTAA A[G/A]ATGCTTCA AATGGTGCAGTT GTTTA	G	A				SILENT- NONCODI NG			
4367- 4368	cg43949223	3202	ACTTGTGAAAGA AGGCAGCACCT GT[C/T]AGCACCA TGGACAGCTCAC AGGAGT	C	T				SILENT- NONCODI NG			
4369- 4370	cg43949223	3204	TTGTGAAAGAAG GCAGCACCTGTC A[G/C]CACCATG GACAGCTCACAG GAGTAG	G	C				SILENT- NONCODI NG			
4371- 4372	cg43949223	3207	GAAAGAAGGCA GCACCTGTCAGC AC[ga/p/G]CATGG ACAGCTCACAGG AGTAGTTG		G				SILENT- NONCODI NG			
4373- 4374	cg43949443	47	AGCGGACGTGC ATCTTGGTCTCA AT[A/G]TCGATCC CCTGCCAGATCT GGAAGG	A	G				SILENT- NONCODI NG			
4375- 4376	cg43949559	290	TTGCCCTTGGTC TCGGGGTTCGCT GT[A/C]GGCGCT GAGGCTGCAGC TATCATGG	A	C				SILENT- NONCODI NG			

4377- 4378	cg43949806	455	CTCCCTTACCA CCCTGGGCTTT AT/GACTCCCTC TCCACCAATCCC TGATG	T	G			SILENT- NONCODI NG		
4379- 4380	cg43949858	2055	TCAAAAGCTGCC GAGTCCTATGAT T/A/G/CACGCGAT GGGACTTGTACA CTTGA	A	G			SILENT- NONCODI NG		
4381- 4382	cg43949858	2060	AGTGCCGAGTC CTATGATTACAC G/C/T/GATGGGA CTTGACACTTG AAGTGA	C	T			SILENT- NONCODI NG		
4383- 4384	cg43949935	901	AATCCATCCACA AGAAAGGAGCCA A/G/A/CGTCAGTT TCCAATGGGG GAACAT	G	A			SILENT- NONCODI NG		
4385- 4386	cg43949954	626	CAGAGAAACAA GGCACTTTGGGA G/C/T/ATTATGGC TTACTCTACTAC ATGTA	C	T			SILENT- NONCODI NG		
4387- 4388	cg43950113	504	TGGATTTTACC TTTGCAGACACC C/A/gap/AAAAAA AAATAAAATAAAT ATTTT	A	-			SILENT- NONCODI NG		
4389- 4390	cg43950155	557	AAGAGCAAGCC AGGAAGTAGCTG A/G/A/CAGAGAC CCCCAAACCGGT TGGCGG	G	A			SILENT- NONCODI NG		
4391- 4392	cg43950281	716	CAACTATATCAT CGGAGGCTCGG TA/A/G/TCAATGA GCTTATTGAAA TCIGGT	A	G			SILENT- NONCODI NG		

4393-4394	cg43950348	1186	CCATGCCGATCA TGCGCTTGGCTA C/GA/TCCAGGT CGCCCTGGTGG TTCTGGC.	G	A				SILENT- NONCODI NG			
4395-4396	cg43950825	743	AGTGGGGACCA CAGGCAAGTGG CAC/C/TACGACT AATTTTTTTTAT TTTTTG	C	T				SILENT- NONCODI NG			
4397-4398	cg43950873	280	CGGTAGTGGCC CCGAATGGCTG GGC/G/CJCGCTG ATATTATTGCAT ACAAGAC	G	C				SILENT- NONCODI NG			
4399-4400	cg43950873	339	GCAGGTAAGG AGGGTGAATCTT CT/A/CJAGTGATT GACAAAGGTGAAG CAAGTC	A	C				SILENT- NONCODI NG			
4401-4402	cg43950873	359	CTTCTAAGTGAT TGACAAAGGTGAA G/C/TJAGTCAAG TGATCATAGGAC AGGGG	C	T				SILENT- NONCODI NG			
4403-4404	cg43950873	366	GTGATTGACAAG GTGAAGCAAGTC A/C/TJGTGATCAT AGGACAGGGGG CCCTTC	C	T				SILENT- NONCODI NG			
4405-4406	cg43950910	494	AAAATGCATTTTA ACTTCTGAGGGT [G/TJGGTGTGCA AAATGTTCAACCA TCCCC	G	T				SILENT- NONCODI NG			
4407-4408	cg43950936	440	TTTACCATCATAGT TTTTCTTTTTTTT gap/TJCTTTTTTTT TTTTTGCATAGG CATT	.	T				SILENT- NONCODI NG			

4409- 4410	cg43950936	453	TTTTCTTTTTTT CTTTTTTTTTTT /gap]TGCATAGGC ATTACTAGGGAC ATAA	T	-				SILENT- NONCODI NG			
4411- 4412	cg43950982	1910	AATGAAAAGAGG CCCCCTGAAGG CC[C/gap]TGAAC CTGGATAGGAAC AATTGCA	C	-				SILENT- NONCODI NG			
4413- 4414	cg43950982	200	ACGTCACATGGT CAAAGTCTCCTC AT[C]TTCAGCCA GTCTCAACACAA AACAC	T	C				SILENT- NONCODI NG			
4415- 4416	cg43950982	233	AGTCTCAACACA AAACACCCCAACA G[G/A]GATGCAC TCAACTTGTGG TTCCAT	G	A				SILENT- NONCODI NG			
4417- 4418	cg43950982	259	GATGCACCTCAAC TTGTTGGTTCCA T[G/T]TGGAACTA GGTGGCAGGGC GAGAGG	G	T				SILENT- NONCODI NG			
4419- 4420	cg43950982	273	GTTGGTCCATG TGGAAGTAGGTG G[C/T]AGGGCGA GAGGAAAGTA GTAGAAG	C	T				SILENT- NONCODI NG			
4421- 4422	cg43950982	292	AGGTGGCAGGG CGAGAGGGAAA GTA[G/T]TAGAAG GGGGCTATGGT GTGCTGTC	G	T				SILENT- NONCODI NG			

4423-4424	cg43950982	299	AGGGCGAGAGG GAAAGTAGTAGA AG[G/C]GGGCTA TGGTGTGTCTGC ATTCAGT	G	C				SILENT- NONCODI NG			
4425-4426	cg43950982	305	AGAGGGAAAGTA GTAGAAAGGGG CT[A/G]TGGTGTG TCTGCATTCACT CCCCCTC	A	G				SILENT- NONCODI NG			
4427-4428	cg43950982	334	TGTGTCTGCATT CAGTCCCCCTCAC AT[C/JAAAGCCAC ATGGATCTAGGG GGGTA	T	C				SILENT- NONCODI NG			
4429-4430	cg43951482	164	GCTTTCAAAGA CATTGTGAAG G[A/G]CATTAAAT TCACATTTAAAA CGTGT	A	G				SILENT- NONCODI NG			
4431-4432	cg43951580	157	ACACACACACAC ACACACACACAC A[C/gap]ACACAC AACCTTCTGTGG CTCAAAA	C	-				SILENT- NONCODI NG			
4433-4434	cg43951635	171	ATGCCTGGCTAA TTTTGTATTTT A[G]GTAGAGACA GGGTTTCACCAT ATTG	A	G				SILENT- NONCODI NG			
4435-4436	cg43951719	570	GTGGCAGGATAA AAGGATATTGT G[A/G]AGTAATCT TAGGGTTGGATA AAAAG	A	G				SILENT- NONCODI NG			

4437-4438	cg43951812	1126	GCAGGTACAGGT GCCAGTTTGTGA CIGAJGATGAA GCACCGACAGC CCACGCG	G	A				SILENT- NONCODI NG		
4439-4440	cg43951812	1284	ACCCAGAGCA AAATGCTCCATG CIAAGACAGCA GGCATTACAGCT ACAAGC	A	G				SILENT- NONCODI NG		
4441-4442	cg43951883	677	ATTACAGACTT GAGTGTGTGT GT/GIGTTTCCAA CCACAGTCATTC ATACT	T	G				SILENT- NONCODI NG		
4443-4444	cg43952028	745	CCCTGGTGTGA GCTAGCAAGCAA TIA/CJACTGACTA CTCGTCACCTAC AGTTG	A	C				SILENT- NONCODI NG		
4445-4446	cg43952230	1440	ACTGCCAATTGC TCATTTTGTCTG AT/CJATTAAACAG ATTATGCATTTT CTCAG	T	C				SILENT- NONCODI NG		
4447-4448	cg43952230	1706	CTGTTTCATGGTC CACATGTATTAA AIC/gap/AAAAAA CATGTCAATTAC TTGGTGC	C	-				SILENT- NONCODI NG		
4449-4450	cg43952230	1710	TCATGGTCCACA TGATTAAACAA A/Agap/AAACATG TCAATTACTTGG TGCAAAC	A	-				SILENT- NONCODI NG		
4451-4452	cg43952230	1711	CATGGTCCACAT GTATTAAACAAA A/Agap/ACATGT CAATTACTTGGT GCAAAACA	A	-				SILENT- NONCODI NG		

4453-4454	cg43952230	1712	ATGGTCCACATG TATTAAACAAAA [A]gap]CATGTCA ATTACTTGGTGC AAACAC	A				SILENT- NONCODI NG			
4455-4456	cg43952399	401	AGGGCACTCTGC TCCTTGCAATAA C[A]GJTCTACTG AACAGTAAGTAC CATGG	A	G			SILENT- NONCODI NG			
4457-4458	cg43953987	655	TACTAAAAAGGA GGGGGGCATGC TT[ga]p/TJCCAAAT GGGATCTACGT CTTCCTC	-	T			SILENT- NONCODI NG			
4459-4460	cg43955058	1808	GCTGCAGGGAG CTGGAAGTGGTC AGT/CJATATATC CGAGCCGCTGT CCGAAAA	T	C			SILENT- NONCODI NG			
4461-4462	cg43955367	370	AGGAGTTCAGA CCAGCCTGACCA A[C/T]ATGGTGAA ACCCCATGTCTA CTAAA	C	T			SILENT- NONCODI NG			
4463-4464	cg43955367	371	GGAGTCAAGAC CAGCCTGACCAA C[A/G]TGGTGAAA CCCCATGTCTAG TAAA	A	G			SILENT- NONCODI NG			
4465-4466	cg43955367	413	CTACTAAAAATA CAAAAAAATGAG C[C/T]GGGCATG GTGGCGCGTGC CTGTAAT	C	T			SILENT- NONCODI NG			
4467-4468	cg43955367	418	AAAAATACAAA AAATGAGCCGG GC[A/G]TGGTGG CGCGTGCCTGTA ATCCCAG	A	G			SILENT- NONCODI NG			

4469- 4470	cg43955553	670	GAAATCTAATGC AAGTAAAGGCAC AAGJTGAATGTG GAGTTGAATGGA ACCAA	A	G				SILENT- NONCODI NG			
4471- 4472	cg43955835	1852	GTCACAGACCAC TCGCCATTGAGA AAGJAGACAGA GTTGGGCTTAT TAGAGT	A	G				SILENT- NONCODI NG			
4473- 4474	cg43955871	1194	TTCCAGTGTGT GGTCTTCTTTGT TIG/CJATGGTGAA TAAACAGGCATT GGGTA	G	C				SILENT- NONCODI NG			
4475- 4476	cg43955877	363	TCAAAGTCCTAT TGTAATATTATTT TT/gapJAAGGGTC TTAGGAGGCCCC TCAGAG	T	-				SILENT- NONCODI NG			
4477- 4478	cg43955877	424	GGTCAGGGCTA GAGTATGAGAAG TC/C/ATTAAGGGT TTTTGTATTTGT TTTTT	C	A				SILENT- NONCODI NG			
4479- 4480	cg43955877	451	AAGGGTTTTTGT ATTTTGTTTTTT T/gapJTCCTATAA ACCTGAGGTTG AAAGC	T	-				SILENT- NONCODI NG			
4481- 4482	cg43955877	461	GATTTTGTTTT TTTTCTATAAA C/gapJCCTGAGG TTGAAAGCTCTG GATAGC	C	-				SILENT- NONCODI NG			
4483- 4484	cg43956161	697	AGAGGCTGTTAT TCCAGGGGAAAGA G/C/TJGGGCAGG TGTCCTGAGGAG TACATT	C	T				SILENT- NONCODI NG			

4485- 4486	cg43956227	2066	TTTCTGAAATTCA CAAAGTTAAACG T/C]GATGTGCTC ATCAGAAACAAT TTCT	T	C				SILENT- NONCODI NG			
4487- 4488	cg43956347	122	TCAACAAATTAGC AGCTTAAGATCT A/T/G]CAACTACA GTGTTAACGTTT ACACG	T	G				SILENT- NONCODI NG			
4489- 4490	cg43956347	146	TCAACTACAGTG TTAACGTTTACA C[gap/A]GTTTAC AAGTGTCAATTC TTTACGT	-	A				SILENT- NONCODI NG			
4491- 4492	cg43956347	152	TACAGTGTTAAC GTTACACAGTTC A/C/T]AAGTGTC TTTCTTTACGTTT CAAT	C	T				SILENT- NONCODI NG			
4493- 4494	cg43956347	154	CAGTGTTAACGT TCACACGTTTAC A/A/G]GTGTCATT TCITTTACGTTTCA ATTC	A	G				SILENT- NONCODI NG			
4495- 4496	cg43956467	844	CTTCACTATCGA GATACCTTGTTGG T[G/gap]GCGTAG CCCATCAGGGCA CCAATAT	G	-				SILENT- NONCODI NG			
4497- 4498	cg43956467	845	CTCACTATCGAG ATACCTTGTTGGT G[G/gap]CGTAGC CCATCAGGGCAC CAATATT	G	-				SILENT- NONCODI NG			
4499- 4500	cg43956696	389	CACCTCCTACTTC TCTCAAAATTAGC A/T/C]TTTAACAT CTTCCAATAACA CACCA	T	C				SILENT- NONCODI NG			

4501- 4502	cg43956870	491	AGGATGGCTGG GTTGAGGTCTTT GCT/C]CAAGTTC TGCTAACATTGA TGACAG	T	C				SILENT- NONCODI NG		
4503- 4504	cg43956870	577	AATTGTTCTCAT CCATTAAACGCTG CT/C]GTGCTCTT CTGGCTCTTTGC AAAAG	T	C				SILENT- NONCODI NG		
4505- 4506	cg43957151	1665	AAGTCCAACATC TCGCCAACTTC A/A/G]CTTCATGG GGCAGCTGCTG GACTTT	A	G				SILENT- NONCODI NG		
4507- 4508	cg43957194	450	ACAAGGCTTCTT GTCTCAGGTCTG C/A/G]GTGTGCA CATGCCAGACTC CTCAG	A	G				SILENT- NONCODI NG		
4509- 4510	cg43957358	203	TGGGCTCCACCA CCGTGGCCGCC GG[C/gap]GGGAC CAGCACAGGCG GCGTTTCT	C	-				SILENT- NONCODI NG		
4511- 4512	cg43957502	725	AGCTGGAGGGA ACGCCAGAGGT GTC[C/gap]TGCC GGGCTCTGGAG CTCTTCGACT	C	-				SILENT- NONCODI NG		
4513- 4514	cg43957567	1342	CAAATGACTACA ATGTTAAATAG A/C/T]AAAACTG CTATACAAGAGC CTCTT	C	T				SILENT- NONCODI NG		

4515- 4516	cg43957735	2014	AAACCCCTTTTGA GCTTGAGTAACC A/C/T/TGAGCTGC CCTTTGTTACCT TTATG	C	T				SILENT- NONCODI NG		
4517- 4518	cg43957996	654	AATATCTTGGAA ATCCACATCATT C/A/G/CAGCTAG AACTTGGTCCCC TTCCCTG	A	G				SILENT- NONCODI NG		
4519- 4520	cg43958045	733	CTCAGCTAGTCC AGAAATTGCTGC A/T/gap/TTCCCAT ATTACTTAGTTCT TTATT	T	-				SILENT- NONCODI NG		
4521- 4522	cg43958093	1678	GGTCTTGCTCTT TATGAGAGGGCA A/T/C/GTGTITTT AATTGTGTTAATT AGAA	T	C				SILENT- NONCODI NG		
4523- 4524	cg43958290	239	ACTAAGGAGGCT GAGGTAGGAGA A/T/G/C/ACTTGAA CCTGGGAGGCA GAGGTG	G	C				SILENT- NONCODI NG		
4525- 4526	cg43958290	257	GGAGAATGACTT GAACCTGGGAG GC/A/G/GAGGTT GTAGTGAGCTGA GATCITG	A	G				SILENT- NONCODI NG		
4527- 4528	cg43958316	930	GGTCCGGGGAG CAATGGCATCCT CC/T/G/TGATATC ATTGGCTGGCTC CTCCAG	T	G				SILENT- NONCODI NG		

4529- 4530	cg43958316	963	ATTGGCTGGCTC CTCCAGGGCCTT G[C/gap]CCCCGC GGTGGTACAAGA GGACCAG	C	-				SILENT- NONCODI NG		
4531- 4532	cg43958676	1234	ATTCTTTAAATTC TCCAATCCTCTT A/GTTTTCTCCT CTTCCTCTGCCG CAG	A	G				SILENT- NONCODI NG		
4533- 4534	cg43958676	1237	CTTTAAATTCCTC AATCCTCTTATT T/CCTCCTCCTCT CCTCTGCCGCAG TCA	T	C				SILENT- NONCODI NG		
4535- 4536	cg43958676	1240	TAAATTCCTCAAT CCCTTATTTC C/TCTCCTCTCCT CTGCCGCAGTCA CTC	C	T				SILENT- NONCODI NG		
4537- 4538	cg43958676	1280	CGCAGTCACTCC CCACTGGCCCTC A[A/G]TTTCACGC TGTTCTTTTTCT CTTC	A	G				SILENT- NONCODI NG		
4539- 4540	cg43958676	1297	GGCCCTCAATTT CACGCTGTTTCT T/T/C]TCTCTTC AAACTGCAATCG CCTCT	T	C				SILENT- NONCODI NG		
4541- 4542	cg43958676	1309	CACGCTGTTTCT TTTTCTCTTCAAA [C/T]TGCAATCG CTCTGCAACTCC TCCA	C	T				SILENT- NONCODI NG		

4543- 4544	cg43958676	1326	TCTTCAAACGTC AATCGCCTCTGC A/A/GJCTCCTCCA GAGCAGCTCTGT ACATT	A	G				SILENT- NONCODI NG			
4545- 4546	cg43958676	1353	TCTCCAGAGCA C GCTCTGTACATT G/C/TJGCTTGG GCATTCTGAAGT TCAATG	C	T				SILENT- NONCODI NG			
4547- 4548	cg43958676	1363	CAGCTCTGTACA A TTGGTCTTGGG C/A/GJTCTGAAG TTCATGATTTG ATCAA	A	G				SILENT- NONCODI NG			
4549- 4550	cg43958676	1477	TGGTGTCAGGA A ACGCCTCGTGTG C/A/CJGCAATAAT GTGATCCAAATC CTGGG	A	C				SILENT- NONCODI NG			
4551- 4552	cg43958676	1480	TGTCCAGGAACG A CCTCGTGTGCAG C/A/GJATAATGTG ATCCAAATCCTG GGCCT	A	G				SILENT- NONCODI NG			
4553- 4554	cg43958676	1504	CAATAATGTGAT C CCAAATCCTGGG C/C/TJTGCTGGAC TCTGTTCCAAAG CTCAT	C	T				SILENT- NONCODI NG			
4555- 4556	cg43958676	1522	CCTGGGCCCTGCT A GGACTCTGTTCC A/A/GJAGCTCATC CCAAGAACAACCTC AAGCA	A	G				SILENT- NONCODI NG			
4557- 4558	cg43958736	578	ATACAATAAATAT C ATCAATTGTTTA C/TJATCCCAAAT TTTGAAAATACT GGG	C	T				SILENT- NONCODI NG			

4559- 4560	cg43958770	372	AAGAAAATATTTA CAAAATACAAGG[T/gap]TTTTTTTT CCATTTTTTGTTT TTG	T	-				SILENT- NONCODI NG			
4561- 4562	cg43958770	624	ATTTTATACGAT TACAAAATGGCC[A/gap]AAAAAAA GAGTCCTCTCCC CCCIC	A	-				SILENT- NONCODI NG			
4563- 4564	cg43958939	915	GTGTGTATAAGT ACATCCCTTTGGG GTT/gap]TTTTTTT TTCCTTTTTTTTT AACCA	T	-				SILENT- NONCODI NG			
4565- 4566	cg43958939	924	AGTACATCCTTT GGGGTTTTTTTT TTT/gap]CTCTTT TTTTAACCAAAG TTGCTG	T	-				SILENT- NONCODI NG			
4567- 4568	cg43959547	57	TGGGAGTGTCTT TTAGCATGCTAA TIG/A]CATTATAA TTAGCATATAAT GAAC	G	A				SILENT- NONCODI NG			
4569- 4570	cg43959551	580	AGTTTCAAAGT TAATTTGGCGGG T/A]GGGGCTT GGGAAGTGGGG AGTGCTG	A	G				SILENT- NONCODI NG			
4571- 4572	cg43959551	629	TGATCGGTCAGG TTGGAGATGGAT T/C/T]ATAGGG GTTGAAGTGAGT TTTTCA	C	T				SILENT- NONCODI NG			
4573- 4574	cg43959563	433	AGTCACGTGCCC CTGAGCGGAGA GC/C/T]TCAGCGT AGCCGCGGCAG CCATCGA	C	T				SILENT- NONCODI NG			

4575- 4576	cg43959715	870	GACCAATTCGAAT TCATCTTCAGCT G[C/A]CAAGTGTA TTAGTCCCTGA ACCTG	C	A				SILENT- NONCODI NG		
4577- 4578	cg43959715	876	TCCAATTCATCTT CAGCTGCCAAGT [G/T]ATTAGTC CCTGAACCTGGA TCCA	G	T				SILENT- NONCODI NG		
4579- 4580	cg43959715	883	CATCTTCAGCTG CCAAGTGATTT A[G/A]TCCCTGAA CCTGGATCCAAG GCATC	G	A				SILENT- NONCODI NG		
4581- 4582	cg43959715	918	CTGGATCCAAGG CATCTCCCTGTA G[G/A]AAACATCA GACCGGGGCAG AGATTG	G	A				SILENT- NONCODI NG		
4583- 4584	cg43960167	247	AGACAAATGCCT AGGCAGATAGG GG[C/T]AGGTCA ACAGTGAAACCC CACCTCC	C	T				SILENT- NONCODI NG		
4585- 4586	cg43960464	454	GGCAAGATTCCG AATGCCAGGCC C[T/C]CAAGTGTG CAACAGGGCACA GGTG	T	C				SILENT- NONCODI NG		
4587- 4588	cg43960464	482	TCCGAATGCCAG GCCCTCAAGTG T[G/A]CAACAGG GCACAGGGTGA CCTCATG	G	A				SILENT- NONCODI NG		
4589- 4590	cg43960464	485	GTGCAACAGGG CACAGGGTGAC CTC[A/gap]TGTC GGCAGGTGGGT GCIGTTCGT	A	.				SILENT- NONCODI NG		

4591- 4592	cg43960807	714	TGCTCGATTCCA CGTGTGCTCGG GG[C/T]CCCCAG AAGAACTCATAC TCCACCG	C	T			SILENT- NONCODI NG		
4593- 4594	cg43960917	401	GCCCGGAGCAA TGGAAGTCTCAT CC[C/G]CATCCT GAGCGGCCTCTT TTCTAGG	C	G			SILENT- NONCODI NG		
4595- 4596	cg43960917	415	AAGTCTCATCCC CATCCTGAGCGG C[C/T]TCTTTTCT AGGATCGAGAG GACCAC	C	T			SILENT- NONCODI NG		
4597- 4598	cg43960917	444	TTTCTAGGATCG AGAGGACCACAC T[G/C]CAGCCCA GGACAAAAGCCC ACGGTA	G	C			SILENT- NONCODI NG		
4599- 4600	cg43960917	460	GACCACACTGCA GCCCAGGACAAA A[G/T]CCCACGG TAGCACATTGTC CGGCAG	G	T			SILENT- NONCODI NG		
4601- 4602	cg43960917	461	ACCACACTGCAG CCCAGGACAAAA G[C/G]CCACGGT AGCACATTGTCC GGCAGG	C	G			SILENT- NONCODI NG		
4603- 4604	cg43960917	466	ACTGCAGCCCGAG GACAAAAGCCCA C[G/A]GTAGCAC ATTGTCCGGCAG GAGAGG	G	A			SILENT- NONCODI NG		

4605- 4606	cg43960917	472	GCCCAGGACAAA AGCCACGGTA GCA/TTCATTGTC CGGCAGGAGAG GAGCAGA	A	T			SILENT- NONCODI NG			
4607- 4608	cg43960917	481	AAAGCCACGG TAGCACATTGTC C/G/AJGCAGGAG AGGAGCAGACC CACGTCC	G	A			SILENT- NONCODI NG			
4609- 4610	cg43960917	503	TCCGGCAGGAG AGGAGCAGACC CAC/G/CJTCCAA GAAGATGGTTTT ACCTTGC	G	C			SILENT- NONCODI NG			
4611- 4612	cg43960917	519	CAGACCCACGTC CAAGAAGATGGT TT/GJTACCTTTG CACGCCTCTTCT CTGAG	T	G			SILENT- NONCODI NG			
4613- 4614	cg43960917	524	CCACGTCCAAGA AGATGGTTTTAC C/T/CJTGCACGC CTCTCTCTGAG AAATG	T	C			SILENT- NONCODI NG			
4615- 4616	cg43961283	524	CCATGCCTCCTA GCAAGATGCTGA G/G/CJCTACAGTA GGTCTGGCCTCA AGCTG	G	C			SILENT- NONCODI NG			
4617- 4618	cg43961690	946	CTGAGGCAGGA GAATTGCTTGAA CC/C/TJGGGAGG CAGAGGTTGCAG TGAGCCG	C	T			SILENT- NONCODI NG			

4619- 4620	cg43961969	394	CTATTAGTAAAC AAGGCCTACGTT T[T/G]TTTCTCTA AAATTTAGAAATCT TAAA	T	G				SILENT- NONCODI NG			
4621- 4622	cg43961990	2402	CTTGCCTCATCC CTGTCCTTTGGCA A[G/C]TGCACGG GTGGTGTGGAG GAAAGGA	G	C				SILENT- NONCODI NG			
4623- 4624	cg43962112	1747	CTCCAGGGAGG CTCAGATCATGG TT[C/T]AGGGGTG CCAGGCACCATT CCTACT	C	T				SILENT- NONCODI NG			
4625- 4626	cg43962250	444	TCATGCCACCTG CGAGACGGGCT CC[T/C]CCTGTCC CCACTGTGTCCC CGGGTC	T	C				SILENT- NONCODI NG			
4627- 4628	cg43962322	576	GTGTGGGAAGG GCCAGAATAAGC AA[C/T]AAAGCCA ATTAGATGTGGG TTCCTGG	C	T				SILENT- NONCODI NG			
4629- 4630	cg43962689	1053	TACTGAGGGTCT ATGCATGGTAAT T[G/A]GCAGAAAA CATGATAGAACT AAACA	G	A				SILENT- NONCODI NG			
4631- 4632	cg43962735	477	TAACCTTCTGCAG TACITTTGTTTCATA [T/A]AAAAACACTA GTAAAATAGGCT TCCT	T	A				SILENT- NONCODI NG			
4633- 4634	cg43962735	513	TAAAATAGGCTT CTTAAAAATTAAA [T/C]JAGTGAATA CCAACCAAAATTA TATA	T	C				SILENT- NONCODI NG			

4635- 4636	cg43962735	550	AACCAAAATTATAT ACATTGTTACAGI T/CJACAAAGTGAA TGAGGCAAAATA TCCA	T	C				SILENT- NONCODI NG			
4637- 4638	cg43962735	636	AGTGGTGGCA CGGAGGGGGTG ACA/G/AJGAAAG CCACGTTCCAAT GTCACAGT	G	A				SILENT- NONCODI NG			
4639- 4640	cg43962852	816	TAACAATTTAGC AGCCGTGGCAA CT/G/AJCCAAGG ACACATACAACA AAAAAAT	G	A				SILENT- NONCODI NG			
4641- 4642	cg43962852	899	TGGCCCCAAATG ACTGCAGACCA A/A/GJ/CACCTGCA ACTTAAGGAAGA ATCTG	A	G				SILENT- NONCODI NG			
4643- 4644	cg43962884	351	CAGAAATGCTT TATTTTCTCTTTI G/gapJTTCCCTCC CCATCCTATATTT TTCT	G	-				SILENT- NONCODI NG			
4645- 4646	cg43962884	380	CTCCCCATCCT ATATTTTCTCCT [A/gap]AAAAACC CTATTATCAGAA ATATTA	A	-				SILENT- NONCODI NG			
4647- 4648	cg43963085	1126	GACCGGTGCCA CCTCTGGAATGG TG/T/CJTCGCCG CGAAATAAGCTA CTGGCGA	T	C				SILENT- NONCODI NG			
4649- 4650	cg43963560	799	CTGCTTCAGCCT CCCAAGTAGCTG A/G/AJATTACAGG CACCCACCATCA CGCCT	G	A				SILENT- NONCODI NG			

4651-4652	cg43964079	749	ACCCATCCAAAA TTATTTGTGATA G[G/A]TGAAAAAT GGCCACAAGCTC TTTGT	G	A				SILENT- NONCODI NG			
4653-4654	cg43964913	893	CGCCTTCTTTC CCAGCAGAAAG GG[A/G]TCCGTT CCGGACAGGAC AGAAGTGA	A	G				SILENT- NONCODI NG			
4655-4656	cg43964913	907	AGCAGAAAGGG ATCCGTTCCGGA CA[G/A]GACAGA AGTGAGCAGATG GTTTCCC	G	A				SILENT- NONCODI NG			
4657-4658	cg43964913	911	GAAAGGGATCC GTTCCGGACAG GAC[A/C]GAAGT GAGCAGATGGTT TCCCCTAC	A	C				SILENT- NONCODI NG			
4659-4660	cg43964975	516	CCCAAGTTACTG CATACCAAGCAG CT[C/A]ATAAAA CCAAC TGACTTA AAGTC	T	C				SILENT- NONCODI NG			
4661-4662	cg43965502	387	ACACTCATTATA CTTTTCCCCAA A[C/A]AGGTACAA AGGAGGTTCAAG TGCTC	C	A				SILENT- NONCODI NG			
4663-4664	cg43966333	309	GGTCCGCACAT CTTTGAATCGCT C[C/T]CCTTTGGT GCTCACTACCTG GTTGT	C	T				SILENT- NONCODI NG			
4665-4666	cg43966333	327	ATCGCTCCCTT TGGTGCTCACTA C[C/T]TGGTTGTC GATGTATCGGAT CAGCT	C	T				SILENT- NONCODI NG			

4667- 4668	cg43966536	855	GCCCCTGGCCT GGGTGGCCCGG GGC[C/gap]GCAG CGCAGAGCAGC AGGTGAGCAG	C	-				SILENT- NONCODI NG		
4669- 4670	cg43966551	772	GGTGGCTTCTCA GCACCTTGAGCC T[C/A]TGATGCCC CGCCTCTGACCT CAGGT	C	A				SILENT- NONCODI NG		
4671- 4672	cg43966619	363	ACACAGGAAGTG AGTTCAGATTTA T[C/T]CACAAATG TCCTCTGGTCTA GTCT	C	T				SILENT- NONCODI NG		
4673- 4674	cg43966787	464	CTGTTTAGTGAA AACAGTTAAGGG C[A/C]GGCCACTT CTACACTCCCAG CGCTA	A	C				SILENT- NONCODI NG		
4675- 4676	cg43966806	930	TATATACACAAC ATTCAGATATT C[T/gap]TAATGTA AGACATTTTCAGA TTGAAG	T	-				SILENT- NONCODI NG		
4677- 4678	cg43966806	931	ATATACACAACA TTCAAGATATTCT [T/gap]AATGTAA GACATTTTCAGAT TGAAGT	T	-				SILENT- NONCODI NG		
4679- 4680	cg43966820	2019	CAAACTCGTCAT ACATGAACTGAA G[C/T]GTCAGGG CTGACTTGCCAA CGCCTC	C	T				SILENT- NONCODI NG		

4681- 4682	cg43966864	540	TCTATGGTAAAT CCTTGCAACAT G(G/T)AAACAATG CATTGGCCCGAG TGCTT	G	T				SILENT- NONCODI NG			
4683- 4684	cg43967021	833	TGGAAAAAAG AGAGCCCTCTA A(A/G)GAGGTG TCAACAGTGGA AGAAAT	A	G				SILENT- NONCODI NG			
4685- 4686	cg43967079	1000	ATGACCCCTAC TACACACACACA C(A/gap)CGCAA GTTAGGTCCAGC ATAGGCC	A	-				SILENT- NONCODI NG			
4687- 4688	cg43967102	231	TCCATCACCCCTG CTGGGGCTCGC CGT(C)CAACGT GGTCACCACGCT CGTGCCTC	T	C				SILENT- NONCODI NG			
4689- 4690	cg43967102	454	CCACAGTATTTA TGGCAGTGGGA GC(T/C)TCAATTG CCGCTCGCTTAG GAACCT	T	C				SILENT- NONCODI NG			
4691- 4692	cg43967119	1015	GCAGGGCAAAG ACCAGACTATCT CC(A/G)CCTGTTG TTTGCATTGTTT CTGGG	A	G				SILENT- NONCODI NG			
4693- 4694	cg43967630	660	AGCTGCTGTCCC CAGAGAGGAGA CA(A/G)CAGCTTC TGGAGGCTCTG GGGACTC	A	G				SILENT- NONCODI NG			
4695- 4696	cg43967706	458	CACTGGGCAAG GTAGGTAGCTAG CT(G/T)CCTGACC CCTAGTCTGGGG TTGGAA	G	T				SILENT- NONCODI NG			

4697- 4698	cg43967833	83	AAACATATCAAA ATGTTACAAAA T[G/A]TATGGCTC CCTTGCTGAGGC CCTGT	G	A				SILENT- NONCODI NG			
4699- 4700	cg43967844	250	ACAACTAATAAT CTTCTTTCAAGA G[T/gap]TTTTTTT TTCAATCTTGGA GTAAAC	T	-				SILENT- NONCODI NG			
4701- 4702	cg43967844	928	TCATGCTTCTGG TTTGAAAGTGAC G[A/G]GTAAATAT GTCAGACTGTTT AAAGG	A	G				SILENT- NONCODI NG			
4703- 4704	cg43968063	1565	GCGGCTCGATAC GCAGTGAGAGT C[A/C]CCGCGCT CAAAGGCATCCG CGCCCA	A	C				SILENT- NONCODI NG			
4705- 4706	cg43968079	1255	CTGTGAGCGTGT CTGATGCCCCGA A[C/A]AGGTGCC AGGTCCCCCAAA AGCAGC	C	A				SILENT- NONCODI NG			
4707- 4708	cg43968177	921	AAATGCTGTCCA GTTTTATTTTTT[T/gap]ATGTTGT ATCCTTGGATGT ACAAA	T	-				SILENT- NONCODI NG			
4709- 4710	cg43968179	902	GAAATCTTCAG AGATCTTCAAAG C[A/G]CAAAAAAT ACGTTCTTTTTTC AAAG	A	G				SILENT- NONCODI NG			
4711- 4712	cg43968211	510	TGGAAATGTAG TTGGAGATAAAG T[T/C]TTTGAAG CTTTGCTGAAAA CCTTT	T	C				SILENT- NONCODI NG			

4713- 4714	cg43968211	537	TTGGAAGCTTTG CTGAAAACCTTT C/A/GTTTCTTCT GGAAGCTTTAAA AAAAG	A	G				SILENT- NONCODI NG			
4715- 4716	cg43968211	565	TCTTCTGGAAGC TTTAAAAAAGG T[G/A]ACCGAACT AGCAGTTGCCCA GTGAT	G	A				SILENT- NONCODI NG			
4717- 4718	cg43968211	570	TGGAAGCTTTAA AAAAGGTGACC G/A/G]ACTAGCA GTTGCCCAGTGA TCTTCA	A	G				SILENT- NONCODI NG			
4719- 4720	cg43968211	598	TAGCAGTTGCCC AGTGATCTTCAT A/T/C]TAGATGAA TTTGATCTTTTG CTCA	T	C				SILENT- NONCODI NG			
4721- 4722	cg43968211	642	TTGCTCATCATA AAAACCAACAC T/T/C]CTCTATA TCTTTTGGACATT TCTC	T	C				SILENT- NONCODI NG			
4723- 4724	cg43968211	669	TCTATAATCTTT TGACATTTCTCA] G/A]TCTGCACAG ACCCCAATAGCA GTTA	G	A				SILENT- NONCODI NG			
4725- 4726	cg43968211	699	CACAGACCCCAA TAGCAGTTATTG G/T/C]CTTACATG TAGATTGGATAT TTTGG	T	C				SILENT- NONCODI NG			
4727- 4728	cg43968242	69	GCGTACTGGCG ACCCGGAGTGAT GA[G/C]CCCCGCC CGAGACGATGC CGCCGGTGG	G	C				SILENT- NONCODI NG			

4729-4730	cg43968298	404	TTGACAAATTTTG GTTTGGGGCTTT T(G/A)CTTCGGTC CAAGCAGATAAA ACGCA	G	A				SILENT- NONCODI NG			
4731-4732	cg43968298	410	ATTTGGTTTGG GGCTTTTGCTTC G(G/A)TCCAAGC AGATAAAACGCA TGGICT	G	A				SILENT- NONCODI NG			
4733-4734	cg43968308	686	TCTCAGCCTCGG GGCTGCAATCCA G(G/A)GCTGTGC TGAGCAGCAAGA GGAGAG	G	A				SILENT- NONCODI NG			
4735-4736	cg43968538	299	TCTGTTGTTAAT CGGTTACATTGT C(A/T)CCTCTAAT ACCAAGTCATCAA ATCCA	A	T				SILENT- NONCODI NG			
4737-4738	cg43968538	409	TCAGGTCATAGG ATTCCCTTTTTTTT T(gap)AAAGATAA GTAAATGCATCC AGAAA	T	-				SILENT- NONCODI NG			
4739-4740	cg43968629	648	TGGCTCTGGCTG GCTTCCATGGGG G(G/A)CTCATCAC TGGAAGGGCTG GTGACC	G	A				SILENT- NONCODI NG			
4741-4742	cg43968904	268	CCATAGCAATTA GCATATTTCTAA [C/T]AAGCCATGT TGTTAAATTTAT ATT	C	T				SILENT- NONCODI NG			
4743-4744	cg43968904	338	TGAAGAGTATGT GATATATTGTCA A(G/T)GGTGATAA GAAAACTCTCCC TGGTT	G	T				SILENT- NONCODI NG			

4745-4746	cg43969016	620	ACGATCATATTTT GGCGTGAAGAA G A G GGGCAAG AGAAGCAGAAAG GAGAATG	A	G				SILENT- NONCODI NG			
4747-4748	cg43969342	1551	CGGCTCACTGCA TCCTCGCCTCC C A G GGTTCAA GCTATTCTCCTG CCTCAG	A	G				SILENT- NONCODI NG			
4749-4750	cg43969342	1671	ACGGGGTTTCAC CATGTTGGCCAG G C A TAGTTTCG AACTCCTGACCT CAGTG	C	A				SILENT- NONCODI NG			
4751-4752	cg43969665	1260	AGACAGAATGGG GGAAAATGGGG AG A gap AAAAA AAACAAACCTTC CCTTTCCC	A					SILENT- NONCODI NG			
4753-4754	cg43969665	1390	CTGGGAGACCAT GTGGTATAAAA A A gap GTCATTA AAGTTGCTTGCA GAAAA	A					SILENT- NONCODI NG			
4755-4756	cg43970196	570	GACATCCCAAAC TTTACAAAACCTT A G CAATGCTGC TTATCTAAAACCTT TTC	A	G				SILENT- NONCODI NG			
4757-4758	cg43970375	691	ACAGGTAAGCG GGGAAACGTACC TAT G GACTCTG GCAAAATATTCT CGGCAT	T	G				SILENT- NONCODI NG			
4759-4760	cg43970424	1135	AAGGTGCCTGCC TGCCTGGGGCC TA A C CGAGCCA AACAGTGCTAAT TTCATC	A	C				SILENT- NONCODI NG			

4761- 4762	cg43970424	1138	GTGCCCTGCCGCA CTGGGCGCTAAC GACGCGCCAAAC AGTGCTAATTC ATCCAT	A	C				SILENT- NONCODI NG			
4763- 4764	cg43970474	399	TCTATTCCCTC AAAAGTTTTTTT T/gapJCCTGCTA TAAGATAAAGAA AAGGCT	T	-				SILENT- NONCODI NG			
4765- 4766	cg43970521	524	GCCACAGCCTC AGGAACAGCCCA GACJCTGGGA GGCGTGGTCAC ACTACAC	A	C				SILENT- NONCODI NG			
4767- 4768	cg43970521	647	TTAACTGTGGC GATGAGAAAGGT G/GCJTGACTC TCTTACTGGCA GGCCA	G	C				SILENT- NONCODI NG			
4769- 4770	cg43970521	679	CTTCTTACTGGC AGGCCACCTG CGT/GJCTGTGG AGACCCTGGG CCCAGGGT	T	G				SILENT- NONCODI NG			
4771- 4772	cg43970716	290	CGTGGAGGCTTC GTTTTCTATTAT T/CJTACATTAT GGCTTCTTTTG TGAG	T	C				SILENT- NONCODI NG			
4773- 4774	cg43970716	450	TCTGCCGACTCC AAGGTAGGGATG G/GAJGCTGTCC CCAACAGACACC AGCGCA	G	A				SILENT- NONCODI NG			

4775- 4776	cg43970716	454	CCGACTCCAAGG TAGGGATGGG CT[G/gap]TCCCC AACAGACACCAG CGCACATG	G	-			SILENT- NONCODI NG			
4777- 4778	cg43970716	467	AGGGATGGGC TGTCCTCCCAACAG AC[A/C]CCAGCG CACATGCCCTAT TTGGTAT	A	C			SILENT- NONCODI NG			
4779- 4780	cg43970764	1939	CAACGTCCGTGT CGATGCCGAAAT CT[C]TTTTTAA ATCTTTTTTTGGA GGAA	T	C			SILENT- NONCODI NG			
4781- 4782	cg43970764	225	CTCTATTTTGTT CCCATCTCCCTT C/TCTGTTCTCT CCCATCCTCCAA AGAT	C	T			SILENT- NONCODI NG			
4783- 4784	cg43970806	599	AACTAAAGATT TGTTGCGCGCAC G[G/T]GATTCTG CCCCTCTGGCCT TCCCT	G	T			SILENT- NONCODI NG			
4785- 4786	cg43970995	640	TACCAGGAACT GTTACAGACGCC AT[gap]TTTTTTT TTTTTTGAGACG GAGTCT	T	-			SILENT- NONCODI NG			
4787- 4788	cg43970995	652	GTTACAGACGCC ATTTTTTTTTTTT T[gap]TGAGACG GAGTCTTGCTCT GTTGCC	T	-			SILENT- NONCODI NG			

4789-4790	cg43970995	653	TTACAGACGCCA TTTTTTTTTTTT T/gap/GAGACGG AGTCTTGCTCTG TTGCCC	T	-				SILENT- NONCODI NG		
4791-4792	cg43971398	347	TAATAGTAGATTT TTAATCAGCTTT G/CjTGATTCTTT AATAGTTATTGG TTT	G	C				SILENT- NONCODI NG		
4793-4794	cg43971504	1794	ATGGCCGGGAC ATCTCAGAGCAC AC[G/T]CATGACC AGGTGGTGATGT TCATCA	G	T				SILENT- NONCODI NG		
4795-4796	cg43971504	1842	TCAAAGCAAGCC GGGAGTCCCACT C[A/G]AGAGAACT GGCCCTGGTGAT CAGGA	A	G				SILENT- NONCODI NG		
4797-4798	cg43971504	1869	GAGAACTGGCC CTGGTGATCAGG AG[G/A]AGAGCT GTGCGCTCATTT GCTGACT	G	A				SILENT- NONCODI NG		
4799-4800	cg43971504	1871	GAACTGGCCCTG GTGATCAGGAG GA[G/A]AGCTGT GCGCTCATTTGC TGACTTC	G	A				SILENT- NONCODI NG		
4801-4802	cg43971504	1884	TGATCAGGAGGA GAGCTGTGCGCT C[A/G]TTTGCTGA CTTCAAGTCTGA AGATG	A	G				SILENT- NONCODI NG		
4803-4804	cg43971504	1902	TGCGCTCATTTG CTGACTTCAAGT C[TT/A]GAAGATGA ACTGAACCAAGCT TTTCC	T	A				SILENT- NONCODI NG		

4805-4806	cg43971504	1911	TTGCTGACTTCA AGTCTGAAGATG A[A/G]CTGAACCA GCTTTTCCCCGA AGCCA	A	G				SILENT- NONCODI NG			
4807-4808	cg43971504	1916	GACTTCAAGTCT GAAGATGAACCTG A[A/G]CCAGCTTT TCCCCGAAGCCA TTTTG	A	G				SILENT- NONCODI NG			
4809-4810	cg43971504	1929	AAGATGAACCTGA ACCAGCTTTTCC C[C/A]GAAGCCAT TTTCCCCATGTG TCCGG	C	A				SILENT- NONCODI NG			
4811-4812	cg43971504	1938	TGAACCAAGCTTT TCCCCGAAGCCA TTT[G]TCCCCAT GTGTCCGGAGG GTGGGG	T	G				SILENT- NONCODI NG			
4813-4814	cg43971504	2705	CCCATTTACCCA CTGGATATTGTC C[G/A]AAAAATGC GAGACCAGCGC GCCATG	G	A				SILENT- NONCODI NG			
4815-4816	cg43971764	4212	AATTTTTGTATT TTTAGTAGAGAC[G/A]GGTTTCACC GTGTTAGCCAGG ATGG	G	A				SILENT- NONCODI NG			
4817-4818	cg43971764	4255	CAGGATGGTCTC GATCTCCTGACC TTT[C]GTGATCCG CCGCCTCAGC CTCCCA	T	C				SILENT- NONCODI NG			
4819-4820	cg43972205	340	GGTCACCAAGAT GCAGCAGGAAAT C[A/G]CTTTTCAG CAAGTAATGTCT CAGAT	A	G				SILENT- NONCODI NG			

4821- 4822	cg43972259	488	TTTAGTGTCAA AATATAGCGTTG A[G/A]GGGAGCT GGACGCTAGGG TCITCAC	G	A				SILENT- NONCODI NG		
4823- 4824	cg43972293	244	TGACATTAAAGA AGAAACAGACAC CT[C]TGGAGAAT TTATGACTCCTTT CICT	T	C				SILENT- NONCODI NG		
4825- 4826	cg43972406	550	GTGATTCCATCT GAAGGCAGTGA GA[G]GTGGTG TTACCATCTGAA GTGGGTC	A	G				SILENT- NONCODI NG		
4827- 4828	cg43972482	348	CTCTGGCTCCGG AGTAGCTGGGAT T[G/A]CAGGCAC CCGCCACCCACG CCTGGCT	G	A				SILENT- NONCODI NG		
4829- 4830	cg43972482	369	GATTGCAGGCAC CCGCCACCCACG CC[T/C]GGCTAAT TTTTGTATTTTA GTAGA	T	C				SILENT- NONCODI NG		
4831- 4832	cg43972482	380	CCCGCCACCAC GCCTGGCTAATT TT[T/gap]GTATTT TTAGTAGAGACG GGTTTC	T	-				SILENT- NONCODI NG		
4833- 4834	cg43972723	824	GTGGTAAGTCTG GGAGTGGAGGA AA[C/A]AACTGGT GTCTGAATATGA CTAAA	C	A				SILENT- NONCODI NG		
4835- 4836	cg43972879	741	ACTGCTGCAGAT CCTTAGCACCAT T[C/T]AGGAACTG TGGAGGGGGCA GCGGGG	C	T				SILENT- NONCODI NG		

4837- 4838	cg43973078	231	ACCTAGAAAGG ACTCATTACCTT G(G/C)TGATATG GTTTGGTTCTAT GTCCCC	G	C				SILENT- NONCODI NG		
4839- 4840	cg43973078	239	AAGGACTCATT CCTTGGTGATAT G(G/C)TTTGGTTC TATGTCCCCACC CAAAAT	G	C				SILENT- NONCODI NG		
4841- 4842	cg43973078	245	TCATTACCTTGG TGATATGGTTTG G(T/gap)TCTATGT CCCCACCCCAAT CTCATA	T	-				SILENT- NONCODI NG		
4843- 4844	cg43973078	246	CATTACCTTGGT GATATGGTTTGG T(T/gap)CTATGTC CCCACCCCAATC TCATAT	T	-				SILENT- NONCODI NG		
4845- 4846	cg43973078	275	TGCCCCACCCA AATCTCATATCG A(A/C)TTGTAATC CCCATATATCCCC CATGT	A	C				SILENT- NONCODI NG		
4847- 4848	cg43973078	314	AATCCCCCATGT TGAGGGAGGGA CC(A/T)TATGGA GGTGACTGGATC ATGGGA	A	T				SILENT- NONCODI NG		
4849- 4850	cg43973114	1339	TAATTAAACAAA CTTAAAAA A(A/gap)ATAGCA TTGGGGGCCCTA TTTTGTG	A	-				SILENT- NONCODI NG		
4851- 4852	cg43973114	1340	AATTAAACAAAC TTAAAAA [A/gap]TAGCATT GGGGGCCCTATT TTTGGA	A	-				SILENT- NONCODI NG		

4853-4854	cg43973149	194	ATCTACTTACAG TCCTAGTATGAA A/GA/TGTTGGG GGGTCCTTGTTA GGTTTG	G	A				SILENT- NONCODI NG			
4855-4856	cg43973149	306	CTAATAGTCATG CAAATGCTTAAG C/A/gap/AAAAAG AAGTTACATTAA GCAGAAC	A	-				SILENT- NONCODI NG			
4857-4858	cg43973149	570	AATCAATGCTTA AAAAACAAAAA A/A/gap/CCTGGG CAGTTCCTAACT ACTTAAA	A	-				SILENT- NONCODI NG			
4859-4860	cg43973267	364	GAAGTGGTGGG AACAAATGAGGGA CA/G/C/CCTGGA TCATGTGGACCA GCCAATG	G	C				SILENT- NONCODI NG			
4861-4862	cg43973267	365	AAGTGGTGGGAA CAATGAGGGACA G/C/G/C/TGGATC ATGTGGACCAGC CAATGC	C	G				SILENT- NONCODI NG			
4863-4864	cg43973459	305	ATTTTATTAAA AATTGATCAGAA[G/A]CTAGTTGAA ATTCTCAATGTA AATA	G	A				SILENT- NONCODI NG			
4865-4866	cg43973531	2966	AACITGGCAGCCA CTATTAATTGATC [A/G]TCAACTCAA GCTCAAGTTGCT GAAA	A	G				SILENT- NONCODI NG			
4867-4868	cg43973531	3033	ACGCAGCCAGA CCTAGCTTGCTA AT[G/A]CAAGGA GAAAAGGGGCA AGTTCITT	G	A				SILENT- NONCODI NG			

4869-4870	cg43973700	896	CTCAATAATCTG GTCCTTCTCAAT GT/CJCCAATCCT GTCAATCTCCAGG TCCAC	T	C				SILENT- NONCODI NG			
4871-4872	cg43973789	649	TTCCAATTGTCC TTTTTTTTTTTTT gap/TJAAGAGAA TCTGGTATGAGA ACCAT	-	T				SILENT- NONCODI NG			
4873-4874	cg43973789	889	AAAAATTTTATTC TCTGTCCCATTT A/TJTTGGTATCT GGAACGGAAGAG AAAA	A	T				SILENT- NONCODI NG			
4875-4876	cg43974402	685	CTGGGATTACAG GCATGCACCACC A/C/TJACCCGGCT AACTTTTGATTT TTAG	C	T				SILENT- NONCODI NG			
4877-4878	cg43975023	579	TTGATAAACAAAC CTCAAAGACACC C/C/TJGAGCCTTT GAACGGAGCCC TCTGCA	C	T				SILENT- NONCODI NG			
4879-4880	cg43975313	284	GCACITAGGATG TTCTGGAATGA G/A/GJGGAATC CACATTCTGCG CCAGGA	A	G				SILENT- NONCODI NG			
4881-4882	cg43975716	333	GAGGATCCAGTT CAGGTTGATGTC C/T/AJGGGAACC AGTGAGGCTCTC GCTTAA	T	A				SILENT- NONCODI NG			
4883-4884	cg43975716	342	GTTCAGGTTGAT GTCCTGGGAACC A/G/AJTGAGGCT CTCGCTTAAATC TATGTG	G	A				SILENT- NONCODI NG			

4885- 4886	cg43975716	354	GTCCTGGGAACC AGTGAGGCTCTC G/C/T/TTAAATCT ATGTGTTGAAAG TGGCA	C	T				SILENT- NONCODI NG			
4887- 4888	cg43975716	360	GGAACCAAGTGA GGCTCTCGCTTA AA/T/CJCTATGTG TTGAAAGTGGCA TTTTGT	T	C				SILENT- NONCODI NG			
4889- 4890	cg43975716	372	GCTCTCGCTTAA ATCTATGTGTG A/A/TJAGTGGCAT TTTGTGTTGTA GCITG	A	T				SILENT- NONCODI NG			
4891- 4892	cg43975716	373	CTCTCGCTTAA TCATATGTGTGA A/A/TJGTGGCATT TTGTTGTTGTAG CTTGT	A	T				SILENT- NONCODI NG			
4893- 4894	cg43975716	379	CTTAAATCTATGT GTTGAAAGTGGC [A/T]TTTGTGT TGTAAGCTTGTAT CATA	A	T				SILENT- NONCODI NG			
4895- 4896	cg43975716	385	TCATATGTGTGA AAGTGGCATTTT G/T/CJTGTTGTAG CTTGTATCATAT GTTGT	T	C				SILENT- NONCODI NG			
4897- 4898	cg43975716	398	AGTGGCATTTTG TTGTTGTAGCTT G/T/CJATCATATG TTGTTTCAAAGT AGTGT	T	C				SILENT- NONCODI NG			
4899- 4900	cg43975716	402	GCAATTTGTTGT TGTAAGCTTGTAT C/A/GJATGTTGT TTCAAAGTAGTG TCCAA	A	G				SILENT- NONCODI NG			

4901- 4902	cg43975716	414	TGTAGCTTGAT CATATGTTGTT C[AG]AAGTAGTG TCCAAACTGGGA AGGCA	A	G				SILENT- NONCODI NG		
4903- 4904	cg43975716	418	GCTTGATCATA TGTTGTTTCAAA GT/CJAGTGCCA AACTGGGAAGG CAAGGG	T	C				SILENT- NONCODI NG		
4905- 4906	cg43975716	456	GGGAAGGCAAG GGTTGGGCTGC AC[G/A]ATATTCC TCAGGTCATATC TTTCCT	G	A				SILENT- NONCODI NG		
4907- 4908	cg43975716	468	GTTTGGGCTGCA CGATATTCCTCA G[G/A]TCATATCT TTCTGGTTCCA GTTGC	G	A				SILENT- NONCODI NG		
4909- 4910	cg43975716	516	TGCCCCATCAGGG TACGGTTTGAAT A[G/C]GTATTCTC ATTAGTGGTGCA TCGCC	G	C				SILENT- NONCODI NG		
4911- 4912	cg43975856	277	TGTTGCTAATGT GCTCAACTCCTT C[A/C]CGGGGA GAGATCAGTTTG CAAAGT	A	C				SILENT- NONCODI NG		
4913- 4914	cg43975884	671	AAGGCATATACA CACCTCATCCCC C[C/Π]ACATGCAC ATCAGCAAAGTCT ATCAG	C	T				SILENT- NONCODI NG		
4915- 4916	cg43975884	728	TCATTGGGCCAA ATGTTTGGCATA T[C/gap]AGAAATTT GTGATGTGAGAG GGCAAG	C	.				SILENT- NONCODI NG		

4917-4918	cg43976147	241	CCTCTCCTCTGT CCTCCTCTCCCA T[A/G]TGCTGCAA ACTCACCCCTG ATGTC	A	G				SILENT- NONCODI NG			
4919-4920	cg43976147	272	CAAACTCACCCC CTGATGTCCAG C[A/T]GCCAGC CCTGGGCCAG GTTGGTC	A	T				SILENT- NONCODI NG			
4921-4922	cg43976147	273	AAACTCACCCC TGATGTCCAGC A[G/C]CCAGCCC CTGGGCCAGG TTGGTCG	G	C				SILENT- NONCODI NG			
4923-4924	cg43976147	286	GATGTCCAGCA GCCAGCCCCTG GG[C/G]CCAGGT TGGTCGTTTCTC CTGCTTT	C	G				SILENT- NONCODI NG			
4925-4926	cg43976147	352	AGCACGGTACTG TCCCACCTGCAC C[A/C]TGCTGCAT TCTCTCAGCACC ACCTG	A	C				SILENT- NONCODI NG			
4927-4928	cg43976147	374	ACCATGCTGCAT TCTCTCAGCACC A[C/T]CTGTGATT CTGCCACTGGCC TAATT	C	T				SILENT- NONCODI NG			
4929-4930	cg43976147	385	TTCTCTCAGCAC CACCTGTGATT T[G/C]CCACTGG CCTAATTCTGTA TCTCAG	G	C				SILENT- NONCODI NG			
4931-4932	cg43976643	1177	TGGTCTGTCCAG AAGAACTACATC T[T/A]TATTAGC ATGCAGTTTGTG GCAAT	T	A				SILENT- NONCODI NG			

4933-4934	cg43976643	1178	GGTCTGTCCAGAT AGAACTACATCT TTT/ATTTAGCA TGCAGTTTGTGG CAATT	T	A				SILENT- NONCODI NG			
4935-4936	cg43976643	1215	AGTTTGTGGCAA TTCTATTGAGGA GG/CJAAACAGG ATAGTATGTACA GTAACA	G	C				SILENT- NONCODI NG			
4937-4938	cg43976643	1283	ATGCAGATTCTT GGCATTCCATTC CIG/ATTTCTGCT GATTATTTTCAGA ATTAT	G	A				SILENT- NONCODI NG			
4939-4940	cg43976643	1290	TTCTTGGCATTC CATTCGGTTTCT GIC/TJTGATTATT TCAGAAATTATCT GTTGG	C	T				SILENT- NONCODI NG			
4941-4942	cg43976643	1313	TGCTGATTATTT CAGAAATTATCTG TTT/GJGGAATGAA CGCGGCGTGTT GCTGCA	T	G				SILENT- NONCODI NG			
4943-4944	cg43976643	1325	CAGAAATTATCTG TTGGAATGAACG CIG/CJGCGTGTT GCTGCAACTGTG CGCTGG	G	C				SILENT- NONCODI NG			
4945-4946	cg43976643	1331	TATCTGTTGGAA TGAACGCGGCG TGTC/JTGCTGCA ACTGTGCGCTGG TGAGAG	T	C				SILENT- NONCODI NG			
4947-4948	cg43976643	1339	GGAATGAACGC GGCGTGTGCTG CA/GJCTGTGC GCTGGTGAGAG CCTGCTGG	A	G				SILENT- NONCODI NG			

4949-4950	cg43976643	1343	TGAACGCGGCG TGTTGCTGCAAC TGTT/CJGCGCTG GTGAGAGCCTG CTGGTAGT	T	C				SILENT- NONCODI NG			
4951-4952	cg43976643	1352	CGTGTGCTGCA ACTGTGCGCTGG TTG/CJAGGCCT GCTGGTAGTGCA AGACGC	G	C				SILENT- NONCODI NG			
4953-4954	cg43976643	1385	GCTGGTAGTGCA AGACGCTGGG TTG/AAGACCG CGCTGGTACCAT TGCTTT	A	G				SILENT- NONCODI NG			
4955-4956	cg43976643	1436	TTTCAAGTGCTT GTCTCTTTGGTA A/A/GJGGATGAA GAGCACCAGGG GGAAAGG	A	G				SILENT- NONCODI NG			
4957-4958	cg43976707	188	GAATGCGTTTCC CCCTTCAGGAAG A/G/gapJAACCTCA GTTACACATCAC GAAGTCA	G	-				SILENT- NONCODI NG			
4959-4960	cg43976754	301	GATGCAAAAGCGA CCTGGACAAGG CTG/TJACCTCAG TGCCAGGAGGG TCCCTGG	G	T				SILENT- NONCODI NG			
4961-4962	cg43976910	368	CTGGTGTTCATC GTGGCTGAAG GG/A/GJCTCCCT GGTGTGCTACAA TCCCTTG	A	G				SILENT- NONCODI NG			
4963-4964	cg43976910	801	ACTGCTGCTGCT CAGCTGGTTGCT TTG/AJAAC TGACA GTAGGCCAGCCT GTTCT	G	A				SILENT- NONCODI NG			

4965- 4966	cg43977247	1098	TTGGCCTCCTTG CTGTCCTGCTTC T[gap]/GTTGGTTT CAGAAACTTCTG ACTTCCG	-	G				SILENT- NONCODI NG		
4967- 4968	cg43977442	3330	TTCTGCCTGTGC TCCTCAAGGGCA G[C/A]TGTGAG GCCTGGAATTCC TCACTG	C	A				SILENT- NONCODI NG		
4969- 4970	cg43977442	3453	AGTCCCCTGGCT CGATTACAGGC TC[A/G]TGCTCC ^A GGTGTGCAGG CTGTGG	A	G				SILENT- NONCODI NG		
4971- 4972	cg43979051	205	TAAAGATAAATG AAGAAATCAAAA AT[A/A]ATAAAG TGAAACTTCTTC TAAGA	T	A				SILENT- NONCODI NG		
4973- 4974	cg43979107	674	GTAGGCCAGAAT ATAAATCTCCTTA [G/gap]GAAGAAG TTTGGTTAGGCA AAACCA	G	-				SILENT- NONCODI NG		
4975- 4976	cg43979107	675	TAGGCCAGAATA TAAATCTCCTTA G[G/gap]AAGAAG TTTGGTTAGGCA AAACCA	G	-				SILENT- NONCODI NG		
4977- 4978	cg43979152	326	TTCTTTGGACCT TTTCAGAACAT GT/GTACTTCCC TGCCTCAGTTAG AAGTT	T	G				SILENT- NONCODI NG		
4979- 4980	cg43979411	429	GCACAGTGGCTC ATGCCTGTAATC CT/CJAGCACTTT GGGAGGCTGAG GCAGGT	T	C				SILENT- NONCODI NG		

4981- 4982	cg43979439	706	GAAATCAGAAAG CAAGGCTTGTTT T[A/G]GGCAAC GTGCCACATATC TTGTAA	A	G				SILENT- NONCODI NG			
4983- 4984	cg43979495	1524	AGAGTGACCGTC TAAAGGTGGTTC A[C/G]AAGGAA GGATCCACAAGT TAGTGA	C	G				SILENT- NONCODI NG			
4985- 4986	cg43979568	523	AGCGGTGAGGG CGCCTCGAAGAA GG[G/gap]CCTCT GGCCAGCGGG GAGCGCAGC	G	-				SILENT- NONCODI NG			
4987- 4988	cg43979574	2158	ATTGCAATTCTA ATCAATCAATCA A[A/gap]ACAGAC CAAAAGGTCATA CTTCTAA	A	-				SILENT- NONCODI NG			
4989- 4990	cg43979594	1114	TAAGGCCATTTC ACTAAGTTTGA A[T/A]TGGAGGA GAGGCAAGCCA AGAATCA	T	A				SILENT- NONCODI NG			
4991- 4992	cg43979615	347	CTGCAGACCACT CTGTGGCACGG GA[T/C]GAGGAT GGGACAGGAT TGCCTCTC	T	C				SILENT- NONCODI NG			
4993- 4994	cg43979647	503	TTGCTCAGAGCA CAAGGCCTACCC C[A/G]TCCTGCGT CTCCAGCCCCGAC TTGGA	A	G				SILENT- NONCODI NG			

4995- 4996	cg43979647	62	TCITTATTACAA AATGCGGTGAAG [A/G]GAAAAATATC TAGATATTTGGG TGTA	A	G				SILENT- NONCODI NG		
4997- 4998	cg43979837	468	GTGGAGTTTGGG GAGGGGGCGA AA[G/gap]CAACG GGACTGCTGGG AGAGGAGGG	G	-				SILENT- NONCODI NG		
4999- 5000	cg43979896	1026	TAAGACCAATTC AGAACAAAGGCA G[G/A]TTGCCCTT AAACACAGGTTG ACCTT	G	A				SILENT- NONCODI NG		
5001- 5002	cg43980073	405	ATTTATGAAGAA ATGGACTTGGAA A[G/T]GAAATTCT AACAGAGAAGAG CTTAA	G	T				SILENT- NONCODI NG		
5003- 5004	cg43980088	288	AATCACAAATTTA GTATTATAGAAA A[A/gap]GAGTTT CTCAGTAATCTC TTGACCA	A	-				SILENT- NONCODI NG		
5005- 5006	cg43980276	1636	TTTCAAAATATAAA TCATTTAACTAT gap/A/AAATATTC AGAGGACATTCA GGAGA	-	A				SILENT- NONCODI NG		
5007- 5008	cg43980513	491	AACGCATGCCCG CTCGGCCGTCA GG[G/gap]CGCTG ATCTGCCCGTTG AGGGTGCT	G	-				SILENT- NONCODI NG		

5009-5010	cg43980531	318	TCCTCCTCTGTT GTCATCGGTGAA GIC/AJTAAAAAA AGTTTTCTGAAA GTAGC	C	A				SILENT- NONCODI NG		
5011-5012	cg43980531	327	GTTGTCATCGGT GAAGCTAAAAAA A/Agap/GTTTTCT GAAAGTAGCAAG TTGTGT	A	-				SILENT- NONCODI NG		
5013-5014	cg43980531	397	GCCAAAAAGGCT CAGTCTTTGGCT C/A/GJCAGATGTC AGTGACAAAATC ATGGC	A	G				SILENT- NONCODI NG		
5015-5016	cg43980543	177	ATTATTGAATACT TTTTGAGTATTI G/AJCTATATACC AGGCAAAAGGCA CAGA	G	A				SILENT- NONCODI NG		
5017-5018	cg43980543	188	CTTTTGAGTATT TGCTATATACCA G/AJGCAAAAGGC ACAGAACAATT ATT	G	A				SILENT- NONCODI NG		
5019-5020	cg43980655	314	CACCCAGGCTG GAGTGCAGTGG CGC/G/AJATCTC GGCTCACTGCAA CCTCCGCC	G	A				SILENT- NONCODI NG		
5021-5022	cg43980827	204	TTCATATCAAAAT TCCCATAAAAAA gap/AJTTACATTC CCCCCTCCCCAG TTCTA	-	A				SILENT- NONCODI NG		
5023-5024	cg43980859	160	ACTGGTAGGAAG AGCAGAGAGATG C/AJGGGAACG TGGTCAGAGGCT GTGAAC	A	G				SILENT- NONCODI NG		

5025- 5026	cg43981033	461	GATTGTTGTTAA CACTGAAAAAAA A[A/gap]CATGGT GGCTCCTGAAAC AAGACAG	A	-			SILENT- NONCODI NG		
5027- 5028	cg43981033	483	AAACATGGTGG CTCCTGAAACAA GAGCAGGTTA GCAACTGGTACA GCTTTC	A	G			SILENT- NONCODI NG		
5029- 5030	cg43981094	350	TTCATAAGACTT GAGTAAGTAGAT CIC/A/AAATTTGT TATCACTAATGG CTCAA	C	A			SILENT- NONCODI NG		
5031- 5032	cg43981141	589	GAACACGGTGCT AGCAGCTAACGA C/C/TTTCCCCTG TGCCCTGTCCTC CTGAC	C	T			SILENT- NONCODI NG		
5033- 5034	cg43981141	673	GGAGGGTGGAA CTATGTTTGAAG GC/C/TTCCAC ACTCTGTACATT CATAAG	C	T			SILENT- NONCODI NG		
5035- 5036	cg43981267	187	GCCAGGAGGAC CAGCATGGGA CAC/A/CJGGAGC TATCAGGCAGGA GTCAGGCT	A	C			SILENT- NONCODI NG		
5037- 5038	cg43981280	707	ATTTGTTCTGC AAGATAATTAC A/T/CJAGTTCTCT CTGCTATATGTG TCCAC	T	C			SILENT- NONCODI NG		

5039-5040	cg43981323	1351	GTGGCTCCGCTG GGGACAGGGCC TC[C/gap]TGGCG CGCCGGCATCC CCCTCTCGG	C	-			SILENT- NONCODI NG			
5041-5042	cg43981356	178	TGCTGCTGCCAC GGGGTAGGGT GC[G/A]GGAGGC GGCTGGCCTC ATGGCCGC	G	A			SILENT- NONCODI NG			
5043-5044	cg43981449	338	TCCAATGGGATC TTAGAATTCCTA G[A/C]GTTGCAG AATTTACTGACT AGACC	A	C			SILENT- NONCODI NG			
5045-5046	cg43981449	437	CAAGGGAGCTCA TAACTCCATGGG G[C/G]CCAGAGT TCCTGGCTCGG GAACAT	C	G			SILENT- NONCODI NG			
5047-5048	cg43981504	1638	TTTAAACCCCC AAATCTTAAATC [A/G]ATATTATAT ATTCTATTTGAAT TTT	A	G			SILENT- NONCODI NG			
5049-5050	cg43981615	906	AATCTTGAGGGC TGAAGGTTCCAA A[G/T]AAATGGTA TATATAGAATTCT ATCT	G	T			SILENT- NONCODI NG			
5051-5052	cg43981615	928	AAAGAAATGGTA TATATAGAATTCT [A/C]TCTGACTTG AAATTTCCCTTC CTG	A	C			SILENT- NONCODI NG			

5053-5054	cg43981615	936	GGTATATAGA ATTCTATCTGAC TTTCJGAAATTTT CCCTTCCTGGAG CTCCG	T	C				SILENT- NONCODI NG		
5055-5056	cg43981615	943	ATAGAAATCTAT CTGACTTGAAT TTTGJTCCTTCC TGGAGCTCCGG ATGCTG	T	G				SILENT- NONCODI NG		
5057-5058	cg43981615	887	ACTGAGGTCATG ATGTTGGAATCT TIG/AJAGGCTG AAGGTTCCAAAG AAATGG	G	A				SILENT- NONCODI NG		
5059-5060	cg43981624	402	TGGCAGCCCT GCTTTTTTTTTT TTT/gapJTTAGCTC CCTAAAGACTGT AGCAGG	T	-				SILENT- NONCODI NG		
5061-5062	cg43981624	403	GGCAGCCCTG CTTTTTTTTTTT TTT/gapJTAGCTC CCTAAAGACTGT AGCAGGA	T	-				SILENT- NONCODI NG		
5063-5064	cg43981624	404	GCAGCCCTGCT TTTTTTTTTTTTT T/gapJAGCTCCCT AAAGACTGTAGC AGGAT	T	-				SILENT- NONCODI NG		
5065-5066	cg43981644	791	CTGTTTGCTTGT TGGTGTGAGTTT TTT/gapJCTTCTG GAGACTTTGTAC TGAATGT	T	-				SILENT- NONCODI NG		
5067-5068	cg43981789	24	CGGGGAGAAGC ACAGTTGCTGCA [G/A]GGAATCTTT TAAACGAGAGCG AGAA	G	A				SILENT- NONCODI NG		

5069-5070	cg43981889	10053	CTAATCTGTTGT GAAAGATCTTTT A/C/TTTTGTATTT CCATTCTTCGAT TATCT	C	T				SILENT- NONCODI NG			
5071-5072	cg43981889	10096	GATTATCTCTCT CAAGTACAGATG AT/AJTGCTTGT GGCTTTATCAGT GTCT	T	A				SILENT- NONCODI NG			
5073-5074	cg43981997	10376	AGTAGTACTGGA GGCCTTGAGG GG[C/gap]CCACA GACAGATCCCAT CCATCAGC	C	-				SILENT- NONCODI NG			
5075-5076	cg43982038	584	AAATGCTTCTCT CCTCTGGTCTC C[C/gap]TAAGGT CCTCCTCCTAGT ACACAGG	C	-				SILENT- NONCODI NG			
5077-5078	cg43982123	443	ACACACACACAC ACACACACACAC A[C/gap]ACACAC AGCACCATGTCC TGAGCTG	C	-				SILENT- NONCODI NG			
5079-5080	cg43982123	445	ACACACACACAC ACACACACACAC A[C/gap]ACACAG CACCATGTCCTG AGCTGCT	C	-				SILENT- NONCODI NG			
5081-5082	cg43982123	504	GACTCCCGCCA GACTGCACCTGA CA[G/C]ACAAAG CCAACTAGGAGG GAGGGGA	G	C				SILENT- NONCODI NG			

5083- 5084	cg43982153	3639	TTAAGTACTTTTCA GTGCTCAAAAAA A/gapJTGCAATCA CTGTGTTGTATA TAATA	A	-				SILENT- NONCODI NG			
5085- 5086	cg43982189	305	GCAGCTTTGCGG GCCCCGACCGG TC/C/TJGCGTGG CAGGTGAAGTGC ACCGGTT	C	T				SILENT- NONCODI NG			
5087- 5088	cg43982232	617	GGCAAAACACAA TACAATGAAATG G[A/gap]AAAAATA ATGTTTGTACA GGAGTGC	A	-				SILENT- NONCODI NG			
5089- 5090	cg43982403	3113	TGCCTAAAATTT CTTCTGGAATA C[A/G]TCATCTAA TACACTATATAC ATATT	A	G				SILENT- NONCODI NG			
5091- 5092	cg43982403	3122	TTTCTTCTGGAA TAACATCATCTA A/T/CACACTATA TACATATTTGTAA AACT	T	C				SILENT- NONCODI NG			
5093- 5094	cg43982403	3152	TATATACATATTT GTAAACTTATCT A/GJAACGAGGTA GACATGAGTTCC ATAC	A	G				SILENT- NONCODI NG			
5095- 5096	cg43982403	3170	ACTTATCAAACG AGGTAGACATGA GT/CJTCCATACA GATCCCAACAGTC ACCCCT	T	C				SILENT- NONCODI NG			
5097- 5098	cg43982403	3215	CACCCCTCTCTGA AGAGTGCACCAT A[A/G]AACTGAAC AATGTATGGGCA ATCAC	A	G				SILENT- NONCODI NG			

5099- 5100	cg43982551	554	TCATAAACAGT GTCACCCGCAAA A/A/C/AAGCCATA CAGATATCATGA CGGTG	A	C			SILENT- NONCODI NG			
5101- 5102	cg43982652	5530	AAAAAAATTA GGCAGGCATGG TG[G/A]TGGCG CCTGTAGTCCCA GCTACTC	G	A			SILENT- NONCODI NG			
5103- 5104	cg43982782	1091	AGTTCGGGACA CCCCCATTTACA A/C/T]GACGAGG CGGACCCGCTG GTGGGCT	C	T			SILENT- NONCODI NG			
5105- 5106	cg43983113	476	TTGACTCATGGA GGCTCTGTAAGA G/C/gap]CCAGGA TTGGGGGCGCTG GGTCAGGG	C	-			SILENT- NONCODI NG			
5107- 5108	cg43983113	568	AGCCCAGAAAG AGACCCATTTT TTT/gap]GGCGG GGGAGCTGAG TCCCAGAGG	T	-			SILENT- NONCODI NG			
5109- 5110	cg43983122	650	TGCACCTGAAGG TGCCCCCATGT G[G/gap]CCAAAG CCCCCTTGCCTG ACCAAGGC	G	-			SILENT- NONCODI NG			
5111- 5112	cg43983294	961	CAGGGGCGCTG GCACATTCCTCA GAT/C]TCTGGCA TGTCATCCTGGA AGTACT	T	C			SILENT- NONCODI NG			

5113-5114	cg43983294	1012	CAGCCTGGCGG TACTGCCACAGA CG[C/T]AGGTTCC CGTCCCACGAAC TGCTGA	C	T				SILENT- NONCODI NG		
5115-5116	cg43983294	1016	CTGGCGGTACTG CCACAGACGCA GGT[C/T]CCCGT CCCACGAACTGC TGACAAT	T	C				SILENT- NONCODI NG		
5117-5118	cg43983294	1021	GGTACTGCCACA GACGCAGGTTCC C[G/A]TCCCACG AACTGCTGACAA TCITTT	G	A				SILENT- NONCODI NG		
5119-5120	cg43983486	3852	CTAGCACACCGT CTCCAAGGGTAC C[G/A]CGTCGAT GCTATGTGCTCA GTTCTA	G	A				SILENT- NONCODI NG		
5121-5122	cg43983486	4093	AATGGTATTTGT AAAGTTTTTTTTT [T/gap]AATTTATT CAAAAAAAGACA TAGTA	T	-				SILENT- NONCODI NG		
5123-5124	cg43983790	479	CAACTGGAATA CTAAACAAATAC T[G/T]GAATTCAC ATTACAGACAGA CGAAA	G	T				SILENT- NONCODI NG		
5125-5126	cg43983790	525	CGAAACCAACAT GGATGCCACACA T[A/C]ACTTCCTT TGTAGTTTCACA GAGAG	A	C				SILENT- NONCODI NG		
5127-5128	cg43983790	572	AGAGCCTATTG TGGTTGCTCAGG T[G/gap]GGGTCA TACATTGCTTGC AGAAATG	G	.				SILENT- NONCODI NG		

5129-5130	cg43983790	589	GCTCAGGTGGG GTCATACATTGC TT[G/A]CAGAAAT GGCCTGATCATA GCTCTA	G	A				SILENT- NONCODI NG			
5131-5132	cg43983790	714	AAGTTGAGATAA TAATATTTACAT [A/G]TTTATATAC AGAGAATCACTC TCAA	A	G				SILENT- NONCODI NG			
5133-5134	cg43983790	783	AATAGGATTTGG GGGTGACTTGTA C[A/G]CATTTCTA AAAACACTTTTCT TTTT	A	G				SILENT- NONCODI NG			
5135-5136	cg43983873	1192	CTACTGTCAGTT TTCTGATTGAGA A[C/T]ATTTCATCG CCCAAGAAACAG CTCAT	C	T				SILENT- NONCODI NG			
5137-5138	cg43983994	831	TGGCGGTGGGT ACCGACTCAAAG GC[A/G]GCAATG CCATTCCCTAGC TCAGACA	A	G				SILENT- NONCODI NG			
5139-5140	cg43984006	1046	CACCATGCAGAC ACGCAGCTGTGA A[C/T]GACAGTTC AGAACTCAGCGT AAGCT	C	T				SILENT- NONCODI NG			
5141-5142	cg43984006	1058	ACGCAGCTGTGA ACGACAGTTTCAG A[A/G]CTCAGCGT AAGCTTGCTA TGAAC	A	G				SILENT- NONCODI NG			
5143-5144	cg43984006	1063	GCTGTGAACGAC AGTTCAGAACTC A[G/A]CGTAAGCT TGTGCTATGAAC GAGCA	G	A				SILENT- NONCODI NG			

5145-5146	cg43984006	1065	TGTGAACGACAG TTCAGAACTCAG C[G/A]TAAGCTTG TGCTATGAACGA GCACC	G	A			SILENT- NONCODI NG		
5147-5148	cg43984006	1069	AACGACAGTTCA GAACTCAGCGTA A[G/A]CTTGTGCT ATGAACGAGCAC CGTCA	G	A			SILENT- NONCODI NG		
5149-5150	cg43984006	1078	TCAGAACTCAGC GTAAGCTTGTGC T[A/G]TGAACGAG CACCGTCAGAGA ATTCC	A	G			SILENT- NONCODI NG		
5151-5152	cg43984006	1084	CTCAGCGTAAGC TTGTGCTATGAA C[G/A]AGCACCG TCAGAGAAATCC CACCCA	G	A			SILENT- NONCODI NG		
5153-5154	cg43984065	2278	GACTCCGGCGG AGCAGAAAGCCTT CGT[C/T]GGGG CGGCACAGGGG TCCTTAAA	T	C			SILENT- NONCODI NG		
5155-5156	cg43984242	229	GCCCACGTCCCA GCTGGACCATG GC[G/gap]CCTCC GCGGAACGTGG TGAAGATTG	G	.			SILENT- NONCODI NG		
5157-5158	cg43984242	260	GCGGAACGTGG TGAAGATTGCCA TC[A/C]AGATGCG TGACGCCCATCCC GCAGCT	A	C			SILENT- NONCODI NG		

5159- 5160	cg43984508	555	CCTCGTCGCTGT CCAGCGAGGCC ATC/AITCCGTGG GGTCCTCAGTGT TGGCGA	C	A				SILENT- NONCODI NG			
5161- 5162	cg43984651	383	TCCTGTTTGAAC TTGGTGCCAAAT A/G/AJAGTAACTC GGACTCCAGTTG GAGGG	G	A				SILENT- NONCODI NG			
5163- 5164	cg43984671	2361	ATACCGTGTACA CTGATATACACG A/A/GJGCTGCTC CTCATTTTTTTGT CAGAT	A	G				SILENT- NONCODI NG			
5165- 5166	cg43984751	661	AAACACTGCCAT GGTCAGCGGGG GT[G/]GCCGAA GGGGTAACGCC CCAGCAGT	G	T				SILENT- NONCODI NG			
5167- 5168	cg43984751	664	CAC TGCCATGGT CAGCGGGGGTG GC[C/]GAAGGG GTAACGCCCCAG CAGTCCG	C	T				SILENT- NONCODI NG			
5169- 5170	cg43984751	673	GGTCAGCGGGG GTGGCCGAAGG GGT[A/]ACGCC CCAGCAGTCCGA GGCCAGCT	A	G				SILENT- NONCODI NG			
5171- 5172	cg43984751	692	AGGGGTAACGC CCCAGCAGTCC GAG[G/]CCAGC TCCGAGGGTCTA ACTTCTCC	G	A				SILENT- NONCODI NG			

5173- 5174	cg43984865	135	ACACATCAGGGT AAATGGGGTATC CIACTGACCTCA AGCACCCCTCAC AAAT	A	C				SILENT- NONCODI NG		
5175- 5176	cg43984865	158	CCATGACCTCAA GCACCCCTCACA A/GATCTGAGT ACTCACAAGATC TGGT	A	G				SILENT- NONCODI NG		
5177- 5178	cg43984865	160	ATGACCTCAAGC ACCCCTCACAA AT/CCTGAGTAC TCACAAGATCTG GTGT	T	C				SILENT- NONCODI NG		
5179- 5180	cg43984962	683	ACGCTCGTGAAA GCTAATCATCCA C/ATGTGATGTT CCGAAAAGGTA AGCCA	A	T				SILENT- NONCODI NG		
5181- 5182	cg43985092	888	CAGGAGGGAAG AGGCCGCTGGG CCC[C/gap]AGGC ATCCTAGGCCTC TCTTCCCGG	C	.				SILENT- NONCODI NG		
5183- 5184	cg43985377	526	ATAATAATTTTCAG GGAAAAA A/gap]AGGCACAT CCAGGCACCACA TTCAA	A	.				SILENT- NONCODI NG		
5185- 5186	cg43985471	317	GCCCCTCCAGG CAGCTGGGGA GAG[C/]GGAGG CAGGGTCGCTCA GGTTCTA	C	T				SILENT- NONCODI NG		

5187-5188	cg43985734	1960	GGTGAAGAGTGT CTGATGCCAGCG G[C/gap]CATCTT GGACCTTGACG CATCCAT	C	-			SILENT- NONCODI NG		
5189-5190	cg43985772	718	ATGGACTCAGCC TGGGTCAGAGA GG[G/A]AATTCT GAAGCTACACGA ACAAGC	G	A			SILENT- NONCODI NG		
5191-5192	cg43986072	633	TATCAGTAAACA TTAATTTTTTTT T[gap]CCTTGAGG CACAGCATGATC TTGGC	T	-			SILENT- NONCODI NG		
5193-5194	cg43986256	742	CTTCGAGGATC CCAGGACAGGG CC[A/G]CCAGCA GGGAGGCCCT CAATACCT	A	G			SILENT- NONCODI NG		
5195-5196	cg43986256	805	TCAATACCTGAG CCCAAACAACAA T[G/A]AGCAGATT CCCAGGCTTTGC TTTCA	G	A			SILENT- NONCODI NG		
5197-5198	cg43986313	1767	CAGAGATCCTGC AGGAGTTGGAGT A[T/C]GGCCCCT CCGTGGACTGGT GGCCCC	T	C			SILENT- NONCODI NG		
5199-5200	cg43986313	1993	CTGTGTGGCATC GCAGAATGGCG AG[G/A]ACGCCA TCAAGCAGCACC CATTCIT	G	A			SILENT- NONCODI NG		

5201- 5202	cg43986510	757	TGATTCTGTTTA CTTAGCATCATC[T/A]TCATCATCAT CATCATCATCTG TAT	T	A				SILENT- NONCODI NG			
5203- 5204	cg43986519	1047	TAATTTAACAGT GACAGAACGACA G[G/A]CAGTGTC CATAAGCAAACA ACACAC	G	A				SILENT- NONCODI NG			
5205- 5206	cg43986519	568	GACAGCAGAATT AAGATTTAAAA A[C/T]GAAAGCAT TTCATCAAAACA AAAA	C	T				SILENT- NONCODI NG			
5207- 5208	cg43986519	593	GAAAGCATTTCA TCAAAACAAAA A[gap/A]CTAACTT CCTCACAGGAAG TCCACT	-	A				SILENT- NONCODI NG			
5209- 5210	cg43986639	11198	TGGGGGCCACTT TTCCTCCCAAT C[T/C]GAACACG CCCTTAGCTTAA CTGCAG	T	C				SILENT- NONCODI NG			
5211- 5212	cg43986776	817	AGAGCTCCAGG GTTGCAGAAGGC GTT[?gap]GCACA GGTCACGAAGG AATGGCTGT	T	-				SILENT- NONCODI NG			
5213- 5214	cg43986966	1069	TAGCAATATCGT TAATCACTGCTC TTT/GJATTTTGA GACAAAAGGACC AACTT	T	G				SILENT- NONCODI NG			
5215- 5216	cg43986974	506	ATGGTGAATTGG GAATGAAGCTGT C[G/A]GAAATCCC CTTGACTCTGCA TTCIG	G	A				SILENT- NONCODI NG			

5217- 5218	cg43987185	368	CACAAATGTCAG AACATTAAAGTA G/C/TATTTTTC CATAGGAATATA TAAAA	C	T				SILENT- NONCODI NG		
5219- 5220	cg43987473	3583	CCGTTACAACAA GCTTCCCTGATG GT/CJGTCCACA GCTTTTACAAAT GCTGGT	T	C				SILENT- NONCODI NG		
5221- 5222	cg43987479	147	ATCAGACAGACA TGACCTCCTACG C/A/GJGCACCAG TATGCATGAGCG GGTGAA	A	G				SILENT- NONCODI NG		
5223- 5224	cg43987639	326	ATAATAAATCGTT TGGTTTTCTTAA[G/AJAAACTGGGT TTTTCTTTTCCCT TGT	G	A				SILENT- NONCODI NG		
5225- 5226	cg43987678	5773	CCCGGAGCTGA AGATGGGGCAG AAG[C/gap]CCAG GCCCCATCTCCA CCCCCAGCT	C	-				SILENT- NONCODI NG		
5227- 5228	cg43987682	1501	AGAACTGCAGG GTGTTCTCACTA AA[C/TJAGTGGCC CTGCCAGCTGG CGGATCA	C	T				SILENT- NONCODI NG		
5229- 5230	cg43987769	493	TAAAGTTAATTAC CTTACCCCTTGCA[A/GJCTATTTTCTG TATAAGAAATCTC AAA	A	G				SILENT- NONCODI NG		

5231-5232	cg43987787	584	ACTGAAATATAT AGAAAACCCCAA T[G/A]TATGAAAC AAGTTTTAGGCA TTGGT	G	A				SILENT- NONCODI NG			
5233-5234	cg43987853	2041	AATCTTAGTTTAA CTATATATTATT T/C[GGTACTCCT GGATTACAGTAGT TGGG	T	C				SILENT- NONCODI NG			
5235-5236	cg43987853	2076	GGATTACAGTAGT TGGGGTAAAAA A[G/A]TTTCTATA TTCAAACATATCT ACAG	G	A				SILENT- NONCODI NG			
5237-5238	cg43987853	2082	AGTAGTTGGGT AAAAAAGTTTC T[A/G]TATTCAAA CATATCTACAGA ATGTC	A	G				SILENT- NONCODI NG			
5239-5240	cg43987905	5415	GGCAGAAAGCG CACCAGCTTCAG CA[C/T]ACGCAG CAGCCGGAAGG TGCGCAGC	C	T				SILENT- NONCODI NG			
5241-5242	cg43988015	150	ACCTTGGCCTCC CAAAGTGCTGGG A[T/C]TACAGGCA TGAGCAACCGCA CCCGG	T	C				SILENT- NONCODI NG			
5243-5244	cg43988019	551	GTGGTAGAGACA TGATTGGTATTG C[C/A]AAAAACAGG TAGTGGGAAAC TGCAG	C	A				SILENT- NONCODI NG			

5245- 5246	cg43988355	4953	GGTTTGTGGG ACAGCCTGTGAA CTTGCTGTGCTC CTGGTGCCTTTG GGCC	T	G				SILENT- NONCODI NG		
5247- 5248	cg43988355	5275	ACTGTAGCCAGG TAGGAACAATGG TCTTACTTGAC CTGCCCTGCCCGA CTACG	C	T				SILENT- NONCODI NG		
5249- 5250	cg43988355	7341	ATCTTGCCCTTT TCCAAGCGGT GATTCTCCGGTC CCACTGAAGTGA GCCCTTC	T	C				SILENT- NONCODI NG		
5251- 5252	cg43988361	280	CCATGACGGTGC GCTCGGGGTG ATGTAJCCGTATT CCTGGGACACG CAGTCGA	G	A				SILENT- NONCODI NG		
5253- 5254	cg43988361	283	TGACGGTGGCT CGGGTTGATG CCGTAJTATTCCT GGACACGCAG TCGAAAA	G	A				SILENT- NONCODI NG		
5255- 5256	cg43988361	337	AGCGGCTGGGC TTCCCGATGATG TCGTCJGCTGG CGCTGGGCGGC CATCTCCA	G	C				SILENT- NONCODI NG		
5257- 5258	cg43988588	995	CAAAAACAGCTA AAGCAGCAAATT CICAJAAGTCAAA AGAGAGTGATGA ACCTC	C	A				SILENT- NONCODI NG		
5259- 5260	cg43988588	481	AAAGCGCAGGC CCAGCTCCAGAA GCJGTAJCTACAAA GACCTTGAACAA CAAGAC	G	A				SILENT- NONCODI NG		

5261- 5262	cg43988624	151	CCCAGAGCCTG CGTTCTTGGA CA[G/C]ACACAG AGAGAAATGGAA TAAATTA	G	C				SILENT- NONCODI NG		
5263- 5264	cg43988652	1774	GCTCCACTTTGC AGGTGACCGTGA C[A/G]CCATCTGC TCGGCCCCAAGG GCACCA	A	G				SILENT- NONCODI NG		
5265- 5266	cg43988652	1780	CTTTGCAGGTGA CCGTGACACCAT CTT[C]GCTCGGC CCAAGGGCACC AAGGTGA	T	C				SILENT- NONCODI NG		
5267- 5268	cg43988747	294	AGAGGAATCGGT CCACAGCCTTCC G[G/A]GTTGTGG GTGTAAGTGCCA GCACIT	G	A				SILENT- NONCODI NG		
5269- 5270	cg43989086	914	TGCCACTCCAGG TGGGGGGAGTG GT[G/A]CCCCAG CCACGCTTCAAC CCTTCTC	G	A				SILENT- NONCODI NG		
5271- 5272	cg43989459	265	GCAGGTGTATCT GCACAGTGGTC GC[C/T]CCACAG CAGACCATGTGT TCACGGG	C	T				SILENT- NONCODI NG		
5273- 5274	cg43990145	285	CCTTGAATTCCA GAAGAAGGAAGA A[A/G]CCTTATGT CTAGCAGTCTGA GCCTG	A	G				SILENT- NONCODI NG		
5275- 5276	cg43990145	513	CCCTGTCTCTAG AAAGAAAAAAA Algap[A]GGAAC GTGTGAGAGGAA ATTCATG	-	A				SILENT- NONCODI NG		

5277- 5278	cg43990709	196	CACGTTTTCCAC TGACATAAAGTT G/C/TTTCGCCCC TTGCAGCTTATC TCCAC	C	T				SILENT- NONCODI NG			
5279- 5280	cg43990709	201	TTTCCACTGACA TAAAGTTGCTTC G/C/GCCCTTGC AGCTTATCTCCA CCITCA	C	G				SILENT- NONCODI NG			
5281- 5282	cg43991361	1679	AACCTTCGAGAT ATGACTGGCCGC C/G/AJAGCTTCTC TGCTTCTGCATA AAGGT	G	A				SILENT- NONCODI NG			
5283- 5284	cg43991427	999	CTGGTCATATGT GACGAGGGACA CA/G/TGCTCAAG AACTCTGAGAAT CAGACT	G	T				SILENT- NONCODI NG			
5285- 5286	cg43991837	372	GAGTATCAACTA CACATTTTTTTT T/gap]CAAGCAG CATATTATTATAA AGCCC	T	-				SILENT- NONCODI NG			
5287- 5288	cg43991837	651	TTTTAATTGCTTT TTTAGGAAAAAG[A/gap]AAAAAAA AGGTGCTTTTAA TACTT	A	-				SILENT- NONCODI NG			
5289- 5290	cg43992019	642	CGGAAGCTTTTT TCTCAGGAGGTA AT/AJCTCTAATA ACAAGCAGAGTG CCCTC	T	A				SILENT- NONCODI NG			
5291- 5292	cg43992019	769	ATCCCAACACAC AGCCAGTCAACG A/G/gap]CCTCTG GCCCTTCCTCT GGGTCCT	G	-				SILENT- NONCODI NG			

5293-5294	cg43992029	319	GGGGCAGCTAC AGGGTTCAGCTC TG[G/A]GCAGGG CTTGGCCAGGG ACAGTGTG	G	A				SILENT- NONCODI NG		
5295-5296	cg43992029	570	CGCACAGCCAG ACACACACACAC AC[A/gap]CCCTG CCACGCACAGCA CGCAGGCA	A	-				SILENT- NONCODI NG		
5297-5298	cg43992029	604	CGCACAGCACG CAGGCACACACA CA[C/gap]TTGTG CATGCACACGCG TTCATATA	C	-				SILENT- NONCODI NG		
5299-5300	cg43992178	216	ATAAACACGTAA GAGTAACACTTT G[C/T]ACTCCAAT AGCACCTGTTGG TCAAA	C	T				SILENT- NONCODI NG		
5301-5302	cg43992186	626	TGGCCTTGGTAA AGGAAATGACAC A[C/T]ATTCCCC AATTGGAAGCA ATCTT	C	T				SILENT- NONCODI NG		
5303-5304	cg43992349	1091	CAGGAGAGCTG CCTCATTAGACT TC[G/A]CCAGTG GCTCCAGGAGA CCCACAAG	G	A				SILENT- NONCODI NG		
5305-5306	cg43992349	1094	GAGAGCTGCCTC ATTAGACTTCGC C[A/G]GTGGCTC CAGGAGACCCCA CAAGGGC	A	G				SILENT- NONCODI NG		

5307-5308	cg43992349	1210	CAGAGAGATCAT GTGTCAGTCTTT G/A/GJCGTGGAG AAAGCAGCATCA GGTAGA	A	G			SILENT- NONCODI NG			
5309-5310	cg43992895	1776	GCACCACCACAC CCGGCTAATTTT TTT/GJATATCTTT AGCAGAGATGG GGTTTC	T	G			SILENT- NONCODI NG			
5311-5312	cg43993206	1428	ATGTGTAGAGTA GATTGTCTGGTG CT/CJCTCAGTTG TTTTTATTTACAT TTGT	T	C			SILENT- NONCODI NG			
5313-5314	cg43993206	524	CTAACCAGCGT ACGACAACCTGGT G/A/CJAAACAAAC TCAAGTGCAAAG GAAAC	A	C			SILENT- NONCODI NG			
5315-5316	cg43993218	1043	CTTTCTGTCAG CAAAAAAGGTAC A/A/TJTTTTTTTAA AACTTGAAAATC AATA	A	T			SILENT- NONCODI NG			
5317-5318	cg43993644	250	TGAAGCAGCCC GAAAACAAGTGA AA[gap/A]GGAAA CCAAGATAACTC TCTCTCCC	-	A			SILENT- NONCODI NG			
5319-5320	cg43993836	672	ATAGCCCGGGC AAGCGGCACCC AGG[G/A]GAGCC TCGACACAGGTA GTGACCTG	G	A			SILENT- NONCODI NG			

5321- 5322	cg43993844	1286	GTGCACTTCTCG CCGGGGGCCCCG GGC/G]GCTCAC CACACCTGCAGT GCATGTC	C	G				SILENT- NONCODI NG			
5323- 5324	cg43993844	1655	GTGGCTGATGGT GGACACTGTCAT A[G/A]GAGAAGG AGAGTTTGGGA AGTGTA	G	A				SILENT- NONCODI NG			
5325- 5326	cg43993844	845	GGTGACCCCG CATGCACTGCAG CC[C/gap]TGATG GCGAGTGGCTG GTGCCTGTA	C	-				SILENT- NONCODI NG			
5327- 5328	cg43993862	346	AGGCTGGAGTG AAGTGGCAGGAT CC[C/]GGGTCA CTGCAACCTCTG CCTCCCG	C	T				SILENT- NONCODI NG			
5329- 5330	cg43993862	556	CCTGGGCTCCC AAAGTGCTAGCA TT[C/]ACAGGCGT GAGCCACCATGC CTGGC	T	C				SILENT- NONCODI NG			
5331- 5332	cg43994222	151	GAGAAACGCAG GTTGCTGCCGTGG TT[A/gap]AAAAAA ATATTGGAGAT CATCCCTA	A	-				SILENT- NONCODI NG			
5333- 5334	cg43994222	158	GCAGGTGCTGCA GTGGTTAAAAAA A[A/gap]TATTTGG AGATCATCCTAT TCCACA	A	-				SILENT- NONCODI NG			

5335-5336	cg43994222	326	CGAGTCAGAAGC CAAGTATCTTCA A/G/AJACCTTCTC ATGGAGAGTGTG AATT	G	A				SILENT- NONCODI NG			
5337-5338	cg43994840	281	CACAGCAAGTCC GATGAGTCCGG CC[A/T]GTCCCG CCACACCCAGG GCCATGCC	A	T				SILENT- NONCODI NG			
5339-5340	cg43994860	908	TTTGAAGAAAT AAAAAGAAAAA A[gap]/AJTGAAGT CTCTTGCTCTCA TGTTGAA	-	A				SILENT- NONCODI NG			
5341-5342	cg43994987	774	CTTGAAAAGGTG CTAAGATTGGTT T[C/T]TGTTAACA TCAAAAAA AACAG	C	T				SILENT- NONCODI NG			
5343-5344	cg43995124	399	AAGAGGCTTTGA AAATGTAGAACT G[G/gap]GAGTCA TAGGAAAAAAGA AGAAAGT	G	-				SILENT- NONCODI NG			
5345-5346	cg43995124	400	AGAGGCTTTGAA AATGTAGAACTG G[G/gap]AGTCAT AGGAAAAAAGAA GAAAGTC	G	-				SILENT- NONCODI NG			
5347-5348	cg43995294	902	AAAAAGGTACAT CAGAAACAGAAA CIA/GITGCTACTA TCAGGGCAACTG AGCTT	A	G				SILENT- NONCODI NG			
5349-5350	cg43995376	1299	GCCATGCTGTG GTAGAGGGTGA GT[A/C]JAGAGGC CAGAGCTGAGG GTGAGGIG	A	C				SILENT- NONCODI NG			

5351- 5352	cg43995405	988	CTGCCGGTGGCC AGGGCCGTGAG TCC[C/T]GTGGCA GAGCCTTCTGGG CGCTGCG	C	T				SILENT- NONCODI NG			
5353- 5354	cg43995405	1135	CTCTCGGTCCGG AACAAAGACGCCT C[A/G]GCCACGG CTCCCCCTCGGC CTATTA	A	G				SILENT- NONCODI NG			
5355- 5356	cg43995405	389	TACATTGCCAGC TGGAAAGGCCT GGT[C/C]CAGGTT CTGAACAGCCTG GGCACC	T	C				SILENT- NONCODI NG			
5357- 5358	cg43995405	724	ACGCCCTCGCTG GCCGCCCTACCAC CC[C/gap]TGGT CGTGCGCCGTG CCGTCACCG	C	-				SILENT- NONCODI NG			
5359- 5360	cg43995405	739	CCTACCACCCCT GGTCGTGCGC CGT[C/C]GCCGTC ACCGTGGCCTTC TGCACGC	T	C				SILENT- NONCODI NG			
5361- 5362	cg43995762	733	GCACCCTAACAC CCCGACTGGTGT T[G/C]CTGGGTC CCTAACATTGTC TGTACC	G	C				SILENT- NONCODI NG			
5363- 5364	cg43995779	317	AAGGACTGCCCC ACAGGAAACCTG A[A/C]CGTGGAC GAGTTCAAGAAG ATCTAC	A	C				SILENT- NONCODI NG			

5365-5366	cg43996227	1000	CCCATCTATATA CAGATGTGGCAT G[G/gap]CTCTGC CCTGGCACAGC CAGCTGGC	G	-				SILENT- NONCODI NG			
5367-5368	cg43996227	1441	TGTGTCAGGCCA GGGAGTCCCTG GC[C/gap]TGCCC TGGATAGAGTGG AGGGCCCT	C	-				SILENT- NONCODI NG			
5369-5370	cg43996450	295	ATTAAAGAAAGAA GAAAGAAAAAA A[gap/A]CAACCA AAAACCTGGAGA ATAAACA	-	A				SILENT- NONCODI NG			
5371-5372	cg43996554	621	AAGGAAGAAAGA AAAGAAAAAGAA G[A/gap]AAAAA CGGAAGCACAAA TCTTCCA	A	-				SILENT- NONCODI NG			
5373-5374	cg43996590	227	GAGCCCGGCCT TACCTGGGTAG GG[C/G]GTGAG TCCGTCCTCATT GCACAAA	C	G				SILENT- NONCODI NG			
5375-5376	cg43996743	617	AGCAAGGGCAC AGAGTCACCAA AC[C/T]TGCCCA ACAATCCCCAGA CAATAT	C	T				SILENT- NONCODI NG			
5377-5378	cg43996869	1106	TCTATCATAAGA ATGTGAACGAGG C[T/C]GAAGATCT CTGGACCAAGAT CTTGA	T	C				SILENT- NONCODI NG			

5379-5380	cg43997723	481	GCGCGCGCGG CCCACGGAGGA CCC/C/TACTCA ACGTGTAAACAG AAACAGA	C	T				SILENT- NONCODI NG		
5381-5382	cg43997723	639	TGGCCCTGCGT GGCCAGCAGGG CC/G/A/GCTCCT CCGAGGGCTCC CTGCCTTG	G	A				SILENT- NONCODI NG		
5383-5384	cg43997865	487	CCGGCTCCAGC AAGAGTCCAGC CA/C/TCCCCCG GCTCCTGGGTGT GCACCA	C	T				SILENT- NONCODI NG		
5385-5386	cg43997865	788	GTAGCGGCGGC GGCGAGCTCG GGC/T/C/CAGTT CTCGGCTCAGC GTCTCCTC	T	C				SILENT- NONCODI NG		
5387-5388	cg43998250	755	GAGAAGTCCCCA CTTAAAAA A/A/gap/TATCTG CAGTTTGAAGGG CAAAGGG	A	-				SILENT- NONCODI NG		
5389-5390	cg43998355	1583	CACCACTACACC TTGAGGGGAACA T/G/A/CAGTCATT TTCCCGGTACAG TCTGT	G	A				SILENT- NONCODI NG		
5391-5392	cg43998922	2634	AGGAGGGAGGA AAAGCTCCTAAT GG[G/gap]AGAGA AGGGTGCAGTAA GAGTTTAC	G	-				SILENT- NONCODI NG		

5393-5394	cg43998972	992	GTTTGGAGGATC ATCCAGGTCACA C[G]gapTTCTCAG GTAGAAATGCAG GGTTTGA	G	-				SILENT- NONCODI NG			
5395-5396	cg43999061	561	AGCAGATAGTTG TCAGAAAGTCAT A[A/C]AAAAACTG GCITTCAGGTCA TATAT	A	C				SILENT- NONCODI NG			
5397-5398	cg43999507	203	ATTCTAGAAAGC AAATAAAGTCAC T[C/T]TCTACAAT AAATAGAGCATC ATGTG	C	T				SILENT- NONCODI NG			
5399-5400	cg43999507	242	GAGCATCATGTG CTTCACAGCAGA C[G/C]CGACAGA GACACATAGGCC CCGTGC	G	C				SILENT- NONCODI NG			
5401-5402	cg43999507	287	CCGTGCCACAG CAGGATCTGAGC CGT[C/T]TCCCGT TCTAAAAGAGCA TTTTAA	T	C				SILENT- NONCODI NG			
5403-5404	cg43999507	292	CCACAGCAGGAT CTGAGCCGTTTC C[C/T]GTTCTAAA AGAGCATTTTAA AAAAT	C	T				SILENT- NONCODI NG			
5405-5406	cg43999507	307	AGCCGTTTCCCG TTCTAAAAGAGC A[T/G]TTTAAAAA ATGAGACTCAGA GAGAG	T	G				SILENT- NONCODI NG			
5407-5408	cg43999702	1061	AGTTGGCCTCG TTCTCCCGCTCC C[G/A]CTGCTCAT CGGAGTGGCCT GGCTGG	G	A				SILENT- NONCODI NG			

5409-5410	cg43999702	758	ATGCATGCTGGA CGGTTCTCCAAA T[Agap]AAAAAA GCCCAAGGGTT TGCTAC	A	-			SILENT- NONCODI NG		
5411-5412	cg43999766	1224	CAGGCTTTACCA AGACCTTGTTA A[G/A]TCCAGTC ACATTTACTTTCT GTCT	G	A			SILENT- NONCODI NG		
5413-5414	cg43999810	479	CATGAAGATGTG GACTTTTTTTTT [T/gap]GAGACAA GAGCCTCACCCCT GTCGCC	T	-			SILENT- NONCODI NG		
5415-5416	cg43999946	348	AAGGTACCACAG CAGGTTATGGTT C[A/G]TACAGGA CTTTAAATGACC CATGTT	A	G			SILENT- NONCODI NG		
5417-5418	cg43999946	388	TGACCCATGTTG ACAATACAATTT G[C/T]AAAAATA TGAGAAAAGCAA TACAT	C	T			SILENT- NONCODI NG		
5419-5420	cg43999946	418	AATATGAGAAAA GCAATACATATT T[C/T]TGAAACAA AAACATACCTGT TGTA	C	T			SILENT- NONCODI NG		
5421-5422	cg43999946	488	CAGAATAGAACA GTTAACAGAGCA G[C/T]AGTTACTG AAGACAGACGG CAACAG	C	T			SILENT- NONCODI NG		
5423-5424	cg43999946	505	CAGAGCAGCAGT TACTGAAGACAG A[C/T]GGCAACA GGCAGCTGCGC CAGCCAT	C	T			SILENT- NONCODI NG		

5425- 5426	cg44000241	413	CTCCCTCACGGA GCCAGCGCCG GG[A/gap]ATGCA GACATCAGAACG TGAGGGGA	A	-			SILENT- NONCODI NG			
5427- 5428	cg44000319	578	AAC TTGAAAGAC AGATTAAAAAA A[gap]A]CTTTTG GCAATAATTAG AATAAT	A	A			SILENT- NONCODI NG			
5429- 5430	cg44000319	686	TGCAGGGAGCT CTTCTAGGTACT TA[G/A]CTGTTTT TAAGGTCTGCAC TTTACC	G	A			SILENT- NONCODI NG			
5431- 5432	cg44000319	826	AACATAATTACA ATTCTGATTATA G[C/gap]ACAGAA CCAGAGATGGCA AACTGAC	C	-			SILENT- NONCODI NG			
5433- 5434	cg44000319	847	ATAGCACAGAAC CAGAGATGGCAA A[C/T]TGACGACC CAAAAGCAGAGC AGGAA	C	T			SILENT- NONCODI NG			
5435- 5436	cg44000399	1278	GCCTTCAATGAT CTCACTTGCTTT C[C/T]CAGGTCG CTGAGAGTCCCA CCATGT	C	T			SILENT- NONCODI NG			
5437- 5438	cg44000405	316	CCCTTCTAATCT GAGGAAACTAAG C[G/A]TGAAAGAA TGTGAGCATGCA TAAAA	G	A			SILENT- NONCODI NG			

5439-5440	cg44000405	478	GAGTGTGTTT TAACCTCTGTAC A/G]TATTTAGA CCAGTAAATGC AGAA	A	G			SILENT- NONCODI NG		
5441-5442	cg44000551	548	CCAGAGGTTGCA ATAGAGAGACAA A/G]AATGCTCT CTCCCTAGATG CCAAG	G A	A			SILENT- NONCODI NG		
5443-5444	cg44000551	626	TGTCAGCCTAGG AATGAAGAACCA A/G]AAAAAGAT CAAACTGAGTGC CACAA	G	A			SILENT- NONCODI NG		
5445-5446	cg44001055	2038	GTTGACTGAACT CTGGAAGAGAA A/C]TAGCAGCTG ATCCTGACTGCT TTTGT	C	T			SILENT- NONCODI NG		
5447-5448	cg44001055	2071	GATCCTGACTGC TTTTGCTGTCTAT A/G]TTTCCAGAA CTCTGGACTGTC TGGT	A	G			SILENT- NONCODI NG		
5449-5450	cg44001055	2079	CTGCTTTTGTCT GTCATATTTCCA G/A/G]ACTCTGG ACTGCTCTGGTTG AATTGT	A	G			SILENT- NONCODI NG		
5451-5452	cg44001055	2080	TGCTTTTGTCTG TCATATTTCCAG A/A/G]CTCTGGAC TGCTCTGGTTGAA TTGTC	A	G			SILENT- NONCODI NG		
5453-5454	cg44001055	2101	CAGAAGCTCTGGA CTGCTCTGGTTGA A/T/C]TGTCTGGAG GATCTCTCTGTTG CTTTC	T	C			SILENT- NONCODI NG		

5455- 5456	cg44001055	2116	TCTGGTTGAATT GTCCGAGGATCT CTTCJCGTTGCTT TCTGACGTACCA GGTGT	T	C				SILENT- NONCODI NG			
5457- 5458	cg44001055	2170	GAGCGGCACGC TTCTGGGTCCTC ATTA/GJGGGTG CCCTTGTTGAGA TGCTGGG	A	G				SILENT- NONCODI NG			
5459- 5460	cg44001076	176	CAAAGCCTGTAG TTGCTGCTTCTT GG/AJTTGGAAG ATTCTGGACAGC CTGAAA	G	A				SILENT- NONCODI NG			
5461- 5462	cg44001185	222	TATTGGGGGATG TCAGCAGAGAAC GTTCJGGGACAT GAAAACAAGTCT TAGGAG	T	C				SILENT- NONCODI NG			
5463- 5464	cg44001185	706	CAAGACCCAAAGC CTTGACCCCTAAG T[A/gap]ACAGAT GCAAGGATCACG AACAAACC	A	-				SILENT- NONCODI NG			
5465- 5466	cg44001210	852	TGGGTATGGGG CCGTTGGCCCG GGG[C/T]CCGGA TATGGTGGAGG GTTCCTCTTG	C	T				SILENT- NONCODI NG			
5467- 5468	cg44001481	385	ACCTGATGAAT TATTTTAAAAAG [T/A]TTATATTCC ACAGAGTTTCAG TTTC	T	A				SILENT- NONCODI NG			

5469-5470	cg44001539	1485	GAGCGGGTCGG CCGTGCGGACC CCG[C/A]TGAAG AACAGCATAACA GCCGAGTC	C	A			SILENT- NONCODI NG			
5471-5472	cg44001588	346	AACAATAACAAC AACGACGAGGG TC[G/T]CTGTGAA GCTGAAAGTTGC AGAGTG	G	T			SILENT- NONCODI NG			
5473-5474	cg44001596	1064	CAATCCCAGCAT AGCACACACCCAC C[A/G]TATAGACG ATCCATTATCAT CGCAA	A	G			SILENT- NONCODI NG			
5475-5476	cg44002106	324	CCCGGGGAAGA GACGGCATGAAT TC[T/A]AAGAGTG CCCAGGGTCTG GCTGGTC	T	A			SILENT- NONCODI NG			
5477-5478	cg44002106	390	ACACGTGCTTCA TGAACCTCAATTC T[G/T]CAGTGCCT GAGCAACACCC GGGAGT	G	T			SILENT- NONCODI NG			
5479-5480	cg44002106	396	GCTTCATGAAC CAATTCTGCAGT G[C/T]CTGAGCAA CACCGGGAGTT GAGAG	C	T			SILENT- NONCODI NG			
5481-5482	cg44002106	411	TTCTGCAGTGCC TGAGCAACACCC G[G/C]GAGTTGA GAGATTACTGCC TCCAGA	G	C			SILENT- NONCODI NG			

5483- 5484	cg44002106	456	TCCAGAGGCTGT ACATGCGGGAC CT[G/C]GACCAC AGCAGCAGTGCA CACACAG	G	C				SILENT- NONCODI NG			
5485- 5486	cg44002106	483	ACCACAGCAGCA GTGCACACACAG C[C/T]CTCGTGA AGAGTTTGCAAA ACTAA	C	T				SILENT- NONCODI NG			
5487- 5488	cg44002106	487	CAGCAGCAGTG CACACACAGCCC TC[G/A]TGGAGA GTTTGCAAACT AATCCA	G	A				SILENT- NONCODI NG			
5489- 5490	cg44002125	1264	GGCCGTTCTCCT GGAGGAGGATT CT[C/T]GCCACCT GCTGGCCCATGAA GCTGGA	C	T				SILENT- NONCODI NG			
5491- 5492	cg44002131	511	ACTCCAGAGGCA GAGTGGGACCT GG[G/C]CTCCCG AGGGCAGACCG CAGCAGAG	G	C				SILENT- NONCODI NG			
5493- 5494	cg44002131	517	GAGGCAGAGTG GGACCTGGGCT CC[G/C]JAGGGC AGACCGCAGCA GAGACCCCA	G	C				SILENT- NONCODI NG			
5495- 5496	cg44002258	914	GCAAGTAACACT GAATGTCCAAAA AT[C]ACGGCTGT GTTAAACTAACA AGCCA	T	C				SILENT- NONCODI NG			

5497- 5498	cg44002457	636	GAGGAAGTGTCA GCAACATGAAA A[A/gap]GCAAAT CCGGCCATAACT ATATAGA	A				SILENT- NONCODI NG			
5499- 5500	cg44002457	703	TCAGCCACGTA CCCGTAGATAAA T[C/T]CAACTATT GCAGAAAAAAGA ATAAT	C	T			SILENT- NONCODI NG			
5501- 5502	cg44002457	795	CCATCTGCGTGG GCAGCGAGCTC AG[A/G]TGCTCCA GCATGGCTGGCT GAGGAG	A	G			SILENT- NONCODI NG			
5503- 5504	cg44002584	380	TTAGCGTAGGCT GCTGCTGCTGCT G[G/A]CCTGGGA GCTGCCCATACC TGGGTG	G	A			SILENT- NONCODI NG			
5505- 5506	cg44002584	783	TCAGGCAGGAA GTTACTTAGCTT CT[C/T]CTTCACC TTCTTCCACAG AATTTA	C	T			SILENT- NONCODI NG			
5507- 5508	cg44002588	872	TCTGTCTATGGC AATAATACGATG C[A/G]TATTGAGA AACTGCTTCAAA GATGG	A	G			SILENT- NONCODI NG			
5509- 5510	cg44002594	3440	CGCCTGGCCGTT GGCGCTGCCCA GC[C/T]GCCTGC AGATCAGGCTCT GGATGCC	C	T			SILENT- NONCODI NG			
5511- 5512	cg44002594	434	CCCCATCCAAGG AATTGTGGCATC T[C/T]GGAGGGC TGGACCGGCAC ACGCCGG	C	T			SILENT- NONCODI NG			

5513-5514	cg44003017	1726	CATCTATTGAAT CTTTGGCTTTGT C[G/A]TTGCAATG CATGGTGCACCG GGCCA	G	A				SILENT- NONCODI NG			
5515-5516	cg44003017	1751	GTTGCAATGCAT GGTGCACCGG CC[A/G]GGCGGT CCTGGAACTTCT CCAGCTC	A	G				SILENT- NONCODI NG			
5517-5518	cg44003792	750	TGCCAGGGAAG GAGGACCTATA GG[G/gap]TGCC AGCAAAGGGCC ACTGGCGGT	G	-				SILENT- NONCODI NG			
5519-5520	cg44003959	1466	GCCCCCTCCAC TCTGCAGGGCCT C[C/A]ACACGA CAGGGGGCCG CGACGGA	C	A				SILENT- NONCODI NG			
5521-5522	cg44004084	251	TCACCATGTTGC CCAGACTGGTCT T[G/A]AACTCCTG GGCTCAAGCAAT CCATC	G	A				SILENT- NONCODI NG			
5523-5524	cg44004084	261	GCCCAGACTGGT CTTGAACCTCCTG G[G/C]CTCAAGC AATCCATCCACC TTGGCC	G	C				SILENT- NONCODI NG			
5525-5526	cg44004084	274	TGAACTCCTGG GCTCAAGCAATC C[A/T]TCCACCTT GGCCTCCCAAAG TGCTG	A	T				SILENT- NONCODI NG			

5527- 5528	cg44004120	470	GGACTTCCTATG TCACITTTCCAAG G[G/gap]CTTCAG CCCACCTTGAAGG GCCAAGG	G	-				SILENT- NONCODI NG			
5529- 5530	cg44004303	485	AGGGTGTAGTCC ACCCGCCAGCC CA[C/gap]ACCTG CCAACCTATTCA TGCGTAGG	C	-				SILENT- NONCODI NG			
5531- 5532	cg44004427	388	ATCCCTGAATTA ACAAGCAGCCAG T[G/C]GCGAGTG TTCATGATAAAA CTGAAT	G	C				SILENT- NONCODI NG			
5533- 5534	cg44004474	172	CCGAGGATTGAG AGCTCCCAATAT T[C/gap]TTTTGGA GAATAAGCAGTA GTTTTGC	C	-				SILENT- NONCODI NG			
5535- 5536	cg44004688	376	GCCTGTCAGCTG GTGGGCAGCCC TG[G/A]AGTGTG GATGGAAGAACA GGCATGC	G	A				SILENT- NONCODI NG			
5537- 5538	cg44004731	2145	CTGTGGGTCTTC TTTTTCTGTGG C[A/T]AATTCACC TTCTCAAAAACA ACAGG	A	T				SILENT- NONCODI NG			
5539- 5540	cg44004731	2146	TGTGGGTCTTCT TTTTTCTGTGGC A[A/T]ATTACCT TCTCAAAAACAA CAGGT	A	T				SILENT- NONCODI NG			

5541-5542	cg44004731	2147	GTGGGTCTTCTT TTTTCTGTGGCA AATTTTACCTT CTCAAAAACAAC AGGTT	A	T				SILENT- NONCODI NG			
5543-5544	cg44004731	236	AAGTTTCTTGT CTGAATTTTCAA GT/GJGGGTGA ACAATGACTGAG AGGAAA	T	G				SILENT- NONCODI NG			
5545-5546	cg44004823	232	GCTGCCACAGTC CTGACCCCTGGCC CT/CJGCTGGC AATGCCCATGCC TGCTCC	T	C				SILENT- NONCODI NG			
5547-5548	cg44004831	367	GGACTCACCCAA CAAAATGTGCTC T[G/A]TTAACACA ACCAGCAGTACA ATCAT	G	A				SILENT- NONCODI NG			
5549-5550	cg44005101	1800	AGTGCCCTTTGA GGCAAATCCATA C[G/C]TCGTCGG GGAGCAAAGGAT TGCTGA	G	C				SILENT- NONCODI NG			
5551-5552	cg44005101	1803	GCCCTTTGAGGC AAATCCATACGT C[G/C]TCGGGA GCAAAGGATTGC TGATCT	G	C				SILENT- NONCODI NG			
5553-5554	cg44005101	1806	CTTTGAGGCAAA TCCATACGTCGT C[G/A]GGGAGCA AAGGATTGCTGA TCCTCG	G	A				SILENT- NONCODI NG			
5555-5556	cg44005150	313	ACACTGAAATCA GAGCCTGCACAC A[G/A]AGCAGCA GATGCTTCAATG TAAAGG	G	A				SILENT- NONCODI NG			

5557-5558	cg44005150	333	ACACAGAGCAGC AGATGCTTCAAT GTT/CJAAAGTCA TTTCCAGGTCCT TGACA	T	C				SILENT- NONCODI NG			
5559-5560	cg44005468	307	CCAGGAGTCAC GGATGGGAAAGT AAJ/GJCTTTGG AGGGGCTGGGA GCTGGGG	A	G				SILENT- NONCODI NG			
5561-5562	cg44005989	642	TCTTGGCCGCAG ACTGAGCCTGTA C/C/TTCACCCGT CTCCACCAACT CTTGG	C	T				SILENT- NONCODI NG			
5563-5564	cg44006130	5030	AATGGCAGCACT TCCGAGAGTGG CA/C/TJAGAGTCT GTTGTGGCCAG CACAGG	C	T				SILENT- NONCODI NG			
5565-5566	cg44006486	287	CTCCCTCACTCA TTCATTATTCACA [C/A]JAGAGTATAT AACAGTTTTTTTT TTT	C	A				SILENT- NONCODI NG			
5567-5568	cg44006536	341	TTATGGTTTCGA CTAACATTAAGT A/T/CJACCCTTTT TTGAATCAACAG GATGA	T	C				SILENT- NONCODI NG			
5569-5570	cg44006660	463	AAGACCTGTGGA GACCATCATCGA G/G/gap CCATGG CCCCACATCTGT GATATGG	G	-				SILENT- NONCODI NG			
5571-5572	cg44007198	670	TTATAACAACAT GATCCCCACAGT C/A/GJCTCAGTG CATGGTACACAG GTTTAT	A	G				SILENT- NONCODI NG			

5573- 5574	cg44007371	81	GTACAGTGGTAA TCCTTCCATCAT A/C/TAGGTAATA TATAATAACATTG AAAA	C	T			SILENT- NONCODI NG			
5575- 5576	cg44007434	650	TATGGACCCCTG ACCCCGCGGG TC[G/A]TTCGGAC TCTTAACGTGTG GACTGA	G	A			SILENT- NONCODI NG			
5577- 5578	cg44008138	404	TGCTGGTTTAAT ATAATTAGTATAC [T/G]AAATAGTTT TCTGCATTTATTT GGT	T	G			SILENT- NONCODI NG			
5579- 5580	cg44008187	672	GTGCAGGTCCCA CACACAGGCCAA A[A/gap]GCTCTA GCTTTGGCCTGG AGGCAGC	A	-			SILENT- NONCODI NG			
5581- 5582	cg44009119	418	AGGTGGTGGAG TCTGAGATTTAG AG[G/gap]CTGAG CCTTTGGGGGTG GGGGCAGA	G	-			SILENT- NONCODI NG			
5583- 5584	cg44009213	829	TAATACCCTCCC CCATCCTTAACT CT[C/J]AGAACCCC GGTTGGTGGG GAGGAG	T	C			SILENT- NONCODI NG			
5585- 5586	cg44009645	5420	GCAGAGTGGTG GCAATGTCATGT GG[G/gap]CACAT GCCCGTCGCTCT GCTAATTG	G	-			SILENT- NONCODI NG			

5587- 5588	cg44009958	974	CCAAAAATACCA TATGCATTTCAG GT/CJGTCAATCA TTATCTCTCAGT CACAA	T	C			SILENT- NONCODI NG			
5589- 5590	cg44010401	208	AGTCTGTTTTTG AAACAGCTTTCC A/C/TTCATCTC CCTTCTGGGGC TCAGG	C	T			SILENT- NONCODI NG			
5591- 5592	cg44010528	549	GGCATGGATGAT ACCTCTCTTCAG G/C/gap/GCTCCA TGGCGCTCTTGC TGCCAGC	C	-			SILENT- NONCODI NG			
5593- 5594	cg44010528	826	CTGGAGCCAGG GGTGTGCTGG GAG/C/TJAGGG CGATGGGTTTGT AGGACATC	C	T			SILENT- NONCODI NG			
5595- 5596	cg44010626	505	GGGCTGGGGCT GGGCCTTCCAAG AC/G/CJATCGACA GAACCACCAACA GGACCG	G	C			SILENT- NONCODI NG			
5597- 5598	cg44010683	1046	ATTCCTTTGGTCT GTTGTCATCCCTI C/TJACGAGCGGA GAATATTAACCA TATT	C	T			SILENT- NONCODI NG			
5599- 5600	cg44011509	1825	ACAAGCCACTGG ATCTGTCCGATT C/C/TJACATTGTC TTACACTGAAAC GGAGG	C	T			SILENT- NONCODI NG			
5601- 5602	cg44011509	1846	ATTCCACATTGT CTTACACTGAAA C/G/CJGAGGCTA CCAACCTCCCTCA TCACTG	G	C			SILENT- NONCODI NG			

5603-5604	cg44011509	1852	CATTGCTTTACA CTGAACGGAG GCT/CJACCAACT CCCTCATCACTG CTCCGG	T	C			SILENT- NONCODI NG			
5605-5606	cg44011509	1891	TCACTGCTCCGG GTGAATTCTCAG A/C/TGCCAGCAT GTCTCCGGACG CCACCA	C	T			SILENT- NONCODI NG			
5607-5608	cg44011509	1909	TCTCAGACGCCA GCATGTCTCCGG A/C/TGCCACCAA GCCGAGCCACT GGTGCA	C	T			SILENT- NONCODI NG			
5609-5610	cg44011594	145	TGTCACCTCATTC TTATCACTCTGT CT/CJTCTTGGT CCAACCCATCAG CTGGC	T	C			SILENT- NONCODI NG			
5611-5612	cg44011736	566	CCACGTGGGGC TCAGACGGGCAT TG/T/AJGCTGCTC TGGGAGGCAAG TCCATGG	T	A			SILENT- NONCODI NG			
5613-5614	cg44012172	31	GAACGCCGGCT CTTCGCCCTCTCA GC[G/gap]GCGGC TTGTCCTTTGTT CCGGACGC	G	-			SILENT- NONCODI NG			
5615-5616	cg44012500	533	GTAACCTGGAGAG AGATTCTTTCAC CT/CJGGGTGAG GAAGTCCGGC TAGGCAT	T	C			SILENT- NONCODI NG			
5617-5618	cg44012840	1068	ACTTTCTGTCC CAATAATTGAGA G[G/T]GCTGTTTC ATTCCAAAAA GGGAA	G	T			SILENT- NONCODI NG			

5619-5620	cg44012840	1437	CAGTGAATCTAT GAATTGTTTAAG A[G/C]AAAGGTCA CTCCGTTACTGA CTTCT	G	C				SILENT- NONCODI NG			
5621-5622	cg44012840	1475	GTTACTGACTTC TGCTACATCTAA T[A/T]TCCAGGG AAGTAATATTTA GAGAT	A	T				SILENT- NONCODI NG			
5623-5624	cg44012940	1427	GTGAGCCTCCAG GATTCAGGGTT C[T/C]GGGGAGG ACAGATTGCTC GGGGTG	T	C				SILENT- NONCODI NG			
5625-5626	cg44013863	1136	TGGTCCGACCGT GGATGGTGATT T[C/T]TCACTGAC ATGCCAGACATA TTACT	C	T				SILENT- NONCODI NG			
5627-5628	cg44013918	156	TTCAAAGTCTCT ATCCCTATCCCA G[A/T]TAGGCCAC TTGGCCCAGGG CAGGGC	A	T				SILENT- NONCODI NG			
5629-5630	cg44014420	316	TCCTCTTCATTT GACCCAAAATAT C[C/gap]TGGGAG GTCCAGCATCCT CTGCTCA	C	-				SILENT- NONCODI NG			
5631-5632	cg44014643	1165	CACCACGCGTGT GAGGTGGGTCC CA[G/gap]AGGGG GGCCCCAGATG GGCCCCAGTC	G	-				SILENT- NONCODI NG			

5633- 5634	cg44014643	1172	CGTGTGAGGTG GGTCCAGAGG GGG[G/gap]CCCC AGATGGGGCCA GTCCTGTGAG	G	-				SILENT- NONCODI NG			
5635- 5636	cg44014643	1340	GGGGCTGGAGG TGCCCCCGGC ATGTCJTTTG TGGCAACACTGA TAACCTA	T	C				SILENT- NONCODI NG			
5637- 5638	cg44014666	14	CGGAGATCTGCT GIA/CJCGCGTTCT ACCTTCCGGCC CGTGT	A	C				SILENT- NONCODI NG			
5639- 5640	cg44014666	133	GGCGGGCCCTT CGGGCGCCCGA GCC[C/gap]GCAA TGTCGGGGCCC AACGGAGACC	C	-				SILENT- NONCODI NG			
5641- 5642	cg44014666	142	TTCGGGGCGCC GAGCCCGCAAT GTC[G/gap]GGCC CCAACGGAGAC CTGGGGATGC	G	-				SILENT- NONCODI NG			
5643- 5644	cg44014666	460	AGGCTCTGGCCT GGGCACTCACC CC[C/gap]TGGCT TAGACACCTTCT CAAGGGCT	C	-				SILENT- NONCODI NG			
5645- 5646	cg44015725	717	AGCCCGGCTGA TGCAGGAGGAG GTG[C/A]GGAGG GTAGAGTGGTAC TACCTCCG	C	A				SILENT- NONCODI NG			

5647- 5648	cg44015725	796	CGGAGCGAGGA GGCAGCGCTTTT TTTgap/TJGGAGG CTTGGCTTCCCG TGGCTTC	-	T				SILENT- NONCODI NG			
5649- 5650	cg44016438	508	GTCTATGCAACA TCCTCCAGATAA TTC/TJCGCAACAT CACTGAGCTGG GATACA	C	T				SILENT- NONCODI NG			
5651- 5652	cg44016438	518	CATCTTCCAGAT AATCCGCAACAT C[A/G]CTGAGCT GGGATACAGTCA GATCTT	A	G				SILENT- NONCODI NG			
5653- 5654	cg44016639	417	CTCTCCACGTAC TGCACAGGCTT GG/TJCCCGCCC TCACCGGCTGG GCCACCA	G	T				SILENT- NONCODI NG			
5655- 5656	cg44017116	349	AAGTCCTGATAA TGATCATCACTT TTC/TJTAATGAG AGGCTTTGAGGA AGATG	C	T				SILENT- NONCODI NG			
5657- 5658	cg44017116	551	GAATAAAAAATA ATTAAAAAATA [A/gap]CCTAATT GTACAAGCTACA CTGTGT	A	-				SILENT- NONCODI NG			
5659- 5660	cg44017354	687	GCCAGAGCTGG TGCCAGGGCTG AGG[C/gap]CCAA GCCAGAGCCGA GCACAGAAAC	C	-				SILENT- NONCODI NG			

5661- 5662	cg44018484	3085	CCATTGTCACCT CCTCTCAGGTTT TTT/C]GATGAAGT CATCTAGTTTCA TCCTT	T	C			SILENT- NONCODI NG			
5663- 5664	cg44018633	263	CCAAAGAAGCAC CAAGGGAGCATC T[G]gap]GACCCAC CAGGCTGCACAC CAACCCCT	G	-			SILENT- NONCODI NG			
5665- 5666	cg44018633	264	CAAAGAAGCACCT AAGGGAGCATCT G[G]gap]ACCACCT AGGCTGCACACCT AACCCCT	G	-			SILENT- NONCODI NG			
5667- 5668	cg44018633	400	TTTCCAGATCTTT CCAAAGCTGATA T/C]CAATGGCA GAATCCAAATAT CCAG	T	C			SILENT- NONCODI NG			
5669- 5670	cg44018633	409	CTTCCAAAGCT GATATCAATGGG C[A]G]GAATCCAA ATATCCAGGTCA CCATA	A	G			SILENT- NONCODI NG			
5671- 5672	cg44018634	458	GATTATAAGATG CTTCATCGGTTT A[G]T]GTTTACT ACCATATTAGTTT GTTT	G	T			SILENT- NONCODI NG			
5673- 5674	cg44019895	416	CTTTTAAAAAAA ATGAGGGCATAG T[G]GGGGGGGT AATAAAGTCTAC CTAGC	T	G			SILENT- NONCODI NG			

5675-5676	cg44019895	481	CAAAAGCATGGT TTCCATTGAATA A[G/A]ATTAAATA TATATAAAACAA GTACA	G	A				SILENT- NONCODI NG		
5677-5678	cg44020396	1361	GGCAGCCATGA GGATCCATGCCC AG[C/T]GTGGG TGGGACGAGGC ATGGGAGA	C	T				SILENT- NONCODI NG		
5679-5680	cg44020396	1390	GGGTGGGACGA GGCATGGGAGA ATA[T/C]GGAACA GCTTTCCTGGTG TCACGAC	T	C				SILENT- NONCODI NG		
5681-5682	cg44020396	1566	CTGCCCCAGGG CTCCTAGCTGCC AA[G/C]TGGCAG AGCAGGGGCCCG GCCCCAGA	G	C				SILENT- NONCODI NG		
5683-5684	cg44020396	1738	AGCTGTTCTTC TCAGCCTTCCGC C[G/A]GGCCAGC AGCTCCTCCTGC TCACGC	G	A				SILENT- NONCODI NG		
5685-5686	cg44020584	3045	GCAACTTCAAAC AGGTGGAGGCC GA[G/T]TTGATTG ACAAGCTGGACA GCATGG	G	T				SILENT- NONCODI NG		
5687-5688	cg44020584	3067	CGAGTTGATTGA CAAGCTGGACAG C[A/G]TGGTGCA GAAGGGAAAGG TGACGA	A	G				SILENT- NONCODI NG		

5689- 5690	cg44021710	102	AAGGGATTCTTC CTTTGAGAGAAG A/C/TATGGAGAG CGAGACCGTCGT GACAA	C	T				SILENT- NONCODI NG			
5691- 5692	cg44021758	1155	ACCTTCTCTCT GCTCCGGCTCA G[G/gap]CTCCGC GGCTGGCTCC AGCAGCCG	G	-				SILENT- NONCODI NG			
5693- 5694	cg44021807	95	AGGTTTCATCCA CATCTTCACATC TTC/TACCCCTCCC ACCGTCAAAACA GGTCC	C	T				SILENT- NONCODI NG			
5695- 5696	cg44022224	442	GACCAGCAACG CCCACGCTTCCT GG[G/gap]CTTTG CCTCGAGGATCC CCGGGGAC	G	-				SILENT- NONCODI NG			
5697- 5698	cg44023097	868	TGCCACGGACCT CACTCCGGCAGT G[G/A]CTGCAGT ACACGCCGAACT CGATCC	G	A				SILENT- NONCODI NG			
5699- 5700	cg44023097	880	CACTCCGGCAGT GGCTGCAGTACA C[G/A]CCGAACT CGATCCCCTTTGT GAGGGT	G	A				SILENT- NONCODI NG			
5701- 5702	cg44023097	883	TCCGGCAGTGG CTGCAGTACACG CC[G/A]AACTCGA TCCCTTTGTGAG GGTCAG	G	A				SILENT- NONCODI NG			

5703-5704	cg44023097	913	CGATCCCTTTGT GAGGGTCAGGA GG[A/G]CAGGAG ACAAACTTCAAC ACTTCAG	A	G				SILENT- NONCODI NG			
5705-5706	cg44023097	919	CTTTGTGAGGGT CAGGAGGACAG GA[G/C]ACAACT TCAACACTTCAG CTCGCT	G	C				SILENT- NONCODI NG			
5707-5708	cg44023097	930	TCAGGAGGACA GGAGACAACTT CA[A/G]CACTTCA GCTCGCTTCTCT CTCAGA	A	G				SILENT- NONCODI NG			
5709-5710	cg44023097	937	GACAGGAGACAA ACTTCAACACTT C[A/T]GCTCGCTT CTCTCTCAGACC CCAAC	A	T				SILENT- NONCODI NG			
5711-5712	cg44023776	1315	TACACAAAATGA TCATTCCATAAAT [A/C]TTTACATGA CAAGGGAAAAA TGGA	A	C				SILENT- NONCODI NG			
5713-5714	cg44023776	1393	GGTGTGATAATC CTTTCTCATGAC A[C/T]TTTAGTTA GGAATCATGCAA GCITT	C	T				SILENT- NONCODI NG			
5715-5716	cg44023776	1444	TAAAATGAAAAT AATTGTAGAAGC GT[gap]TAACATA AATATTCCATTTT AGTTT	T	-				SILENT- NONCODI NG			
5717-5718	cg44023776	1445	AAAATGAAAATA ATTGTAGAAGCG TT[gap]AACTAAA ATATTCCATTTTA GTTTT	T	-				SILENT- NONCODI NG			

5719-5720	cg44023776	1560	GTTTAATTTTCAGT TATCAGATCTTTI T/CJCTTCATCT CTCATGATGAAA CTAA	C			SILENT- NONCODI NG		
5721-5722	cg44023776	1710	CAGTTGTCCATG C CTCAAGGCATCT G/C/AJCTTCCTC GGAGTCGATCAT CACGG	A			SILENT- NONCODI NG		
5723-5724	cg44023776	1730	ATCTGCCCTTCCT T TCGGAGTCGATC A/T/CJACGGTAT ACTTTTGCTGCA TACTG	C			SILENT- NONCODI NG		
5725-5726	cg44023776	1895	GAAGTCCTTGTT A GACATAATAAAC A/A/CJACCCCAAG TTTTCTGTTTGA TTTT	C			SILENT- NONCODI NG		
5727-5728	cg44023886	609	TTCAGTGTAAC G TTGACACGTTCC G[G/gap]CTGCGA GCAGCCACGGG TCTGGTAC	-			SILENT- NONCODI NG		
5729-5730	cg44024241	517	GGGGGACTATG A AAATCCACGATG GGW/GJGAAAC TGGAGCTTTATT ATCAATA	G			SILENT- NONCODI NG		
5731-5732	cg44024241	591	CCCGCTTTCCTC C TCCCATCCTCAT C/C/TJCCACACT GGGATAGATGCT TGTTT	T			SILENT- NONCODI NG		

5733-5734	cg44024241	615	CCCCACACTGG GATAGATGCTTG TTT/CJTGTAAAA CTCACCTTAATA AAGAC	T	C				SILENT- NONCODI NG			
5735-5736	cg44024675	933	GTCACTGGAATT ATTATTATGAGA AT/CJGTCTTTGG GCCCCATTTGTG CCAAA	T	C				SILENT- NONCODI NG			
5737-5738	cg44025359	318	GGTTAGAGGAGA CAGAAAAACAAAG C/CJA/CAGCTCTT CCAAAGCTCACCA CCTAG	C	A				SILENT- NONCODI NG			
5739-5740	cg44025363	364	GTCAAGTTCATA TTGTATCACATT GTT/CJTGGTGGAT GACACTGGGCTCC AGATA	T	C				SILENT- NONCODI NG			
5741-5742	cg44025788	201	CTAATAGGAAAA CGAAGACCCCAAG AT/gapTTTTTTTT TAAATTAAGGT TATTTT	T	-				SILENT- NONCODI NG			
5743-5744	cg44026589	829	TGACACTGACTT TCTAAATATTCCA [G/C]AACTATTTT CCTGAACGTGAA GGTC	G	C				SILENT- NONCODI NG			
5745-5746	cg44026882	1328	TTTGTGAGATTCTT CTCAATAATTTT G/AJCCAAATCTG GTTGGCGTCATC TCAT	G	A				SILENT- NONCODI NG			
5747-5748	cg44027139	531	GTGCAGCGGCT CACACCTGTAAT CC/T/CJAGCACTT TAGGAGACTGAG GTGGGA	T	C				SILENT- NONCODI NG			

5749-5750	cg44027365	965	AGAAGTGCCCTA TCTGCAGACAGG C[G/A]ATCACCC GGGTGATACCCC TGTACA	G	A				SILENT- NONCODI NG			
5751-5752	cg44027572	117	CTGGATTAAAGG TCAGGGCCGGT GG[C/gap]TGTGG GAGGTGACACTG AGCCGCTC	C	-				SILENT- NONCODI NG			
5753-5754	cg44027650	1369	TTACAAGAGATT TCGACTGTGGAA GT[C/A]ACAAATA CTTTTAAGAAAA CAGAT	T	C				SILENT- NONCODI NG			
5755-5756	cg44029982	1121	GGGGTGCACAT CATCTGGTGGTG AT[G/C]GTGGCT GTAGGGGATGTT GGTCTCC	G	C				SILENT- NONCODI NG			
5757-5758	cg44030068	216	AGAAATATTCATT GAAGTTGATTAT A[G]GAGGAAAGA GGAAAGTTGGCA TATT	A	G				SILENT- NONCODI NG			
5759-5760	cg44030287	796	TTGCCCTTTTGAA GAAGAGCCCGC ATT[A]ATGAGTG GACGGCAGACA GCTATAT	T	A				SILENT- NONCODI NG			
5761-5762	cg44030433	1910	GATCAAAAGTCTA TTTTGCATAAAAT [G/C]TCCAATAAT TAAATATTGTTAT AAA	G	C				SILENT- NONCODI NG			
5763-5764	cg44030437	376	CAGCCTGCCACC AAGACTCAAGCA A[C/T]GTAAGAGT CATCTCCCCAGA CTGGC	C	T				SILENT- NONCODI NG			

5765- 5766	cg44030903	284	GGCGTTCGGGA AGGGCCGCGG CCG[G]ATCCGG GGCCGTGCGC TTGGGGGCC	G	A				SILENT- NONCODI NG			
5767- 5768	cg44031455	577	CCTGCTCCCCAA CTACAGCAGGGT CT[C]TGGGTCCT GGGTCTGAGGG TTTATT	T	C				SILENT- NONCODI NG			
5769- 5770	cg44031677	488	CCAGTGGCATTG CAGACTTCAGAT C[G]CCGGGA GTGGCCTGTACA GCAACC	G	T				SILENT- NONCODI NG			
5771- 5772	cg44032154	1138	GGCCTCTCTCTG CTACGGAGGG GG[G]GGAATC TAACCCCTCTGC CCTGGCT	G	T				SILENT- NONCODI NG			
5773- 5774	cg44032208	846	CATTTTATGTAC TCATCTGCTGTG[A/gap]AAAGTCTT TAGGTTCAATTAA AAAA	A	-				SILENT- NONCODI NG			
5775- 5776	cg44032208	848	TTTTATGTACTC ATCTGCTGTGAA[A/gap]AGTCTTTA GGTTCATTAAAA AAACA	A	-				SILENT- NONCODI NG			
5777- 5778	cg44032208	849	TTTTATGTACTCA TCTGCTGTGAAA[A/gap]GTCCTTAG GTTCAATTAAAA AACAG	A	-				SILENT- NONCODI NG			

5779-5780	cg440322208	904	TAGAAATGATCT TAGATCTAATATA [G/C]TGATTTTAA GCATCCCGTCAA AGGC	G	C			SILENT- NONCODI NG			
5781-5782	cg440322216	626	CTGAGTATTTTAT GCTATATGTGTG[T/gap]GAGTATAT ATATGTGTGTAT ATCTA	T	-			SILENT- NONCODI NG			
5783-5784	cg440322244	302	CTTGAGCCTGGG AGGTGAAGGTTG C/A/G]GTGAGCC AAGATCACGCCA CTGCAC	A	G			SILENT- NONCODI NG			
5785-5786	cg44034193	633	GGCCATCTCAG TGGGCTGGTACA C/A/G]CTGGTCA GCAGCTGCCCAT TGTACC	A	G			SILENT- NONCODI NG			
5787-5788	cg44034193	648	GCTGGTACACAC TGGTCAGCAGCT G/C/A]CCATTGTA CCCGCTGTATGG TGACA	C	A			SILENT- NONCODI NG			
5789-5790	cg44034193	657	CACTGGTCAGCA GCTGCCCATTTGT A/C/G]CCGCTGT ATGGTGACACCG GCCTCT	C	G			SILENT- NONCODI NG			
5791-5792	cg44034691	981	GAGTGGCCACCT GCGAAGACAGG G/C/T]GTCATTA TGGGCCAGAGG GCTGCTC	C	T			SILENT- NONCODI NG			
5793-5794	cg44034774	2714	GTGGTACTCCAG GTCCTCTGTCAG C/C/T]GCTGGAG CATGGACAGGG GCTCATT	C	T			SILENT- NONCODI NG			

5795-5796	cg44034830	306	GGGGACCCAGG CATTCCGGTCCC CC[C/gap]TGGCG GTGAGGGTACCA ATGGCCTC	C	-				SILENT- NONCODI NG			
5797-5798	cg44034830	574	ATGGCCTTGGCA GGGACATCACAG C[G/A]AAACACAT GGCACTTGAGCA TACAG	G	A				SILENT- NONCODI NG			
5799-5800	cg44034830	684	GTAGAGCTGGT TAGAGGCAGGA GC[C/gap]TGCAG GAGGCTGGAAA GTCAGGCTA	C	-				SILENT- NONCODI NG			
5801-5802	cg44034889	296	GGCCGTCGGG ACTGCGTGGAGA GG[G/A]ACGGGC TCCACAGCGTGG TGGATGA	G	A				SILENT- NONCODI NG			
5803-5804	cg44034889	391	CGCCGGCCGCT GCGCTGCCCGG GAC[G/A]GAGAC AGAGGGGCCCG ACCTCCCAG	G	A				SILENT- NONCODI NG			
5805-5806	cg44035239	429	TTTTATCAGCTAT ATATATATATAT ap[A]GAGAAATATA TATATATTTTGT GTT	-	A				SILENT- NONCODI NG			
5807-5808	cg44035419	3031	ACTCCAAGACCG TGAGTCCCCTAG A[A/G]GTTACTCA TCCACTTTGACT GACAT	A	G				SILENT- NONCODI NG			

5809-5810	cg44035528	808	GGAGCTCGGG TGGGTCGTGG GAC[G/C]GTGG CGATAGCATCAG TCCACAGG	G	C			SILENT- NONCODI NG			
5811-5812	cg44036050	1163	AGCTCGAAGGA GCCAAAGCCAG CGG[C/gap]TGCG AAACTTTCTTCG TATCTTCCC	C	-			SILENT- NONCODI NG			
5813-5814	cg44036050	2199	GGTCGATGTAGA CCTTAGTACCAT GT[C]CCGATGA GATACTGTCCGT GTTTGT	T	C			SILENT- NONCODI NG			
5815-5816	cg44036050	472	TAAGACCAAAA CAAACTCAAAA A[gap/A]CCTTCA ATATGAAGGCAG CAGCTGG	-	A			SILENT- NONCODI NG			
5817-5818	cg44036247	309	GTACAAAAATT ACATAACAAGAG G[A/gap]AAAAATA GGCAGTGCAGC ACCTTTAG	A	-			SILENT- NONCODI NG			
5819-5820	cg44126480	287	GTGGTGCATCTA TCTATGGCAAC A[A/G]TTTGAAGA TGAACCTTCATCC AGACT	A	G			SILENT- NONCODI NG			
5821-5822	cg44126938	147	GGTACTTTTTCG CCCGTCCTCGAT G[A/G]AATCCCCT GATGGCAAGAAC TGTTT	A	G			SILENT- NONCODI NG			
5823-5824	cg44126938	74	GGCTCCCGCAA CGCGGATACTT CGT[C]CGGTGA CACGCTTCGTGC GTGGTTG	T	C			SILENT- NONCODI NG			

5825-5826	cg44126946	137	CCACGTTCTTGG TCACGCTGGATC C[C/T]CAAACGCA TACCGGGGTAG CAGCCC	C	T				SILENT- NONCODI NG			
5827-5828	cg44127370	230	GGGCCCCAAG ACACCGTGCTCG TC[A/G]CAGGTGT GGGACAACACCA GGTGCG	A	G				SILENT- NONCODI NG			
5829-5830	cg44127374	194	GTGGGCTCCTG CGGCGTTTGTG A[T/G]CGGGTGC TCGACCCCTTAC AGCCCA	T	G				SILENT- NONCODI NG			
5831-5832	cg44127374	86	CTGATCAGGCCC CGGCGTTGCTGT GT[C]TCGCTGG AGCGACGGATC GAGTGGC	T	C				SILENT- NONCODI NG			
5833-5834	cg44127378	316	GTGCGCCATCGT CACGAAGCAGCT G[G/T]CCCCCTCA GCCAGGGGAAAA GCATCCG	G	T				SILENT- NONCODI NG			
5835-5836	cg44127419	184	TCCCCTCAGCAA TGGCCTCAGAAA C[C/T]TCGGCAC GAATCTCCTCGA TACGCC	C	T				SILENT- NONCODI NG			
5837-5838	cg44127419	235	GACGCAAGCCCTA CGCCACCCTCTT C[A/G]JACAACAAA GAGGCCCTCTCA CCACGT	A	G				SILENT- NONCODI NG			

5839-5840	cg44127419	37	GAACGTCACCAG CCTCGACGACGA G[A/T]CGGGCC GGGTACGGGTC TTCTCCC	A	T				SILENT- NONCODI NG			
5841-5842	cg44127465	1990	GGCCTCCTGG GCCGCAGGGAC CCC[C/gap]TGGG GACAGCCGCCT CCTGTCCACG	C	-				SILENT- NONCODI NG			
5843-5844	cg44127465	2546	GTGACAGGGGC CCTGCTGGGCC ACC[A/G]GGTCAT CCTGGGCCACCT GGCCCTC	A	G				SILENT- NONCODI NG			
5845-5846	cg44127475	210	CACCACTGTATA CACCGACGATG GT[A/G]GGAAAA CGTGGAACGG GGAATCCC	A	G				SILENT- NONCODI NG			
5847-5848	cg44127475	213	CACGTATACAC CGACGATGGTAG G[A/G]AAACGTG GCAACGGGGAA TCCCGAT	A	G				SILENT- NONCODI NG			
5849-5850	cg44127475	497	GGGAACAGCTTC CTGCGCTCATTG T[C/T]GTCTCAGC AGATGACCCGAG GCGTC	C	T				SILENT- NONCODI NG			
5851-5852	cg44127475	544	CGTCGACATGGC ATTGCCCATGTG G[C/T]AGTTATCC ATCGATCCTCGA GGACG	C	T				SILENT- NONCODI NG			

5853-5854	cg44127493	230	CATCTACGACCG CCGAGACCTGAC GIC/TTCGTTGGC CGCCGAGATGA CAACGA	C	T			SILENT- NONCODI NG			
5855-5856	cg44127493	331	AAGCCCTTCTTG CCAAAGGCGAGC GT[G/A]CGCCGC TACGCGGGCAA GCTCGATA	G	A			SILENT- NONCODI NG			
5857-5858	cg44127493	336	CTTCTTGCCAAG GGCAGCGTGCG CC[G/A]CTAGGC GGCAAGCTCG ATAGCATA	G	A			SILENT- NONCODI NG			
5859-5860	cg44127499	10	TCCGGACTT[T/C] GGTCTGGCCTCT CCTGACGGGCC AG	T	C			SILENT- NONCODI NG			
5861-5862	cg44127556	341	AGGCCGCCCTCAA GGCGGAGTGCG GT[T/C]TACCTCC GGCCGACCCCG CCCGTGA	T	C			SILENT- NONCODI NG			
5863-5864	cg44127556	376	CCGACCCCGCC CGTGAGGCTGA GCA[G/A]ATCGC GCGGTTGCGGC AGTTAGCGG	G	A			SILENT- NONCODI NG			
5865-5866	cg44127556	478	TGGCCGAGGTG GTGCGTCACCAC GA[A/G]GCTATTG CTGACGATTCTG GCGACG	A	G			SILENT- NONCODI NG			

5867- 5868	cg44127556	493	GTCACCACGAAG CTATTGCTGACG A/T/G/TCTGGCGA CGACTCTGGAGT GGCGG	T	G				SILENT- NONCODI NG		
5869- 5870	cg44127556	509	TGCTGACGATTC TGCGGACGACTC T/G/A/GAGTGGC GGATACGGGGG AGGCGGA	G	A				SILENT- NONCODI NG		
5871- 5872	cg44127560	100	GCAAAGTCGTTT CTGGCATGAATG A/T/C/GCTCAGAT GCGGGCGCTGC GTCGGC	T	C				SILENT- NONCODI NG		
5873- 5874	cg44127560	107	CGTTTCTGGCAT GAATGATGCTCA G/A/T/TGGGGC GCTGCGTCCGC ACCACGT	A	T				SILENT- NONCODI NG		
5875- 5876	cg44127560	136	GGCGCTGCGT CGCGACCCACGT CTC/A/G/ATGGTT TTCAGCACTTC GCACTAC	A	G				SILENT- NONCODI NG		
5877- 5878	cg44127560	145	GTGCGGACCAC GTCTCAATGGTT TTC/TTCAGCACT TCGCACTACTTC CTCATC	C	T				SILENT- NONCODI NG		
5879- 5880	cg44127560	34	AGTCCACCCTCA TCAGGATGATTA A/C/T/JGGGCTGT GGTCCCCGTCTG AGGGTA	C	T				SILENT- NONCODI NG		

5881-5882	cg44127560	79	AGGGTACCGTTG AGGTGCGCGC AA/GJGTCGTTT CTGGCATGAATG ATGCTC	A	G				SILENT- NONCODI NG			
5883-5884	cg44127560	90	GAGGTTGCCGG CAAAGTCGTTTC TG[G/A]CATGAAT GATGCTCAGATG CGGGCG	G	A				SILENT- NONCODI NG			
5885-5886	cg44127562	181	GGTCATCCTTGC TTGGGAGCTGAG C[C/A]AGGGCCC GCACGTCATCCC GATTCC	C	A				SILENT- NONCODI NG			
5887-5888	cg44127562	193	TTGGGAGCTGAG CCAGGGCCCCG AC[G/A]TCATCCC GATTCCCGGGTC TCACCG	G	A				SILENT- NONCODI NG			
5889-5890	cg44127562	213	CGCAGTCATCC CGATTCGCGGT C[T/C]CACC GTT CCAGACGATTCT TGACT	T	C				SILENT- NONCODI NG			
5891-5892	cg44127562	237	CTCACCGTCCC AGACGATTCTTG A[C/T]TCCCTCAG GTCCGTCGACGT CACGC	C	T				SILENT- NONCODI NG			
5893-5894	cg44127562	265	CCTCAGGTCCGT CGACGTCACGCT G[G/A]ACGACGA GGAGCTTGCCCA GCITCC	G	A				SILENT- NONCODI NG			
5895-5896	cg44127564	110	GTTGGCATGCCG TAGGCGCGGGC GGT[G/T]TTGGTC GTGCAACTCAAT GACCTGG	T	G				SILENT- NONCODI NG			

5897-5898	cg44127564	214	AGGGTGTCCAAT AGCCACGTGGA CC[A/G]ATGGAC GTCCTTTTGGTA ACCTGGC	A	G				SILENT- NONCODI NG			
5899-5900	cg44127564	219	GTCCAATAGCCA CGTGGACCAATG G[A/G]CGTCCTT TGGTAACCTGGC TTGCT	A	G				SILENT- NONCODI NG			
5901-5902	cg44127564	236	ACCAATGGACGT CCTTTTGGTAAC C[T/C]GGCTTGCT CGGACGGCATA GCCGCC	T	C				SILENT- NONCODI NG			
5903-5904	cg44127564	322	CCCACGTGAAAT AGCCAATGCCG CA[G/gap]CCCCA GGTTTGAAGGTG TCCATTGC	G	-				SILENT- NONCODI NG			
5905-5906	cg44127564	348	CCCCAGGTTTGA AGGTGTCCATTG C[G/A]CCGGTGC GAGACCGGGTG CCCTCCG	G	A				SILENT- NONCODI NG			
5907-5908	cg44127568	38	ACGATGTGGATC GTGCTCCTTGGA G[T/gap]TTTCATC TTTGTCACGAG ATGTTT	T	-				SILENT- NONCODI NG			
5909-5910	cg44127585	95	TCCAGCTGGAGC GGATGGATGAGA G[T/A]GATGACG GTGACGCCACTA CCGGCA	T	A				SILENT- NONCODI NG			
5911-5912	cg44127585	164	CAAGGACGGCC TTTGACCCCCCG AC[C/T]TCGCACT CGGCGATGGAC AAATGT	C	T				SILENT- NONCODI NG			

5913-5914	cg44127585	173	CCTTTGACCCCC CGACCTCGCACT C[G/A]GCGATGG ACAAAATGTGGC GTAATG	G	A			SILENT- NONCODI NG			
5915-5916	cg44127585	185	CGACCTCGCACT CGCGATGGAC AA[G/A]ATGTGGC GTAATGGCAAGC GGGTAC	A	G			SILENT- NONCODI NG			
5917-5918	cg44127585	221	ATGGCAAGCGG GTACGACGGGT CAA[G/A]CTGGA CGAGAACCGCAA CTGGGAAA	G	A			SILENT- NONCODI NG			
5919-5920	cg44127585	230	GGGTACGACGG GTCAAGCTGGAC GA[G/A]AACCGC AACTGGGAAAAG TTCCGAG	G	A			SILENT- NONCODI NG			
5921-5922	cg44127585	247	CTGGACGAGAAC CGCAACTGGGAA A[A/T]GTTCGAG AGGCCATGCCG GACGCT	A	T			SILENT- NONCODI NG			
5923-5924	cg44127585	254	AGAACCGCAACT GGGAAAAGTTCC G[A/G]GAGGCCA TGCCGGACGCT GTGGTGA	A	G			SILENT- NONCODI NG			
5925-5926	cg44127585	287	TGCCGGACGCT GTGGTGATGTTT GT[C/T]GTTAAGC CTTCTTCGGTGA ACGTTG	C	T			SILENT- NONCODI NG			

5927-5928	cg44127585	328	GTGAACGTTGCC ACCAACGGGATG A/G]TGTCCCA AAGAGGACTACA CCATC	A	G			SILENT- NONCODI NG			
5929-5930	cg44127585	331	AACGTTGCCACC AACGGGATGAAT G/T/C]TCCAAAG AGGACTACACCA TCATT	T	C			SILENT- NONCODI NG			
5931-5932	cg44127585	345	CGGGATGAATGT TCCCAAAGAGGA C/T/G]ACACCATC ATTATCTGGGT GACGA	T	G			SILENT- NONCODI NG			
5933-5934	cg44127585	362	AAGAGGACTACA CCATCATTATCT [G/A]GGTGACGA GTGAAAGACG CTCCGG	G	A			SILENT- NONCODI NG			
5935-5936	cg44128033	262	ACCACCTCAGCG ATCTGCAAAGCC T/G/A]GTGTGAGC ATCCACCTCCGA GCTCG	G	A			SILENT- NONCODI NG			
5937-5938	cg44128033	286	TGGTGTGAGCAT CCACCTCCGAGC T/C/T]GGCGATAT TAAGGGGGTCG GCCTCA	C	T			SILENT- NONCODI NG			
5939-5940	cg44128033	31	GCCGGTTGCTCA CTGATGACTATC G/T/C]CCCAATTC CGTCGCTCCTGG CGGGT	T	C			SILENT- NONCODI NG			
5941-5942	cg44128033	67	TCGCTCCTGGCG GGTTTCCCTGT C/A/C]GGATTACA GAAACTGTCCTG GGAAG	A	C			SILENT- NONCODI NG			

5943-5944	cg44128710	2200	GCGTGTGTGACTC GTGAAGGGGCC GCCTTGGCGTC TGAGGAAGGCA CAGCCTG	C	T			SILENT- NONCODI NG			
5945-5946	cg44128803	722	TAACCTTATTGTAT TTTTAGTAGAGA TTCGGGATGTCA CCATGTTGGCCA GGAT	T	C			SILENT- NONCODI NG			
5947-5948	cg44129401	327	AGGGCTGAGTG CCAAAAGCTTGG GGGGAJAGGAGG GACAGGTCCTCG GCAATAA	G	A			SILENT- NONCODI NG			
5949-5950	cg44129401	367	CTCGGCAATAAA CAGTGTACACACA C[G/A]CATCACAG CCATTTGAGAAA TGGCT	G	A			SILENT- NONCODI NG			
5951-5952	cg44129641	102	GCGTGGGGTCT CCTCGCTGGCCT CCGAP/TCCCTCT TCACTTGTGTCT TCCCATTAA	-	T			SILENT- NONCODI NG			
5953-5954	cg44130064	873	ATTTAACACTATT GTATTTTATTAT T/CJATGTAATTTA GTAATATGAATA TAA	T	C			SILENT- NONCODI NG			
5955-5956	cg44130064	991	GTACACTGGTGT TTATATTTGCACA [G/A]AGTATTGAT ATGTGATGIATT AAGT	G	A			SILENT- NONCODI NG			
5957-5958	cg44130288	163	TAGCCAGATGTA ACCAGCTTGCTG T[C/T]TTGTCCCA AGCCTCCCTCTA AGGGG	C	T			SILENT- NONCODI NG			

5959-5960	cg44130288	188	CTTGTCCTCAAGC CTCCCTCTAAGG G(G)gapJACAGTG TGAATCGGTGAA TGTTGAG	G	-				SILENT- NONCODI NG			
5961-5962	cg44130288	264	GGGAATGCTCTG AAATCAGTGTGG G(C/A)ATGGCTGT ACCAACAGGAAT GAACA	C	A				SILENT- NONCODI NG			
5963-5964	cg44130288	299	CCAACAGGAATG AACAGTTGTTCC AT(C/G)ACAGATG ACTCCCAAGTGA CACAC	T	C				SILENT- NONCODI NG			
5965-5966	cg44130288	323	ATGACAGATGAC TCCCAAGTGACA C(A/G)CACGTGT CCTCAAGAAGAC TCACAC	A	G				SILENT- NONCODI NG			
5967-5968	cg44130564	2202	AACCTGATCAAG CAGGATGACGG CG(G/A)CTCCCC CATCAGACACTA TCTGGTC	G	A				SILENT- NONCODI NG			
5969-5970	cg44130564	447	CCTCACCATCTA TAACGCCAACAT C(G/T)ACGACGC CGGCATTTACAA GTGTGT	G	T				SILENT- NONCODI NG			
5971-5972	cg44130566	228	CGTGTGTGTGTG TGTGTGTGTGTG T(G)gapJTGTTTTA ATTTTTATTTTAG AGACA	G	-				SILENT- NONCODI NG			
5973-5974	cg44130566	230	TGTGTGTGTGTG TGTGTGTGTGTG T(G)gapJTTTTAAT TTTTATTTTAGAG ACAGG	G	-				SILENT- NONCODI NG			

5975-5976	cg44130841	918	AGTCCCAAAC TAGGGTGCCAA T[G/A]TCCCTCAC CTTGAAGTTAGC AAGAG	G	A			SILENT- NONCODI NG			
5977-5978	cg44131199	491	AGCAGGACGTC GCTGCCGGGG AGC[C/T]CTCCAG ACACGCAGAAAT GCCACAG	C	T			SILENT- NONCODI NG			
5979-5980	cg44131207	228	GAATTCGGTGCG TTTGGTGGCTAT G[G/A]CACCTC ACCAGCTTTGAC ATCCAT	G	A			SILENT- NONCODI NG			
5981-5982	cg44131588	173	AGCTTCTCACCT CTACGGTGAAAG T[T/C]TCGGTGTC ACCCACATGGG GCTTTT	T	C			SILENT- NONCODI NG			
5983-5984	cg44131588	253	TGCGAACCTCA CACATCGCTGAC G[A/gap]CGGCCG CGGAGTCGATG CTGAGGCC	A	-			SILENT- NONCODI NG			
5985-5986	cg44131588	272	CTGACGACGGC GGCGGAGTCGA TGC[T/C]GAGGC CGACGGCGATG GGGATTTCG	T	C			SILENT- NONCODI NG			
5987-5988	cg44131588	295	GCTGAGGCCGA CGCGCATGGG ATT[T/C]CGTCCG GGCGGCAGACC TACTTGGG	T	C			SILENT- NONCODI NG			

5989-5990	cg44131701	340	GCGGTGCCAGA AAAAGGCCAAAT ACT[<i>gap</i>]CTGCT TTCCCAGGGAC GCGCGTAG	T	-				SILENT- NONCODI NG			
5991-5992	cg44131756	1234	ACAGCAGGGCC ATGGAGGGGG GCC[C/ <i>gap</i>]GGCT CACTCGGCGGA GCCCTTGTTGG	C	-				SILENT- NONCODI NG			
5993-5994	cg44131756	337	AGGCATTGAGCG GAGATCTCACCA CT[C]GCACTCCA GCCTGGGCGAC AGAGCA	T	C				SILENT- NONCODI NG			
5995-5996	cg44131756	380	ACAGAGCAAGAT TCTATCAAAAA G[A/ <i>gap</i>]AAGAAA GAAAGGACAGG ACAGGAAA	A	-				SILENT- NONCODI NG			
5997-5998	cg44131756	388	AGATTCTATCAA AAAAGAAAGAAA G[A/ <i>gap</i>]AAGGAC AGGACAGGAAA GGGAAGGG	A	-				SILENT- NONCODI NG			
5999-6000	cg44131756	389	GATTCTATCAA AAAGAAAGAAAG A[A/ <i>gap</i>]AGGACA GGACAGGAAAG GGAAGGGG	A	-				SILENT- NONCODI NG			
6001-6002	cg44131756	390	ATTCTATCAAAAA AGAAAGAAAGAA [A/ <i>gap</i>]GGACAGG ACAGGAAAGGG AAGGGGT	A	-				SILENT- NONCODI NG			

6003-6004	cg44131756	445	CAGAACTGGGG GCAAAACAAAA AA[gap/A]GAAGG AAGGAAGGAAAG AAAGAAAT	-	A				SILENT- NONCODI NG			
6005-6006	cg44131756	469	AAGAAAGGAAGGA AGGAAAGAAAGA A[AG]TGGGTATG GGCAGAATTGG GGGCAA	A	G				SILENT- NONCODI NG			
6007-6008	cg44910941	371	GGCCAGACTG AGCCATGCCACA CC[C/gap]TTCCT CCTAGTCCCCAT GCTCTCCT	C	-				SILENT- NONCODI NG			
6009-6010	cg44911060	110	TGGAATGGAATG CAATGGAATGGA AT[C/C]GACTGGA ATGGAATGGAAT GGAAT	T	C				SILENT- NONCODI NG			
6011-6012	cg44911060	111	GGAATGGAATGC AATGGAATGGAA T[C/G]GACTGGA ATGGAATGGAAT GGAATG	C	G				SILENT- NONCODI NG			
6013-6014	cg44911060	161	GGAATGGAATGG AATGGAATGGAA T[C/A]AACCCGAG TGCAATGGAATG GAGTG	C	A				SILENT- NONCODI NG			
6015-6016	cg44911343	350	TTTTTTTTTTTG AAACAGGTCTC [A/G]CTCTGCTGC CCAGGCTGGAG TGCAG	A	G				SILENT- NONCODI NG			

6017- 6018	cg44911865	216	ACCGTTGCGTAG ATACCAGGCTGC G[C/gap]CATTCC AATCCCGGATCC GCGTCAC	C	-				SILENT- NONCODI NG			
6019- 6020	cg44911865	217	CCGTTGCGTAGA TACCAGGCTGCG C[C/gap]ATTCCA ATCCCGGATCCG CGTCACA	C	-				SILENT- NONCODI NG			
6021- 6022	cg44911865	548	GTCGATCGATGC TCGCGCCGGTC GC[C/gap]TCTGC GAGGATACGAC GCGT	C	-				SILENT- NONCODI NG			
6023- 6024	cg44912335	209	ACCCTGAGTCAT GGGGTCTTTTG T[A/G]AAAGTCCC CAAAC TGCCCA GGAAG	A	G				SILENT- NONCODI NG			
6025- 6026	cg44912347	613	CTCTAATTGAAG CTCTGGCATCAT CT[A/G]GGGGCTTT ATGAGCCAAGG GAGATA	T	A				SILENT- NONCODI NG			
6027- 6028	cg44913034	265	GTCAGGGTGCTC GGCAAGGGCGA GC[A/G]TCCTCCA TGCAGCAGAGAC ACCAGA	A	G				SILENT- NONCODI NG			
6029- 6030	cg44913283	155	GTTGGCACTCG TCATGAATTGAA G[A/G]ATGAAAAG CCATAGTCACAA GTCTG	A	G				SILENT- NONCODI NG			

6031- 6032	cg44913564	333	CGGCCGTGAAG AGCAGCTGGC GGA[C/A]GGTG AAACCTGCACAG GTGCACTG	C	A				SILENT- NONCODI NG			
6033- 6034	cg44913901	158	AGCGGAGGTT GCAGTGAGCCG AGA[C/T]CACACC ATTGCACTCCAG CCTGGAC	C	T				SILENT- NONCODI NG			
6035- 6036	cg44914000	2432	AACTATTAGGT TGTTTCTAATTT [G/C]ATTATTATA AAGTTGCAGAAA TTTG	G	C				SILENT- NONCODI NG			
6037- 6038	cg44914031	610	GGTGACAGAGT GAGACACTGTCT CC[A/gap]AAAA AAATGTTTAAAA TGAGACC	A	-				SILENT- NONCODI NG			
6039- 6040	cg44914031	965	CAAAAGATTCTA CTTCCTTGCTTG G[G/A]CGGGGCT CCGATTCTCCAA ACTGAT	G	A				SILENT- NONCODI NG			
6041- 6042	cg44914076	277	TGAGGTCAAGCT GTCTGCCCCATCT C[A/G]GCCTCCC AAAGTGCTGGGA TTGCAG	A	G				SILENT- NONCODI NG			
6043- 6044	cg44914681	335	CTTCTAGACACA CCCTGAGCCAGA A[G/T]GGAACCC ACTGCCTTGAAG GGAAGG	G	T				SILENT- NONCODI NG			

6045-6046	cg44914784	261	TCCAGCTGGAGCT GGATGGATGAGA GTTA]GATGACG GTGACGCCACTA CCGGCA	A			SILENT- NONCODI NG		
6047-6048	cg44914784	351	CGACCTCGCACT A CGGCGATGGAC AA]A]G]ATGTGGC GTAATGGCAAGC GGGTAC	G			SILENT- NONCODI NG		
6049-6050	cg44914784	387	ATGGCAAGCGG G GTACGACGGGT CAA]G]A]CTGGA CGAGAACCAGCA CTGGGAAA	A			SILENT- NONCODI NG		
6051-6052	cg44914784	396	GGGTACGACGG G GTCAAGCTGGAC GA]G]A]AACCGC AACTGGGAAAG TTCCGAG	A			SILENT- NONCODI NG		
6053-6054	cg44914784	413	CTGGACGAGAAC A CGCAACTGGGAA A]A]T]G]T]CCGAG AGGCCATGCCG GACGCT	T			SILENT- NONCODI NG		
6055-6056	cg44914784	420	AGAACCCGCAACT A GGGAAAAGTTCC G]A]G]GAGGCCA TGCCGGGACGCT GTGGTGA	G			SILENT- NONCODI NG		
6057-6058	cg44914811	102	CGTGAGCAATGA G CGTCAGCCATAG T]G]A]GTGAGGC GGTCATCGCTGA CCCCGG	A			SILENT- NONCODI NG		

6059-6060	cg44914811	144	TGACCCCGGTCT GCTCGGAGTCGT C[G/A]ACAAAGCT AATGATGTGACG TACCA	G	A				SILENT- NONCODI NG			
6061-6062	cg44914811	155	TGCTCGGAGTCG TCGACAAAGCTA AT/C]GATGTGAC GTACCACCGCGT CGACT	T	C				SILENT- NONCODI NG			
6063-6064	cg44914811	306	AATTCGGGTAGA TCGTCGTAGTCG C[A/G]CCACCTG CGCAGGAAATG GCCATAT	A	G				SILENT- NONCODI NG			
6065-6066	cg44914838	424	TGGCAGTCGGC GGACAGACGCC GCT[A/G]GCATCA GGGCTCTCATGC GCTGGAA	A	G				SILENT- NONCODI NG			
6067-6068	cg44914838	559	TTGACGGTCGG GTGGACCGAACT GCT/C]ACCAATC AGGCATTGATG TGCAC	T	C				SILENT- NONCODI NG			
6069-6070	cg44914838	589	ATCAGGCATTG ATGTCGCACAAA C[C/]TTGTCCGA CGACACAAGAAC CTCGT	C	T				SILENT- NONCODI NG			
6071-6072	cg44914838	646	TCGTAGATACCT CCGTCAACCGAG TT/C]CATCAAAG GGACTGCGAAG CGCTGT	T	C				SILENT- NONCODI NG			
6073-6074	cg44914838	667	GAGTTCATCAA GGGACTGCGAA GC[G/A]CTGTCA GGAATTCTTCAT GCGCCIC	G	A				SILENT- NONCODI NG			

6075- 6076	cg44914862	106	GCCCCGTA CCTCAGACATAG TTT/CJACCCATC TCTTCTGCCCA GGAAC	T	C				SILENT- NONCODI NG		
6077- 6078	cg44914862	113	ACTCACCTCAGA CATAGTTCACCC ATT/CJCTCTTCTG CCCCAGGAACTG GACGA	T	C				SILENT- NONCODI NG		
6079- 6080	cg44914862	135	CCATCTCTTCTG CCCCAGGAACTG GTA/GJCGAGGGT CACGATGGCAAC GAGGGC	A	G				SILENT- NONCODI NG		
6081- 6082	cg44914862	140	TCTTCTGCCCA GGAACCTGGACG AG[G]A/GTCACG ATGGCAACGAG GGCAAAGA	G	A				SILENT- NONCODI NG		
6083- 6084	cg44914862	152	GGAACCTGGACG AGGGTCACGATG GC[A/G]ACGAGG GCAAAGATAACG ATCGCCA	A	G				SILENT- NONCODI NG		
6085- 6086	cg44914862	158	GGACGAGGGTC ACGATGGCAACG AG[G]A/GCAAAG ATAACGATCGCC ACGGCAG	G	A				SILENT- NONCODI NG		
6087- 6088	cg44914862	182	GGGCAAAGATAA CGATCGGCCACG GC[A/G]GCACCG AGCCCTGGTCA TGGTTGA	A	G				SILENT- NONCODI NG		

6089-6090	cg44914862	218	CCTGGTCATGGT TGACGAAGGCTT GGTTCGGTAGA ACAGCGACACCA ACGAGC	G	T			SILENT- NONCODI NG			
6091-6092	cg44914862	238	GCTTGGCGGTA GAACAGCGACAC CA[A/G]CGAGCG AGTCCTCGGCTC AGCCGGG	A	G			SILENT- NONCODI NG			
6093-6094	cg44914862	296	TCCGATCATCG CGTACAGCGCGT C[A/G]AACAACTG GAACCCACCGAT CGTCG	A	G			SILENT- NONCODI NG			
6095-6096	cg44914862	36	ACGAAGCGCGG CTGCGACACGGT GT[C/T]GCCCG CTTGGCAAGGG CCGCCACC	C	T			SILENT- NONCODI NG			
6097-6098	cg44914862	55	CGGTGTCGCC CGCTTGGCAAG GGC[C/T]GCCAC CTCTACAGCGGA GAGTTCGG	C	T			SILENT- NONCODI NG			
6099-6100	cg44914862	81	GCCACCTCTACA GCGGAGAGTTT GG[G/A]CCCCGT ACTCACCTCAGA CATAGT	G	A			SILENT- NONCODI NG			
6101-6102	cg44914862	89	TACAGCGGAGA GTTCCGGCCCC GTA[C/A]TCACCT CAGACATAGTTC ACCCATC	C	A			SILENT- NONCODI NG			

6103-6104	cg44914864	232	CCTCAAGATCAG CCGTACGGCCG GT[A/G]AGGACC GCACTAACCTTC GGGCTC	A	G			SILENT- NONCODI NG			
6105-6106	cg44914864	271	CCTTCGGGCTC GGTCGAAGTCG GC[G/A]CGCGAG CCTGATCCGAAG AAGGACG	G	A			SILENT- NONCODI NG			
6107-6108	cg44914864	277	GGCCTCGGTCG AAGTCGGCCG CGA[G/T]CCTGAT CCGAAGAAAGG CGAGGTGG	G	T			SILENT- NONCODI NG			
6109-6110	cg44914864	283	GGTCGAAGTCG GCGCGCGAGCC TGAT[C]CCGAAG AAGGACGAGGT GGGAGCCC	T	C			SILENT- NONCODI NG			
6111-6112	cg44914864	292	GCGCGCGCGAG CCTGATCCGAAG AA[G/A]GACGAG GTGGGAGCCCC GAAACCT	G	A			SILENT- NONCODI NG			
6113-6114	cg44914864	319	ACGAGGTGGA GCCCGAAACC CTC[G/A]CTTTGA GCCGCCACGCG AGCAGCGA	G	A			SILENT- NONCODI NG			
6115-6116	cg44914864	373	TCTCGACGACCG CTGTTGTGACCG TT[C]AGGGTTCC ACGACTAGCCTT CTCAC	T	C			SILENT- NONCODI NG			

6117- 6118	cg44914864	378	ACGACCGCTGTT GTGACCGTTAGG GTTCTCCACGAC TAGCCTTCTCAC GATTG	T	C			SILENT- NONCODI NG			
6119- 6120	cg44914866	62	GCCCGCTGGTAA TAGCACGAGCTA GTCCTTGGATGG CTGCCGACCCG ACGCCAC	C	T			SILENT- NONCODI NG			
6121- 6122	cg44914870	246	TCCTGTGGAGAC GTGGAGTTTCC GTCCTGCGTACCT GGGAGATTATTT CGCCA	C	T			SILENT- NONCODI NG			
6123- 6124	cg44914873	45	GGCATGAACGAC CAGCTTCTTGTT ATCTTGGCTAGC GTCCTGATCCTC CCAGA	C	T			SILENT- NONCODI NG			
6125- 6126	cg44914940	141	CGCATGTGCTG CTCGCTGACCG GGAGTAACTCT GACGAAGACGG CTAGGGTG	A	G			SILENT- NONCODI NG			
6127- 6128	cg44914951	466	AAATTGGTGACC TCAAGGCCGATG TCTTAAACATGG CTGAGCCGGCT CGCAGA	C	T			SILENT- NONCODI NG			
6129- 6130	cg44914951	511	CGCAGAGTTACA GTGGGTCGCGC AAACATAATGG TGCCCGAACCT ACGTGG	A	C			SILENT- NONCODI NG			
6131- 6132	cg44914951	534	AAAATAATGGTG CCCGAAACCTAC GTCCTGGTACTCA TATTCACCTGGAC AATGT	T	C			SILENT- NONCODI NG			

6133- 6134	cg44914951	601	CAGGGTTCGTGCT CTTGAACAAGA CT/GTGGCCGAG CGCATTGGTGCA C	T	G				SILENT- NONCODI NG			
6135- 6136	cg44914955	102	CAAACCGCTACG AGACCGCCTGC GA/C/TCCACGTC TGAACCGGAACC AGTCCT	C	T				SILENT- NONCODI NG			
6137- 6138	cg44914955	18	GTGCACATCGAG TTGAC/C/T/GGG GACGACGTCAC GGAGTGCTTGG	C	T				SILENT- NONCODI NG			
6139- 6140	cg44914955	212	GTCAGTCCGCTG GCAAGGTTCCGC A/G/A/CATCGACC TATGATCGATCC GGA	G	A				SILENT- NONCODI NG			
6141- 6142	cg44914955	48	ACGACGTACAG GAGTGCTTGGG CGG/G/C/GTCGA CAAGCTAGCAGA GTCCGATC	G	C				SILENT- NONCODI NG			
6143- 6144	cg44914955	60	AGTGCTTGGGC GGGGTCGACAA GCT/A/C/GCAGA GTCCGATCTGAC AAACCGCT	A	C				SILENT- NONCODI NG			
6145- 6146	cg44914955	95	GATCTGACAAAC CGCTACGAGACC G/C/TCTGCGAC CCACGTCCTGAAC CGGAAC	C	T				SILENT- NONCODI NG			
6147- 6148	cg44914955	99	TGACAAACCGCT ACGAGACCGCCT G/C/T/GACCCAC GTCTGAACCGGA ACCACT	C	T				SILENT- NONCODI NG			

6149-6150	cg44914965	180	GGCTACAAGTTT CAGGCCTAAAGC ATTATCACCACCC AGGAAAGCAACA CCACG	T	A				SILENT- NONCODI NG		
6151-6152	cg44914965	198	TAAAGCATCACC ACCCAGGAAAGC ATA/GCACCACG CAGGAATGGTGT ATTACG	A	G				SILENT- NONCODI NG		
6153-6154	cg44914965	245	TCAGCTGATTAG GACCGAGCCGA CGATGJAATTCCT GAAGAAGCGTAC TCCGCA	A	G				SILENT- NONCODI NG		
6155-6156	cg44915044	114	ACCGCGTCCAAG AGCTCGCGGATA T/GA/GTCTCTGA AAAGTATGCCGA TGCTG	G	A				SILENT- NONCODI NG		
6157-6158	cg44915044	135	ATATGGTCTCTG AAAAGTATGCCG AT/CJGCTGAGCA AGACCTGCTTTT GGTCT	T	C				SILENT- NONCODI NG		
6159-6160	cg44915044	174	TGCTTTTGGTCT GCGTGCTCAAG GGC/TJGCGGCT TTCCTCTGACG GACTTCG	C	T				SILENT- NONCODI NG		
6161-6162	cg44915044	189	TGCTCAAGGGC GCGGCTTTCTTC CT/G/TJACGGACT TCGCGCGCAAG CTATCCA	G	T				SILENT- NONCODI NG		
6163-6164	cg44915044	219	ACTTCGGCGCA AGCTATCCATCC C/C/TJCCGAGCT GGAGTTTATGGC CGTGT	C	T				SILENT- NONCODI NG		

6165- 6166	cg44915044	226	GCGCAAGCTATC CATCCCTCCGA G[C/T]TGGAGTTT ATGCCCGTGTCC TCTTA	C	T				SILENT- NONCODI NG		
6167- 6168	cg44915044	249	AGCTGGAGTTTA TGGCCGTGTCCT CT[G/T]ATGGCG CCTCCACTTCTT CTCCG	T	G				SILENT- NONCODI NG		
6169- 6170	cg44915044	276	ATGGCGCTCCA CTTCTTCTCCG G[C/T]GTGGTGC GCATTTTGAAGG ACTTGG	C	T				SILENT- NONCODI NG		
6171- 6172	cg44915044	84	CAATCCTCATTG GAGAGAGGAA CT[A/G]CAAAACC GCGTCCAAGAG CTCGGG	A	G				SILENT- NONCODI NG		
6173- 6174	cg44915062	214	GTCCTCAATAG TAAGATAGCACA G[C/T]TTATTGAG AAATAACGAGA TTGAG	C	T				SILENT- NONCODI NG		
6175- 6176	cg44915070	21	NTCCGGAGCGG TTCAGCGCG[A/G] JATGCCGCTTTCT ACGCGTGAGAG CG	A	G				SILENT- NONCODI NG		
6177- 6178	cg44915080	491	TGTGTCCACATG TGACCGGAGTG CC[T/C]GCGCCC AGCCGCCCGTG ACACTTCC	T	C				SILENT- NONCODI NG		

6179- 6180	cg44915080	507	CGGAGTGCCCTG CGCCAGCCGC CCG[T/C]GACACT TCCGGGCTGAG ACGCGGTC	T	C				SILENT- NONCODI NG			
6181- 6182	cg44915080	527	GCCCGTGACACT TCCGGGCTGAG AC[G/A]CGGTCT GGTCTTAAGGGG CCCGTCA	G	A				SILENT- NONCODI NG			
6183- 6184	cg44915080	540	CGGGCTGAGAC GCGGTCTGGTCT TA[gap/C]AGGGG CCCGTCACAGC GATGGGCC	-	C				SILENT- NONCODI NG			
6185- 6186	cg44915149	654	TATCGATCCCCG GTTCCGGACCCCT C[C/G]ACGATCAT CAAATCCACCAG AAAAA	C	G				SILENT- NONCODI NG			
6187- 6188	cg44915149	720	TACTGATGCCGA TCGTACAGGCCGA GT[C/G]CCGAGCT GGTGCCCGCTG TGACCAA	T	C				SILENT- NONCODI NG			
6189- 6190	cg44915354	103	CTTGAACGTCAG TCGGTGCCCGG TA[G/A]GCGTACT TTCCCAGACGGC CGTCAC	G	A				SILENT- NONCODI NG			
6191- 6192	cg44915354	116	CGGTGCCCGGT AGCGGTACTTTC CC[A/C]GACGGC CGTCACCTCGAA TGGCGTC	A	C				SILENT- NONCODI NG			

6193- 6194	cg44915354	122	CCGGTAGGCGT ACTTCCCAGAC GGC/TJCGTCAC CTCGAATGGCGT CAAATCG	C	T				SILENT- NONCODI NG			
6195- 6196	cg44915354	193	GACCCGAGTTA CCCTTCTTCATC A/A/CJATGGACCT CTCCGGCCGAA CTGTG	A	C				SILENT- NONCODI NG			
6197- 6198	cg44915354	200	AGTTACCCCTTCT TCATCAAATGGA C/C/TJCTCCGGC CGAACTGTTGCC TTCCA	C	T				SILENT- NONCODI NG			
6199- 6200	cg44915354	207	CTCTTCATCAA ATGGACCTCTCC G/G/AJCCGAACT GTTGCCCTTCCAG CCTGAG	G	A				SILENT- NONCODI NG			
6201- 6202	cg44915354	233	CCGAACGTGTTGC CTTCCAGCCTGA G/T/CJGGCAACG TCACCTTGGCCT CCGTCG	T	C				SILENT- NONCODI NG			
6203- 6204	cg44915354	246	TCCAGCCTGAG TGGCAACGTCAC CTT/CJGGCCTCC GTCGAAATGTCC GGA	T	C				SILENT- NONCODI NG			
6205- 6206	cg44915354	26	GTGCACGCCAA GAGCAGGGCGG CGGT/CJTTGGAT GGGATGGGCCG TCTCCGTCG	T	C				SILENT- NONCODI NG			
6207- 6208	cg44915354	35	AAGAGCAGGGC GGCGGTTGGAT GGG/AJTTGGGC CGTCTCCGTCGA CGATCTCG	A	G				SILENT- NONCODI NG			

6209-6210	cg44915354	62	GGGCCGCTCTCC GTCGACGATCTC GC/TCCTTATG AGAAGCGTCTTG AACGTC	C	T				SILENT- NONCODI NG			
6211-6212	cg44915354	77	ACGATCTGCCCC CTTATGAGAAGC GT/CJCTTGAACG TCAGTCGGTGCC CGGTA	T	C				SILENT- NONCODI NG			
6213-6214	cg44915354	83	TCGCCCTTATG AGAAAGCGTCTTG A/A/GJCGTCAGTC GGTGCCCGGTA GGCGTA	A	G				SILENT- NONCODI NG			
6215-6216	cg44915354	86	CCCCTTATGAGA AGCGTCTTGAAC GT/CJ/CAGTCGG TGCCCGGTAGG CGTACTT	T	C				SILENT- NONCODI NG			
6217-6218	cg44915425	156	TCCAACCGATGA TCAGGAATGGGA CT/CJGTGCTTG ACGGTAACCAAA TGGTG	T	C				SILENT- NONCODI NG			
6219-6220	cg44915425	42	CGCGATGGTGC GCCATAGTCACG AA/G/AJ/CAGCTG GCCCTCAGCCA GGGAAA	G	A				SILENT- NONCODI NG			
6221-6222	cg44915425	49	GTGGCCCATAGT CACGAAGCAGCT GG/TCCTCTCA GCCAGGGGAAA GCATCCG	G	T				SILENT- NONCODI NG			
6223-6224	cg44916342	625	GATGATGAGGAA AAATGTGGTTGT C/G/AJTATTATGT GTCCGGTCAGG CCTCTG	G	A				SILENT- NONCODI NG			

6225-6226	cg44916489	154	CGGGGCCCGCC TCC TTGATGAA GC[C/G]GCCTTC TTGTCGTCGACA AACCCCA	C	G			SILENT- NONCODI NG		
6227-6228	cg44916489	162	GCCTCCTTGATG GAAGCCGCCCTTC TT[C/G]GTCGTCGA CAAACCCCAAC AGACA	T	C			SILENT- NONCODI NG		
6229-6230	cg44917150	298	GGTGCCCGGG CATGAGGTGCG GCC[T/C]CCAGG GCGCCTCCTGC CGGCCCGGA	T	C			SILENT- NONCODI NG		
6231-6232	cg44917278	834	AGCTTTGGGGGA GGGTAATTCCCTG C[C/T]AGGAAGCT GGTCCACCAGT CCTGC	C	T			SILENT- NONCODI NG		
6233-6234	cg44917278	839	TGGGGGAGGGT AATTCCTGCCAG GA[A/G]GCTGGT TCCACCAGTCCT GCTGTAG	A	G			SILENT- NONCODI NG		
6235-6236	cg44917461	96	TTGGAAGATCTG AGCTCCCGCCAT C[G/A]CCTTCTTG GCTTCACCGGC GTCAAC	G	A			SILENT- NONCODI NG		
6237-6238	cg44917712	138	ATCGGCCATCTG CACCCCATGG GG[G/gap]CTAGA GCCCTTTACTTC CTCCTTCA	G	-			SILENT- NONCODI NG		

6239-6240	cg44917712	249	AGTAGACAATAA ATAACTGCTTTT C/C/TJGGCAGAG GCTAGGTTGTCC TGGGGG	C	T				SILENT- NONCODI NG			
6241-6242	cg44918306	542	ATCTTTTGTGTTTG CTTTTTTTTTTTT /gap)AAAAAAGGT CCCAGGAATATA CAGC	T	-				SILENT- NONCODI NG			
6243-6244	cg44918737	493	TCGGTCTGGGAA GCGGTGACGTA GG/A/GJCTCGTC GGCAGACGAGG TGCCACG	A	G				SILENT- NONCODI NG			
6245-6246	cg44918799	129	TATCTCTTCAAC AGATCCGGGTG GC/C/TJATTGACC ATCTACGCAGCA ACGGGG	C	T				SILENT- NONCODI NG			
6247-6248	cg44918799	57	GAAGTCAGCGC CTGTACTCTTTC CG/T/CJGACATCC TCATGCTCAAGG TTGTCA	T	C				SILENT- NONCODI NG			
6249-6250	cg44918799	81	GTGACATCCTCA TGCTCAAGGTTG T/C/TJAAGCGTCT TCTTGACGCTGG GGTAT	C	T				SILENT- NONCODI NG			
6251-6252	cg44918799	90	TCATGCTCAAGG TTGTCAAGCGTC T/C/CJCTTGACGC TGCGGTATCTCT TCAAC	T	C				SILENT- NONCODI NG			
6253-6254	cg44918827	261	TCAGCAAGAACA AGACGCCTGCC CT/C/GJAAGGC TCGCCGACGCG TCGTGGCG	C	G				SILENT- NONCODI NG			

6255- 6256	cg44918827	64	ACCGCTCGAGTT GCTGCGAGAAG GTCTTTGCCCGT GCGGAGTTCCG ACGGCAC	C	T				SILENT- NONCODI NG		
6257- 6258	cg44918840	106	TAGCTGAGGTGA GGAGCAGGGAC GGAGJATCGGC GCCAGCTCGCG AGTGGCGT	A	G				SILENT- NONCODI NG		
6259- 6260	cg44918840	145	CGCGAGTGGCG TGGCGGTCCGA GAGTTCJACAATG ATGGTAGTTCCC TCAGCAA	T	C				SILENT- NONCODI NG		
6261- 6262	cg44918840	160	GGTCCGAGAGTA CAATGATGGTAG TTTCJCCCTCAGC AATGGCCTCAGA AACCT	T	C				SILENT- NONCODI NG		
6263- 6264	cg44918840	184	TCCCTCAGCAA TGGCCTCAGAAA CCTCTCGGCAC GAATCTCCTCGA TACGCC	C	T				SILENT- NONCODI NG		
6265- 6266	cg44918840	235	GACGCAAGCCCT CGCCACCCTCTT CAGJACAACAAA GAGGCCCTCA CCACGT	A	G				SILENT- NONCODI NG		
6267- 6268	cg44918840	37	GAACGTCACCAG CCTCGACGACGA GATTCGGGCC GGTACGGGTC TTCTCCC	A	T				SILENT- NONCODI NG		

6269-6270	cg44920731	1183	TGGAGGAAAATA TGTACATCAATG C[G/A]CACCAGT GATCAGAAAACC CCCAGG	G	A				SILENT- NONCODI NG			
6271-6272	cg44920731	1190	AAATATGTACAT CAATGCGCACCA G[T/G]GATCAGAA AACCCCCAGGAA CCCAA	T	G				SILENT- NONCODI NG			
6273-6274	cg44920731	1197	TACATCAATGCG CACCAGTGATCA G[A/gap]AAACCC CCAGGAACCCAA GCAAGTG	A	-				SILENT- NONCODI NG			
6275-6276	cg44920731	1208	GCACCAGTGATC AGAAAACCCCCA G[G/A]AACCCAA GCAAGTGGGAA CTGAGGG	G	A				SILENT- NONCODI NG			
6277-6278	cg44920731	1216	GATCAGAAAACC CCAGGAACCCCA A[G/C]CAAGTGG GAACTGAGGGG GCCGGCT	G	C				SILENT- NONCODI NG			
6279-6280	cg44920731	1263	GGCTCCTCATCA GCTGGGGAAA GG[G/gap]AAAAT GGCCTCACAG AAGCCATAA	G	-				SILENT- NONCODI NG			
6281-6282	cg44920731	1267	CCTCATCAGCTG GGGAAAAGGGA AA[A/G]TGGGCC TCACAGAAAGCCA TAACAGG	A	G				SILENT- NONCODI NG			

6283- 6284	cg44920731	1290	AAATGGGCCTCA CAGAAAGCCATAA C[A/C]GGGTGGA AAGAGCGAGGC TGCAGTC	A	C				SILENT- NONCODI NG			
6285- 6286	cg44920731	1299	TCACAGAAGCCA TAACAGGGTGGA A[A/G]GAGCGAG GCTGCAGTCCAC AGGGGT	A	G				SILENT- NONCODI NG			
6287- 6288	cg44920731	1304	GAAGCCATAACA GGGTGGAAGA GC[G/A]AGGCTG CAGTCCACAGG GGTTGTGT	G	A				SILENT- NONCODI NG			
6289- 6290	cg44920731	1306	AGCCATAACAGG GTGGAAGAGC GA[G/A]GCTGCA GTCCACAGGG TTGTGTGA	G	A				SILENT- NONCODI NG			
6291- 6292	cg44920731	3395	GTGTGTTGAGT GGCTTGATTTT TT[<i>gap</i>]CTCTGC AGGGGGAGTGG CATCTCCT	T	-				SILENT- NONCODI NG			
6293- 6294	cg44920877	47	GGTCTATGCCC CGCGGCCCGTTG GC[C/ <i>gap</i>]TCGCC CACACCCCGG CCCCACTGC	C	-				SILENT- NONCODI NG			
6295- 6296	cg44920877	62	GGCCGTTGGCC TCGCCACACCCC CC[G/C]GCCCCA CTGCCGGTGGA GAGACGTC	G	C				SILENT- NONCODI NG			

6297-6298	cg43959936	273	TGTGTGATGGGG ACATGGAGAAGC C/C/TATCCAGGT CATGTGCTACGA CTATG	C	T	Pro	Pro	SILENT- CODING	ATPase_ associate d	Human Gene Similar to SPTREMBL- ID:O04042 F7G19.26 - ARABIDOPSIS THALIANA (MOUSE-EAR CRESS), 525 aa.	1.10E-33
6299-6300	cg34407554	235	CCGAACCTGGCC GCACGCGTAGC AGTTC/CCTGCGC GATCAAGGTGTC GTACCCG	T	C	Val	Val	SILENT- CODING	dehydrog enase	Human Gene Similar to TREMBLNEW- ID:E1202273 METHYLENETETRAHYDROFOLATE DEHYDROGENASE - MYCOBACTERIUM TUBERCULOSIS, 281 aa.	8.70E-39
6301-6302	cg34407554	295	CCGTGCTCGTCG GGGAGGACCCG GC/C/TTCGCAC CAGTACGTGCT GGCAAAC	C	T	Ala	Ala	SILENT- CODING	dehydrog enase	Human Gene Similar to TREMBLNEW- ID:E1202273 METHYLENETETRAHYDROFOLATE DEHYDROGENASE - MYCOBACTERIUM TUBERCULOSIS, 281 aa.	8.70E-39
6303-6304	cg34407554	331	ACGTGCGTGGCA AACATCGCGACT G/C/TJGCGCAAG TAGGCATTGAAT CGATTG	C	T	Cys	Cys	SILENT- CODING	dehydrog enase	Human Gene Similar to TREMBLNEW- ID:E1202273 METHYLENETETRAHYDROFOLATE DEHYDROGENASE - MYCOBACTERIUM TUBERCULOSIS, 281 aa.	8.70E-39
6305-6306	cg34407554	412	AGGAACCTGCTC AAAAGATCCGCG G/G/TJCTCAATGC CAACCCGCGATTG CACCG	G	T	Gly	Gly	SILENT- CODING	dehydrog enase	Human Gene Similar to TREMBLNEW- ID:E1202273 METHYLENETETRAHYDROFOLATE DEHYDROGENASE - MYCOBACTERIUM TUBERCULOSIS, 281 aa.	8.70E-39
6307-6308	cg34407554	445	CCAACCCGCGATT GCACCCGGTTACA T/T/CJGTTGAGCT ACCGCTGCCAC GTCATA	T	C	Ile	Ile	SILENT- CODING	dehydrog enase	Human Gene Similar to TREMBLNEW- ID:E1202273 METHYLENETETRAHYDROFOLATE DEHYDROGENASE - MYCOBACTERIUM TUBERCULOSIS, 281 aa.	8.70E-39

6309-6310	cg34407554	487	CACGTCATATCG ACACGAACCTGGG C[G/A]CTTAACCT CATCGACCCTAA CAAGG	G	A	Ala	Ala	SILENT- CODING	dehydrog enase	Human Gene Similar to TREMBLNEW- ID:E1202273 METHYLENETETRAHYDROFOLATE DEHYDROGENASE - MYCOBACTERIUM TUBERCULOSIS, 281 aa.	8.70E-39
6311-6312	cg29344427	340	GACTGGCGGCC TTACGTTGCTTG AC[C/T]AGCTCCC ACCGCGCCTTGC CAGAGC	C	T	Leu	Leu	SILENT- CODING	dehydrog enase	Human Gene Similar to SWISSPROT- ID:P20707 2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.2) (ALPHA- KETOGLUTARATE DEHYDROGENASE) - AZOTOBACTER VINELANDII, 943 aa.	9.40E-31
6313-6314	cg42716656	119	TGACCGGGTTG GCTGAAGTTCTT AA[G/A]GTAACT GTAGTCCCGTG GAGGCT	G	A	Thr	Thr	SILENT- CODING	glycoprot ein	Human Gene Similar to SWISSPROT- ID:Q09332 UDP- GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT) - DROSOPHILA MELANOGASTER (FRUIT FLY), 1548 aa.	2.80E-43
6315-6316	cg42716656	134	AAGTTCCTAAGG TAAACTGTAGTC C[C/T]CGTGGAG GCTGGCCTGTG GTGATGT	C	T	Arg	Arg	SILENT- CODING	glycoprot ein	Human Gene Similar to SWISSPROT- ID:Q09332 UDP- GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT) - DROSOPHILA MELANOGASTER (FRUIT FLY), 1548 aa.	2.80E-43
6317-6318	cg42716656	164	GAGGCTGGCCT GTGGTGATGTCG TA[G/A]CAATGAC CTCCAGTAACA GGTATT	G	A	Cys	Cys	SILENT- CODING	glycoprot ein	Human Gene Similar to SWISSPROT- ID:Q09332 UDP- GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT) - DROSOPHILA MELANOGASTER (FRUIT FLY), 1548 aa.	2.80E-43

6319-6320	cg42716656	176	TGGTGATGTCGT AGCAATGACCTT C/C/TAGTAACAG GTATCCAGCTC ATACT	C	T	Leu	Leu	SILENT- CODING	glycoprot ein	Human Gene Similar to SWISSPROT- ID:Q09332 UDP. GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT) - DROSOPHILA MELANOGASTER (FRUIT FLY), 1548 aa.	'2.8E-43
6321-6322	cg42716656	185	CGTAGCAATGAC CTTCCAGTAACA G/G/A/TATTCCAG CTCATACTCAGC AGCCA	G	A	Tyr	Tyr	SILENT- CODING	glycoprot ein	Human Gene Similar to SWISSPROT- ID:Q09332 UDP. GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT) - DROSOPHILA MELANOGASTER (FRUIT FLY), 1548 aa.	2.80E-43
6323-6324	cg42716656	232	GCCACTACACTG TCCACCTCTTCT A/A/G/JATAAATAT TATCAAGATCAT ATGGT	A	G	Leu	Leu	SILENT- CODING	glycoprot ein	Human Gene Similar to SWISSPROT- ID:Q09332 UDP. GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT) - DROSOPHILA MELANOGASTER (FRUIT FLY), 1548 aa.	2.80E-43
6325-6326	cg42716656	245	CCACCTCTTCTA AATAAATATTATC J/A/C/JAGATCATAT GGTGTCTGACA GATT	A	C	Leu	Leu	SILENT- CODING	glycoprot ein	Human Gene Similar to SWISSPROT- ID:Q09332 UDP. GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT) - DROSOPHILA MELANOGASTER (FRUIT FLY), 1548 aa.	2.80E-43
6327-6328	cg42716656	281	GTGTTCTGACAG ATTCTACCATCC A/G/A/CTCTCAGG TGTGTTCAAATT CAAAG	G	A	Ser	Ser	SILENT- CODING	glycoprot ein	Human Gene Similar to SWISSPROT- ID:Q09332 UDP. GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT) - DROSOPHILA MELANOGASTER (FRUIT FLY), 1548 aa.	2.80E-43

6329-6330	cg42716656	298	ACCATCCAGCTC TCAGGTGTGTTT A/G/ATTCAAAG TAAACAGCGGAG ACTGA	A	G	Leu	Leu	SILENT- CODING	glycoprot ein	Human Gene Similar to SWISSPROT- ID:Q09332 UDP. GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT) - DROSOPHILA MELANOGASTER (FRUIT FLY), 1548 aa.	2.80E-43
6331-6332	cg42716656	334	AACAGCGGAGA CTGAGGCATATC CA/G/JAAATTTT GCGATCGGACC CTTAGCA	A	G	Leu	Leu	SILENT- CODING	glycoprot ein	Human Gene Similar to SWISSPROT- ID:Q09332 UDP. GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT) - DROSOPHILA MELANOGASTER (FRUIT FLY), 1548 aa.	2.80E-43
6333-6334	cg42716656	338	GCGGAGACTGA GGCATATCCAAA AA/T/C/TTTGCGA TCGGACCCCTAG CAAAAC	T	C	Lys	Lys	SILENT- CODING	glycoprot ein	Human Gene Similar to SWISSPROT- ID:Q09332 UDP. GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT) - DROSOPHILA MELANOGASTER (FRUIT FLY), 1548 aa.	2.80E-43
6335-6336	cg42716656	344	ACTGAGGCATAT CCAAAAATTTTG C/G/T/ATCGGAC CCTTAGCAAAAC TACTGT	G	T	Ile	Ile	SILENT- CODING	glycoprot ein	Human Gene Similar to SWISSPROT- ID:Q09332 UDP. GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT) - DROSOPHILA MELANOGASTER (FRUIT FLY), 1548 aa.	2.80E-43
6337-6338	cg42716656	362	ATTTGCGATCG GACCCTTAGCAA A/G/CTACTGTC TGAAGTGAAGA AATCT	A	G	Ser	Ser	SILENT- CODING	glycoprot ein	Human Gene Similar to SWISSPROT- ID:Q09332 UDP. GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT) - DROSOPHILA MELANOGASTER (FRUIT FLY), 1548 aa.	2.80E-43

6339-6340	cg42716656	365	TTGCGATCGGAC CCTTAGCAAAAC T[A/G]CTGTCTGA AGTGAAAGAAAT CTCTG	A	G	Ser	Ser	SILENT- CODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:Q09332 UDP- GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT) - DROSOPHILA MELANOGASTER (FRUIT FLY), 1548 aa.	2.80E-43
6341-6342	cg27241188	130	CGGTGTCGAGG TCCGTGAAGGCC GG[G/T]CTCCAG TTCCCCGTCGGC CGCATCG	G	T	Gly	Gly	SILENT- CODING	histone	Human Gene Similar to SWISSPROT- ID:P40280 HISTONE H2A - ZEA MAYS (MAIZE), 159 aa.	3.90E-48
6343-6344	cg20725546	285	TTGCCAAGGAGG TAGAGGTCCTCG A[A/G]GGCCTGA CCGCCGATCCG AAGCGGC	A	G	Glu	Glu	SILENT- CODING	kinase	Human Gene Similar to SWISSPROT- ID:O06821 PHOSPHOGLYCERATE KINASE (EC 2.7.2.3) - MYCOBACTERIUM TUBERCULOSIS, 412 aa.	9.40E-42
6345-6346	cg20725546	432	GTATGGCGTACA CCTTCCTCAAGG C[G/C]AAGGGTC TCGAGGTCGGT GACTCCC	G	C	Ala	Ala	SILENT- CODING	kinase	Human Gene Similar to SWISSPROT- ID:O06821 PHOSPHOGLYCERATE KINASE (EC 2.7.2.3) - MYCOBACTERIUM TUBERCULOSIS, 412 aa.	9.40E-42
6347-6348	cg44013488	1026	AGAAGGCCAAAG TCCAGGCATCCA C[A/C]GGTCCTG CATCTATAGACT TCATCT	A	C	Pro	Pro	SILENT- CODING	kinase	Human Gene Similar to SWISSPROT- ID:P49695 PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-) - THERMOMONOSPORA CURVATA, 742 aa.	1.30E-33
6349-6350	cg44013488	1098	AGAGACGAATAT GAGCATCTAGAG A[G/A]CTGGAGG CAGCAATGGGCA GGGTGT	G	A	Ser	Ser	SILENT- CODING	kinase	Human Gene Similar to SWISSPROT- ID:P49695 PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-) - THERMOMONOSPORA CURVATA, 742 aa.	1.30E-33
6351-6352	cg44013488	834	TTGCAATATCAA AAATATTGATGA T[T/C]CCATCTAT GGCTCCCACTGG CTAGGT	T	C	Gly	Gly	SILENT- CODING	kinase	Human Gene Similar to SWISSPROT- ID:P49695 PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-) - THERMOMONOSPORA CURVATA, 742 aa.	1.30E-33

6353-6354	cg44013488	849	TATTGATGATTC CATCTATGGCTC C/A/GJCTGGCTA GGTATTTCCCAT CAGGAC	A	G	Ser	Ser	SILENT- CODING	Kinase	Human Gene Similar to SWISSPROT- ID:P49695 PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-) - THERMOMONOSPORA CURVATA, 742 aa.	1.30E-33
6355-6356	cg44013488	855	TGATTCATCTA TGGCTCCACTGG CT/CJAGGTATT CCCATCAGGACT ATATG	T	C	Leu	Leu	SILENT- CODING	kinase	Human Gene Similar to SWISSPROT- ID:P49695 PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-) - THERMOMONOSPORA CURVATA, 742 aa.	1.30E-33
6357-6358	cg44013488	864	CTATGGCTCCAC TGGCTAGGTATT T/CJCCATCAGG ACTATATGCAAT ACTAA	C	T	Gly	Gly	SILENT- CODING	kinase	Human Gene Similar to SWISSPROT- ID:P49695 PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-) - THERMOMONOSPORA CURVATA, 742 aa.	1.30E-33
6359-6360	cg44013488	891	CATCAGGACTAT ATGCAATACTAA G/A/GJATGAATTT TCCTCTAGTGTC CAAAG	A	G	Ile	Ile	SILENT- CODING	kinase	Human Gene Similar to SWISSPROT- ID:P49695 PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-) - THERMOMONOSPORA CURVATA, 742 aa.	1.30E-33
6361-6362	cg42512386	580	TAGGAGAGTATG CTGCAGTGGAAAC T/T/CJCATCAGGC AAAAGATGTCAA CACAG	T	C	Leu	Leu	SILENT- CODING	kinesin	Human Gene Similar to SPTREMBL- ID:O01349 KINESIN-73 - DROSOPHILA MELANOGASTER (FRUIT FLY), 1921 aa.	4.10E-36
6363-6364	cg29345567	426	TAGCTTTCAACG T CCGGTCTGTGC GT/T/CJACCTGCG GTCTGCTGGCAG GACGCG	T	C	Val	Val	SILENT- CODING	phosphatase	Human Gene Similar to SWISSPROT- ID:P06987 IMIDAZOLEGLYCEROL- PHOSPHATE DEHYDRATASE (EC 4.2.1.19) (IGPD) / HISTIDINOL- PHOSPHATASE (EC 3.1.3.15) - ESCHERICHIA COLI, 355 aa.	1.40E-33
6365-6366	cg42529544	421	CACTTTGATACA A CTTCTGAGCGCG T/A/GJCCATATGCC GATGATAGAAAC ATCAG	A	G	Gly	Gly	SILENT- CODING	protease	Human Gene Similar to SPTREMBL- ID:P87892 PROTEASE - HUMAN ENDOGENOUS RETROVIRUS K, 334 aa (fragment).	1.60E-48

6367-6368	cg29358731	175	TCAGCTTCTCGC CTAGGTTGGTCA TTCACATGGC GAAGCTCAGCAG CGGAGA	G	C	Val	Val	SILENT- CODING	struct	Human Gene Similar to SWISSPROT- ID:P93087 CALMODULIN - CAPSICUM ANNUUM (BELL PEPPER), 148 aa.	2.90E-47
6369-6370	cg29358731	178	GCTTCTGCCTA GGTTGGTCATGA CAGTGGCGAA GCTCAGCAGCG GAGATGA	A	G	His	His	SILENT- CODING	struct	Human Gene Similar to SWISSPROT- ID:P93087 CALMODULIN - CAPSICUM ANNUUM (BELL PEPPER), 148 aa.	2.90E-47
6371-6372	cg29358731	193	TGGTCATGACAT GGCGAAGCTCA GCAGGCGGAG ATGAAGCCGTTT TGGTCCT	A	G	Ala	Ala	SILENT- CODING	struct	Human Gene Similar to SWISSPROT- ID:P93087 CALMODULIN - CAPSICUM ANNUUM (BELL PEPPER), 148 aa.	2.90E-47
6373-6374	cg29358731	235	TCTGGTCCTTGT CGAACACACGGA AAGCGCCTCTT GAGCTCCTCCTC AGAGT	G	C	Ala	Ala	SILENT- CODING	struct	Human Gene Similar to SWISSPROT- ID:P93087 CALMODULIN - CAPSICUM ANNUUM (BELL PEPPER), 148 aa.	2.90E-47
6375-6376	cg29358731	280	CAGAGTCGGTGT CCTTCATCTTGC GTTGAGAACT CAGGAA	T	G	Ala	Ala	SILENT- CODING	struct	Human Gene Similar to SWISSPROT- ID:P93087 CALMODULIN - CAPSICUM ANNUUM (BELL PEPPER), 148 aa.	2.90E-47
6377-6378	cg29358731	286	CGGTGCTCTTCA TCTTGCCTGCCA TTCAGGTTGA GAACTCAGGAA AGTCGA	C	G	Leu	Leu	SILENT- CODING	struct	Human Gene Similar to SWISSPROT- ID:P93087 CALMODULIN - CAPSICUM ANNUUM (BELL PEPPER), 148 aa.	2.90E-47
6379-6380	cg29358731	295	TCATCTTGGCTG CCATCAGGTTGA GAGGAACTCAG GAAAGTCGATGG TTCCAT	A	G	Phe	Phe	SILENT- CODING	struct	Human Gene Similar to SWISSPROT- ID:P93087 CALMODULIN - CAPSICUM ANNUUM (BELL PEPPER), 148 aa.	2.90E-47
6381-6382	cg29358731	313	GGTTGAGAACT CAGGAAAGTCGA TTCGTTCCATT GCCATCAGCATC AACCT	G	C	Thr	Thr	SILENT- CODING	struct	Human Gene Similar to SWISSPROT- ID:P93087 CALMODULIN - CAPSICUM ANNUUM (BELL PEPPER), 148 aa.	2.90E-47

6383-6384	cg29358731	325	CAGGAAAGTCGA TGTTCCATTGC C/A/GJTCAGCATC AACCTCATTGAT CA	A	G	Asp	Asp	SILENT-CODING	struct	Human Gene Similar to SWISSPROT-ID:P93087 CALMODULIN - CAPSICUM ANNUUM (BELL PEPPER), 148 aa.	2.90E-47
6385-6386	cg43986867	422	CGCCGGAGTCC TCGAGCTGGACA GC[G/A]GGCAGC ACCAGGCGGCG GACAGTGT	G	A	Pro	Pro	SILENT-CODING	struct	Human Gene Similar to SPTREMBL-ID:Q10466 TITIN, HEART ISOFORM N2-B (EC 2.7.1.-) (CONNECTIN) - HOMO SAPIENS (HUMAN), 26926 aa.	1.90E-34
6387-6388	cg43976004	1947	AGGACGACGAC GACACGCGTGAA GG[G/A]GAGGAG GAGCTAGAGGA CGACGACG	G	A	Ser	Ser	SILENT-CODING	struct	Human Gene Similar to SWISSPROT-ID:Q02817 MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2) - HOMO SAPIENS (HUMAN), 5179 aa. Ipcis:SPTREMBL-ID:Q14878 MUCIN - HOMO SAPIENS (HUMAN), 5179 aa.	7.40E-34
6389-6390	cg44127439	155	CGGCGCCCGCC TCCTTGATGGAA GC[C/G]GCCCTC TTGTCGTCGACA AACCCCA	C	G	Ala	Ala	SILENT-CODING	synthase	Human Gene Similar to SWISSPROT-ID:P19206 BIOTIN SYNTHASE (EC 2.8.1.6) (BIOTIN SYNTHETASE) - BACILLUS SPHAERICUS, 332 aa.	7.90E-45
6391-6392	cg44127439	38	GCGACAGACCAT TGCGCTTGAGGA C[C/T]TCGACGGT ATCCATCCTGTC CTCGT	C	T	Glu	Glu	SILENT-CODING	synthase	Human Gene Similar to SWISSPROT-ID:P19206 BIOTIN SYNTHASE (EC 2.8.1.6) (BIOTIN SYNTHETASE) - BACILLUS SPHAERICUS, 332 aa.	7.90E-45
6393-6394	cg43926631	473	AGAGAGTCCACA CTGGAGAGAAAC C[C/T]TATAGATG TTGTGGATGTGG GAAGG	C	T	Pro	Pro	SILENT-CODING	transcript factor	Human Gene Similar to SWISSNEW-ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa. Ipcis:SWISSPROT-ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.	1.80E-40

6395-6396	cg32152874	139	GCGGCAAGGTG TACGTGTCCATG CC[G/C]GCCATG GCCATGCACCTG CTCACGC	G	C	Pro	SILENT- CODING	transcript factor	Human Gene Similar to SPTREMBL- ID:Q24140 NEURON SPECIFIC ZINC FINGER TRANSCRIPTION FACTOR - DROSOPHILA MELANOGASTER (FRUIT FLY), 664 aa.	1.50E-39
6397-6398	cg32152874	190	ACGACCTGCGC CACAAAGTCCGG CGT[G/C]TGCGG CAAAGCCCTTCTC GCGGCCCT	G	C	Val	SILENT- CODING	transcript factor	Human Gene Similar to SPTREMBL- ID:Q24140 NEURON SPECIFIC ZINC FINGER TRANSCRIPTION FACTOR - DROSOPHILA MELANOGASTER (FRUIT FLY), 664 aa.	1.50E-39
6399-6400	cg32152874	28	GGGACGCGTGC GGCGAGTGCGG CAA[G/G]ACATAC GCCACGTCGTC GAACCTGA	A	G	Lys	SILENT- CODING	transcript factor	Human Gene Similar to SPTREMBL- ID:Q24140 NEURON SPECIFIC ZINC FINGER TRANSCRIPTION FACTOR - DROSOPHILA MELANOGASTER (FRUIT FLY), 664 aa.	1.50E-39
6401-6402	cg43103077	2098	TTCCATAACGGC TGGAAGCTGCAA A[G/A]AAGCTTGT GATTGGTAACC AAAGC	G	A	Phe	SILENT- CODING	transfe se	Human Gene Similar to TREMBLNEW- ID:G2804586 1,4- A -D-GLUCAN: 1,4-A - D-GLUCAN 6-A-D-(1,4-A-D-GLUCANO) TRANSFERASE (EC 2.4.1.18) - AGROBACTERIUM TUMEFACIENS, 734 aa.	3.50E-42
6403-6404	cg43103077	2116	CTGCAAGAAGC TTGTGATTTGGT A[A/C]CCAAAGCT GGCATAGTAAGC ATGCT	A	C	Gly	SILENT- CODING	transfe se	Human Gene Similar to TREMBLNEW- ID:G2804586 1,4- A -D-GLUCAN: 1,4-A - D-GLUCAN 6-A-D-(1,4-A-D-GLUCANO) TRANSFERASE (EC 2.4.1.18) - AGROBACTERIUM TUMEFACIENS, 734 aa.	3.50E-42
6405-6406	cg43103077	2140	AACCAAGCTGG CATAGTAAGCAT G[C/T]TCCATGAT TGCCATCAACTG AATGC	C	T	Glu	SILENT- CODING	transfe se	Human Gene Similar to TREMBLNEW- ID:G2804586 1,4- A -D-GLUCAN: 1,4-A - D-GLUCAN 6-A-D-(1,4-A-D-GLUCANO) TRANSFERASE (EC 2.4.1.18) - AGROBACTERIUM TUMEFACIENS, 734 aa.	3.50E-42
6407-6408	cg43103077	2149	TGGCATAGTAAG CATGCTCCATGA TTT[C/G]GCCATCAA CTGAATGCAGTT GTATC	T	C	Ala	SILENT- CODING	transfe se	Human Gene Similar to TREMBLNEW- ID:G2804586 1,4- A -D-GLUCAN: 1,4-A - D-GLUCAN 6-A-D-(1,4-A-D-GLUCANO) TRANSFERASE (EC 2.4.1.18) - AGROBACTERIUM TUMEFACIENS, 734 aa.	3.50E-42

6409-6410	cg43103077	2173	TTGCCATCAACT GAATGCAGTTGT ATT/CJCCAAGC CTTGATTCTTG GTAGTA	T	C	Gly	Gly	SILENT- CODING	transferrase	Human Gene Similar to TREMBLNEW- ID:G2804586 1,4-A-D-GLUCAN: 1,4-A-D-GLUCAN 6-A-D-(1,4-A-D-GLUCANO) TRANSFERASE (EC 2.4.1.18) - AGROBACTERIUM TUMEFACIENS, 734 aa	3.50E-42
6411-6412	cg20749088	537	TAGGGGTGGCA GTGCCAATGTCC ATC/TJCCCGGAT ACACCACCATCG AGTCAG	C	T	Gly	Gly	SILENT- CODING	transferrase	Human Gene Similar to TREMBLNEW- ID:E1284465 PUTATIVE TRNA DELTA(2)- ISOPENTENYL PYROPHOSPHATE TRANSFERASE - STREPTOMYCES COELICOLOR, 312 aa	9.40E-41
6413-6414	cg38434693	127	TGGAAATGATCG CGAGGGCAAGG ATC/TJCTGTCTAG CGCGTGGCCTG GACCACA	C	T	Ile	Ile	SILENT- CODING	transport	Human Gene Similar to TREMBLNEW- ID:E1237464 ABC TRANSPORTER ATP BINDING PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 542 aa	7.80E-34
6415-6416	cg38434693	139	CGAGGGCAAGG ATCCTGTCAGCG CGT/CJGGCCTG GACCACATACTG GAACGGA	T	C	Arg	Arg	SILENT- CODING	transport	Human Gene Similar to TREMBLNEW- ID:E1237464 ABC TRANSPORTER ATP BINDING PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 542 aa	7.80E-34
6417-6418	cg38434693	43	CCGGTGAAACCC TTCCCGCAGCAG GTT/AJTCAGTACG TCGCACCGGCG AGCTTG	T	A	Gly	Gly	SILENT- CODING	transport	Human Gene Similar to TREMBLNEW- ID:E1237464 ABC TRANSPORTER ATP BINDING PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 542 aa	7.80E-34
6419-6420	cg38434693	55	TTCCCGCAGCAG GTTCAGTACGTC GTC/TJACCGGCG AGCTTGGCTACC TGCCAC	C	T	Arg	Arg	SILENT- CODING	transport	Human Gene Similar to TREMBLNEW- ID:E1237464 ABC TRANSPORTER ATP BINDING PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 542 aa	7.80E-34
6421-6422	cg38434693	64	CAGGTTTCAGTAC GTCGCACCGGC GA/GAJCTTGGCT ACCTGCCACAGG ATCCCC	G	A	Glu	Glu	SILENT- CODING	transport	Human Gene Similar to TREMBLNEW- ID:E1237464 ABC TRANSPORTER ATP BINDING PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 542 aa	7.80E-34

6423-6424	cg38434693	74	ACGTCCGACCCG GCGAGCTTGGCT AC[C/T]TGGCACA GGATCCCCGCG ACCCAGA	C	T	Leu	Leu	SILENT- CODING	transport	Human Gene Similar to TREMBLNEW- ID:E1237464 ABC TRANSPORTER ATP BINDING PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 542 aa.	7.80E-34
6425-6426	cg38434693	94	GCTACCTGCCAC AGGATCCCCGC GA[C/T]CCAGACA TGGAATGATCG CGAGGG	C	T	Asp	Asp	SILENT- CODING	transport	Human Gene Similar to TREMBLNEW- ID:E1237464 ABC TRANSPORTER ATP BINDING PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 542 aa.	7.80E-34
6427-6428	cg43919179	1212	TAAACCTCCCGT TGGGAGTGATCA T[A/G]TAGATACT GGGAGGTTTGAA AGGAA	A	G	Tyr	Tyr	SILENT- CODING	ubiquitin	Human Gene Similar to SWISSPROT- ID:P33296 UBIQUITIN-CONJUGATING ENZYME E2-28.4 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - SACCHAROMYCES CEREVISIAE , (BAKER'S YEAST), 250 aa.	5.20E-41
6429-6430	cg25254092	478	GTGCCGGTCTC GAACGTATTGCC TA[C/T]CTACTCC AGGGCGTCGAC AATATGT	C	T	Tyr	Tyr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:007438 ALANYL-TRNA SYNTHETASE (EC 6.1.1.7) (ALANINE-- TRNA LIGASE) (ALARS) - Mycobacterium tuberculosis, 904 aa.	4.00E-49
6431-6432	cg25254092	562	AAGCGTCCGAGA TGTCGGGCAAG CG[G/T]TACGGT GCTCGCCACGA CGACGACG	G	T	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:007438 ALANYL-TRNA SYNTHETASE (EC 6.1.1.7) (ALANINE-- TRNA LIGASE) (ALARS) - Mycobacterium tuberculosis, 904 aa.	4.00E-49
6433-6434	cg25254092	568	CCGAGATGTCG GGCAAGCGGTA CGG[T/C]GCTCG CCACGACGACG ACGTCCGAC	T	C	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:007438 ALANYL-TRNA SYNTHETASE (EC 6.1.1.7) (ALANINE-- TRNA LIGASE) (ALARS) - Mycobacterium tuberculosis, 904 aa.	4.00E-49
6435-6436	cg42879031	244	TGCATTCCAGT ATGTTGCAAGAT T[C/T]AGAGGAGT GGACTGAATGCC ATTG	C	T	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14526 KIAA0290 - HOMO SAPIENS (HUMAN), 906 aa (fragment).	1.10E-47

6437-6438	cg39517880	323	CGAGCTGCACCT CAGCGGCAGAC AG[G/A]TCAATAT TGGCCCGGTAACA AGTCCA	G	A	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O33207 HYPOTHETICAL 34.4 KD PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 318 aa.	1.60E-47
6439-6440	cg39517880	332	CCTCAGCGGCA GACAGGTCAATA TT[G/A]GCCGGTA ACAAGTCCATGC CCTCGG	G	A	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O33207 HYPOTHETICAL 34.4 KD PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 318 aa.	1.60E-47
6441-6442	cg39517880	386	CAGTGGGCTGG ATGACGTCATGA AC[A/G]TCGTCAC GAGGTGACATCA GCAGGG	A	G	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O33207 HYPOTHETICAL 34.4 KD PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 318 aa.	1.60E-47
6443-6444	cg39517880	398	TGACGTCATGAA CATCGTCACGAG G[T/C]GACATCAG CAGGGTGTAGAT GGAAT	T	C	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O33207 HYPOTHETICAL 34.4 KD PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 318 aa.	1.60E-47
6445-6446	cg29866014	338	GACGCAATCACG AACTCCTCGCGC A[A/G]CGCCGGC GACACCTCGGG GATGGTC	A	G	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:Q41739 THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR - Zea mays (Maize), 354 aa.	5.20E-47
6447-6448	cg43945782	739	ATGTGGCTTCCA GATCCTCTGTCT T[G/A]TTGCGGA GATGTTCCAAGT TTTCCC	G	A	Asn	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60625 ENDOBREVIN - HOMO SAPIENS (HUMAN), 100 aa.	6.80E-47
6449-6450	cg27837466	59	GGTGATAGCCA CCAACTGCTCGC AT[C/G]CCTTTGAC GACCTCGTCGGT CAACC	T	C	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O53715 HYPOTHETICAL 19.9 KD PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 183 aa.	2.30E-46
6451-6452	cg27837466	82	CATCCTTTGACG ACCTCGTCGGTC A[A/G]CCCCGGA CCTTCCGATCCA AAGACC	A	G	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O53715 HYPOTHETICAL 19.9 KD PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 183 aa.	2.30E-46

6453-6454	cg43287601	1497	ACAGGGTTTCAC CGTGTGGCCAG G[C/A]TGGTCTTG AACTCCTGACCT CAAGT	C	A	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39188 !!! ALU SUBFAMILY J WARNING ENTRY !!!! - Homo sapiens (Human), 591 aa.	2.70E-46
6455-6456	cg39527289	240	ACGGCGATGCC AACTTGGCTAAA GG[C/T]GCCACC GTCGGAATCTTG CTTCAGG	C	T	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O53204 ABC-TRANSPOTER ATP BINDING PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 558 aa.	4.80E-46
6457-6458	cg39527289	378	AAGTCTCCGCCG AGATGGCCAAAC C[T/C]GACGCCG ACTTTGACGCC TGATGG	T	C	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O53204 ABC-TRANSPOTER ATP BINDING PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 558 aa.	4.80E-46
6459-6460	cg39527289	405	ACGCCGACTTTG ACGCCCTGATGG C[G/C]GAGATGG GTGAGCTGCAGA CCGAGC	G	C	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O53204 ABC-TRANSPOTER ATP BINDING PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 558 aa.	4.80E-46
6461-6462	cg43918551	207	AGGCTGGCATG GAGCGGGAAC GGA[G/A]AACATC ATCCAGGAGACA GAGAAAG	G	A	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q13438 PROTEIN OS-9 PRECURSOR - Homo sapiens (Human), 667 aa.	7.80E-46
6463-6464	cg43294390	1391	CACCATAATAAT CTGGTGATCAT T[A/G]GGGTCTAC TGGTTCAAGGAA AGGCC	A	G	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O45407 F26H11.3B - CAENORHABDITIS ELEGANS, 510 aa.	1.60E-45
6465-6466	cg34394308	207	TCATCATCCAGC ACGGTCTGACGA C[A/G]AATCGGAA ATCAATGGAGTG GTTTA	A	G	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P50442 GLYCINE AMIDINOTRANSFERASE PRECURSOR (EC 2.1.4.1) (L-ARGININE:GLYCINE AMIDINOTRANSFERASE) (TRANSAMIDINASE) (AT) - Rattus norvegicus (Rat), 423 aa.	1.50E-42

6467-6468	cg34394308	210	TCATCCAGCACG GTCTGACGACAA ATTCJCGGAAATC AATGGAGTGGTT TAAGC	T	C	Asn	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P50442 GLYCINE AMIDINOTRANSFERASE PRECURSOR (EC 2.1.4.1) (L-ARGININE:GLYCINE AMIDINOTRANSFERASE) (TRANSAMIDINASE) (AT) - Rattus norvegicus (Rat), 423 aa.	1.50E-42
6469-6470	cg34394308	216	AGCACGGTCTGA CGACAAATCGGA A(A/G)TCAATGGA GTGGTTTAAGCG TTACT	A	G	Lys	Lys	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P50442 GLYCINE AMIDINOTRANSFERASE PRECURSOR (EC 2.1.4.1) (L-ARGININE:GLYCINE AMIDINOTRANSFERASE) (TRANSAMIDINASE) (AT) - Rattus norvegicus (Rat), 423 aa.	1.50E-42
6471-6472	cg43129081	334	ACTACAGGCACG CGCCACCCACG CC[G/A]GCTAATT TTTTGTATTTTA GTAGA	G	A	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39189 !!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!! - Homo sapiens (Human), 587 aa.	3.70E-41
6473-6474	cg37858342	560	CATGAGAATTCA AATTTTCCTGTAA [G/A]TGACGACAT TTATCTACTGTG CCCT	G	A	His	His	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA83026 KIAA1074 PROTEIN - HOMO SAPIENS (HUMAN), 1709 aa.	1.30E-40
6475-6476	cg42868441	383	CTCTACTAAAA TACAAAAATTAG CTTCJGGGCATG GTGGTGC CGCG CTGTAAT	T	C	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39194 !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!! - Homo sapiens (Human), 593 aa.	6.40E-38
6477-6478	cg42868441	395	TACAAAAATTAG CTGGGCATGGT GGTTCJGCGCGC CTGTAATCCCG CTACTTG	T	C	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39194 !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!! - Homo sapiens (Human), 593 aa.	6.40E-38

6479-6480	cg42868441	452	TGAGGCAGGAG AATTGCTTGAAC CC[A/G]GGAGGC AGAGCTTGCAGC GAGCTGA	A	G	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39194 !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!! - Homo sapiens (Human), 593 aa.	6.40E-38
6481-6482	cg29256713	47	GTGCGATGCGTC GATTCGGTGACG CT[C/G]GAGTCGTT TCTGAACATCAT CGATT	T	C	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O86812 HYPOTHETICAL 52.9 KD PROTEIN - STREPTOMYCES COELICOLOR, 493 aa.	8.70E-38
6483-6484	cg29256713	62	TCGGTGACGCTG AGTCGTTTCTGA A[C/T]ATCATCGA TTCCATTGCTC TCGCT	C	T	Asn	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O86812 HYPOTHETICAL 52.9 KD PROTEIN - STREPTOMYCES COELICOLOR, 493 aa.	8.70E-38
6485-6486	cg29256713	83	TGAACATCATCG ATTCCATTGCT CT[C/G]CGCTGTCC GGAGGTCGGTTT GAGGT	T	C	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O86812 HYPOTHETICAL 52.9 KD PROTEIN - STREPTOMYCES COELICOLOR, 493 aa.	8.70E-38
6487-6488	cg29256713	89	TCATCGATTCCA TTCGCTCTCGCT GT[C/G]CCGGAGG TCGGTTTGAGGT CGAACT	T	C	Cys	Cys	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O86812 HYPOTHETICAL 52.9 KD PROTEIN - STREPTOMYCES COELICOLOR, 493 aa.	8.70E-38
6489-6490	cg33204850	396	TAGTGACGGCC GCGGTAGCCTC GGA[C/T]GTTCC GAGATTCTGCGC GGGGAGA	C	T	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P36176 RECF PROTEIN - Streptomyces coelicolor, 373 aa.	1.80E-37
6491-6492	cg41616497	210	ACTCTGTGCGCC AGGCTGGAGTG CA[A/G]TGCGGT GATCTCAGCTCA CTGCAAA	A	G	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39194 !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!! - Homo sapiens (Human), 593 aa.	9.70E-37
6493-6494	cg43087949	346	GCCTGAAGGCAT GTGCCCTAGCC G[C/T]GTGGTGG TGGTAGCCTCAG CTGCC	C	T	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34077 CGI-82 PROTEIN - HOMO SAPIENS (HUMAN), 318 aa.	1.00E-36

6495-6496	cg30785452	148	TGTTGGGCTTCA TCATGCCGATGC T(G)AATCGACTT AATGCCAAGTCC AGGAA	G	A	Ile	Ile	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O33225 RV1229C - MYCOBACTERIUM TUBERCULOSIS, 390 aa.	4.40E-36
6497-6498	cg30785452	298	CCTCGCGGCCG AGCTGAGCCAG GGC(C)GJAGGGC CAGGTTGACGGT GACAGAGG	C	G	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O33225 RV1229C - MYCOBACTERIUM TUBERCULOSIS, 390 aa.	4.40E-36
6499-6500	cg30793892	93	CGTTGACGTGG GCAGTGAACCT TC(A)GJCCCTTCA GCTCAACGGTGT CGACGC	A	G	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P42015 PTS SYSTEM, GLUCOSE- SPECIFIC IIABC COMPONENT (EIABC- GLC) (GLUCOSE- PERMEASE IIABC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, ABC COMPONENT) (EC 2.7.1.69) (EI- GLC/EII-GLC) - Bacillus stearothermophilus, 324 aa (fragment).	1.20E-35
6501-6502	cg35929441	344	TTACACCATATTA CAAAAATAACTI C/TJAAGATGGAT TAAAGACTTAA TGTA	C	T	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O00363 PUTATIVE P150 - HOMO SAPIENS (HUMAN), 1275 aa.	3.30E-35
6503-6504	cg35929441	419	GAAGAAAATCTA GGCAATAACATT C(A)TJGGACATAG GCATGGGCAAA GATTTC	A	T	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O00363 PUTATIVE P150 - HOMO SAPIENS (HUMAN), 1275 aa.	3.30E-35
6505-6506	cg42667624	891	GTAACCTCCTAA GAAACAGGGTAT G(G)A/JGGATATAT TTTCAAATTCCT GCATA	G	A	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39195 !!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!! - Homo sapiens (Human), 591 aa.	5.00E-35
6507-6508	cg34997905	304	TAACTTTTAAAT TTTTGTAGAGAI T(C)GGGGTCTCA CTATGTTGTCCA GGCT	T	C	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39188 !!!!! ALU SUBFAMILY J WARNING ENTRY !!!!! - Homo sapiens (Human), 591 aa.	7.90E-35

6509-6510	cg43967284	819	TCTCTGAGGGCC TGATCCAGTGAC C[G/A]CAGGGTC CCACGAAGGGC CCCGGCT	G	A	Cys	Cys	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTEMBL- ACC:O88635 SERINE/THREONINE PROTEIN KINASE 51PK - MUS MUSCULUS (MOUSE), 416 aa.	1.00E-34
6511-6512	cg29242150	111	TTGATGCAGGGG CTGCTAAGGAGC TT[G/A]TGCGCAA CCTAGTAAGCAT GCAGT	T	G	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTEMBL- ACC:P93804 PHOSPHOGLUCOMUTASE (EC 2.7.5.1) - ZEA MAYS (MAIZE), 469 aa (fragment).	1.30E-34
6513-6514	cg29242150	36	CTGTGAAGATA TTGTCCGTCAGC A[C/T]TGGGCCA CATATGGTCGCC ATTACT	C	T	His	His	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTEMBL- ACC:P93804 PHOSPHOGLUCOMUTASE (EC 2.7.5.1) - ZEA MAYS (MAIZE), 469 aa (fragment).	1.30E-34
6515-6516	cg29242150	60	ACTGGGCCACAT ATGGTCGCCATT A[C/T]TACACACG CTATGACTATGA GAATG	C	T	Tyr	Tyr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTEMBL- ACC:P93804 PHOSPHOGLUCOMUTASE (EC 2.7.5.1) - ZEA MAYS (MAIZE), 469 aa (fragment).	1.30E-34
6517-6518	cg29242150	87	ACACACGCTATG ACTATGAGAATG TT[C/G]GATGCAGG GGCTGCTAAGGA GCTTA	T	C	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTEMBL- ACC:P93804 PHOSPHOGLUCOMUTASE (EC 2.7.5.1) - ZEA MAYS (MAIZE), 469 aa (fragment).	1.30E-34
6519-6520	cg29242150	93	GCTATGACTATG AGAAATGTTGATG C[A/T]GGGGCTG CTAAGGAGCTTA TGGCAA	A	T	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTEMBL- ACC:P93804 PHOSPHOGLUCOMUTASE (EC 2.7.5.1) - ZEA MAYS (MAIZE), 469 aa (fragment).	1.30E-34
6521-6522	cg39867665	176	TGTAATCCCAGC ACTTTGGGAGGC C[G/A]AGGCGGG CGGATCACCTGA GGTCAG	G	A	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39194 !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!! - Homo sapiens (Human), 593 aa.	1.40E-34
6523-6524	cg39867665	278	TACAAAAATTAG CTGGCGGTGGT GG[C/T]GCGCGC CTGTAATCCCAG CTACTTG	C	T	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39194 !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!! - Homo sapiens (Human), 593 aa.	1.40E-34

6525-6526	cg39867665	359	TGGGAGGTGGA GGTGCAGTGAG CC[G/A]JAGATCAC GCCACTGCACCTC CAGCCT	G	A	Pro	Pro	SILENT-CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT-ACC:P39194 !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!! - Homo sapiens (Human), 593 aa.	1.40E-34
6527-6528	cg43261509	514	ATCAAAAAATTAG CCGGGCATGGT GG[C/T]ACGTGC CTGTAATCCAG CTACTTG	C	T	Gly	Gly	SILENT-CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT-ACC:P39188 !!!!! ALU SUBFAMILY J WARNING ENTRY !!!!! - Homo sapiens (Human), 591 aa.	1.60E-34
6529-6530	cg38629253	309	CCACCCACCTCG GCCTCCCAAAGT G[T/C]TGGGATTA CAGGTGTGAGC CACCGG	T	C	Cys	Cys	SILENT-CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT-ACC:P39194 !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!! - Homo sapiens (Human), 593 aa.	3.90E-34
6531-6532	cg39710199	438	TGATCCCGATGG GAATGACGAGAG C[T/C]JAGTAGCAG CTGCTCACCGTT GCGCA	T	C	Leu	Leu	SILENT-CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:CAB50754 PUTATIVE INTEGRAL MEMBRANE TRANSPORT PROTEIN - STREPTOMYCES COELICOLOR, 269 aa.	1.20E-33
6533-6534	cg29219974	292	ACGACGGCGGT TACCGCCCGGAC CG[C/T]GGCTGG AACAAAGTTTCC CGCGTCG	C	T	Arg	Arg	SILENT-CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT-ACC:P35885 DNA GYRASE SUBUNIT A (EC 5.99.1.3) - Streptomyces coelicolor, 864 aa.	2.30E-33
6535-6536	cg29219974	301	GTTACCGCCCGG ACCGCGGCTGG AA[C/T]AAGTGTT CCCGCGTCGTC GGTGACG	C	T	Asn	Asn	SILENT-CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT-ACC:P35885 DNA GYRASE SUBUNIT A (EC 5.99.1.3) - Streptomyces coelicolor, 864 aa.	2.30E-33
6537-6538	cg38821538	224	AAAAATTAGCCA AGCGTGGTGGT AC[A/G]CGCCTG TAATCCAGCTA CTCAGGA	A	G	Thr	Thr	SILENT-CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT-ACC:P39195 !!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!! - Homo sapiens (Human), 591 aa.	3.50E-33

6539-6540	cg38821538	230	TAGCCAGGCGT GGTGGTACACG CCT[G/A]TAATCC CAGCTACTCAGG AGGCTGA	G	A	Leu	Leu	SILENT-CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT-ACC:P39195 !!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!! - Homo sapiens (Human), 591 aa.	3.50E-33
6541-6542	cg43297632	568	CATGGTGAAACC CTGTCTCTACTA A[A/G]AAATACA GAAAAATTAGCTG GGCGT	A	G	Phe	Phe	SILENT-CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT-ACC:P39189 !!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!! - Homo sapiens (Human), 587 aa.	6.70E-33
6543-6544	cg43297632	604	AAATTAGCTGGG CGTGGTGGCGG GC[G/A]CCTGTA GCCCCAGCTACT TGGGAGG	G	A	Gly	Gly	SILENT-CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT-ACC:P39189 !!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!! - Homo sapiens (Human), 587 aa.	6.70E-33
6545-6546	cg33204852	171	CTTCGAGGCGGT CACGGTGATCAA G[C/T]TGGGGAA GAATCCCAGGTA ACCGTC	C	T	Gln	Gln	SILENT-CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT-ACC:Q10818 HYPOTHETICAL 52.9 KD PROTEIN CY274.28C - Mycobacterium tuberculosis, 503 aa.	1.10E-32
6547-6548	cg43999183	151	GTGAGGCGAGGA GAATCGCCTGAA CC[T/C]AGGAGG CAGAGGCTGCA GTGGGCCG	T	C	Pro	Pro	SILENT-CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT-ACC:P39189 !!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!! - Homo sapiens (Human), 587 aa.	1.70E-32
6549-6550	cg43982145	1315	TCAGGGGACG CGGTAAAAAGTAG TT[C/T]CTCCAGA ACACTTCTTCCT TCACAA	C	T	Arg	Arg	SILENT-CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL-ACC:Q24502 SYNAPSE-ASSOCIATED PROTEIN - DROSOPHILA MELANOGASTER (FRUIT FLY), 347 aa.	2.00E-32
6551-6552	cg21632104	205	GGTCGATGGCG TCGACAGCCCCGT TC[T/C]GGACGG GTCCAGAACAGC CGATTTC	T	C	Pro	Pro	SILENT-CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:CAB38487 PUTATIVE HELICASE - STREPTOMYCES COELICOLOR, 815 aa.	3.00E-32
6553-6554	cg21632104	211	TGGCGTCGACA GCCCGTTCTGGA CG[G/A]GTCCAG AACAGCCGATTT CCGCGAC	G	A	Thr	Thr	SILENT-CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:CAB38487 PUTATIVE HELICASE - STREPTOMYCES COELICOLOR, 815 aa.	3.00E-32

6555-6556	cg21632104	373	GCGGGCCGAGC ACATACGGGTGA TC[C/T]GGGTGC AACACAGTCGAT TCCACCG	C		T	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB38487 PUTATIVE HELICASE - STREPTOMYCES COELICOLOR, 815 aa.	3.00E-32
6557-6558	cg21632104	381	AGCACATACGGG TTATCCGGGTGC A[A/G]CACAGTC GATTCCACCGAG GACGAG	A	G		Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB38487 PUTATIVE HELICASE - STREPTOMYCES COELICOLOR, 815 aa.	3.00E-32
6559-6560	cg21632104	388	ACGGGTTATCCG GGTGCAACACAG T[C/T]GATTCCAC CGAGGACGAGA ACAATA	C	T		Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB38487 PUTATIVE HELICASE - STREPTOMYCES COELICOLOR, 815 aa.	3.00E-32
6561-6562	cg21632104	49	CCGGTTGTATT CGTCGACCAGC CA[T/C]TGATCCC CCTGATGCAGGT ACACCG	T	C		Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB38487 PUTATIVE HELICASE - STREPTOMYCES COELICOLOR, 815 aa.	3.00E-32
6563-6564	cg21659365	81	GGATTGGCATCT TCATTGGCGCTC T[C/T]ACCTTCAC GGGTCGCTGG TGGCCT	C	T		Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P73500 PYRIDINE NUCLEOTIDE TRANSHYDROGENASE BETA SUBUNIT - SYNECHOCYSTIS SP. (STRAIN PCC 6803), 480 aa.	5.80E-32
6565-6566	cg21659365	93	TCATTGGCGCTC TCACCTTCACGG G[G/A]TCGCTGG TGGCCTGGGGC AAGCTCT	G	A		Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P73500 PYRIDINE NUCLEOTIDE TRANSHYDROGENASE BETA SUBUNIT - SYNECHOCYSTIS SP. (STRAIN PCC 6803), 480 aa.	5.80E-32
6567-6568	cg44126917	114	CCTGTGGGACCT TTCCATCAGCAG C[C/G]AGCGTCG CTGCAGCAATGG CCAGAT	C	G		Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q10818 HYPOTHETICAL 52.9 KD PROTEIN CY274.28C - Mycobacterium tuberculosis, 503 aa.	5.90E-32
6569-6570	cg44126917	165	CAAAATGCGTCC CAGCCTTTGGTA G[G/A]CCAGCTG GCGTGAGATTGA TCGTCA	G	A		Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q10818 HYPOTHETICAL 52.9 KD PROTEIN CY274.28C - Mycobacterium tuberculosis, 503 aa.	5.90E-32

6571-6572	cg42286566	177	CAATTTGGTCTC GAACTCCTGAGC T[C/T]AAGTGATC CGCCCGCCCTTG GCCTCC	C	T	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39194 !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!! - Homo sapiens (Human), 593 aa.	1.40E-31
6573-6574	cg43926000	426	AGGTCAGGAGTT CAAGACCAAGCCT A[G/A]CCAAATG GTGAAACCCCGT CTCTA	G	A	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39193 !!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!! - Homo sapiens (Human), 593 aa.	1.90E-31
6575-6576	cg43967015	650	GGGAGGCTGAG GCAGGCGGATC ACCT[C/G]GAGATT AGGAGTTCGAGA CTAGCCT	T	C	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39194 !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!! - Homo sapiens (Human), 593 aa.	2.60E-31
6577-6578	cg43967015	719	CCATCTCTACTA AAAAATACAAAA TT[C/G]AGCCAGG CGTGGTGCGC ATGCCCTG	T	C	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39194 !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!! - Homo sapiens (Human), 593 aa.	2.60E-31
6579-6580	cg43967015	755	GGTGGCGCATG CCTGTAATCTCA GC[T/C]ACTCGG GAGGCTGAGGC AGGAGAAT	T	C	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39194 !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!! - Homo sapiens (Human), 593 aa.	2.60E-31
6581-6582	cg43967015	821	GATGGAGGTTGC AGTGGAGCCGA GA[T/C]TGCGC ATTGCACTCAGC CTGGGTA	T	C	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39194 !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!! - Homo sapiens (Human), 593 aa.	2.6E-31
6583-6584	cg20729392	376	CGATGGCAGTCA ACTCAGCGGATGC C[C/T]GATGTCAT CCAGTTCAGCAT GTACA	C	T	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q49800 LYSP - MYCOBACTERIUM LEPRAE, 244 aa.	7.3E-31
6585-6586	cg20729392	466	CCCGGGCATAG GACACAAAGAA CC[A/G]CTAGAG GGCGGGTGAAT GACCAACT	A	G	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q49800 LYSP - MYCOBACTERIUM LEPRAE, 244 aa.	7.3E-31

6587-6588	cg43273813	294	AACATGGTGAAA CCCCGTCTCTAC T/A/GJAAAATATA AAAAATTAGCCA GGCAT	A	G	Phe	Phe	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSPROT-ACC:P39188 !!!!! ALU SUBFAMILY J WARNING ENTRY !!!!! - Homo sapiens (Human), 591 aa.	7.8E-31
6589-6590	cg42487874	343	AAAAAAAATTAG CCAGGTGTGGT GGT/CJGGGCGC CTGTGGTCCCG GCTGCTCG	T	C	Gly	Gly	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSPROT-ACC:P39194 !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!! - Homo sapiens (Human), 593 aa.	8.5E-31
6591-6592	cg44019253	764	CAGGGTTCCAC TGAGAGGGACT GGC/TJTGCGTAT TTTCCTGAAGAA AATGAA	C	T	Gln	Gln	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to TREMBLNEW-ACC:CAB43242 HYPOTHETICAL 66.9 KD PROTEIN - HOMO SAPIENS (HUMAN), 616 aa (fragment).	9.8E-31
6593-6594	cg27356472	67	GTCTCATCGCA CTGCAGGAAGC CA/G/AJAGATATC TGTGAGGGGCA GGTCAAC	G	A	Arg (6809)	Lys (6810)	CONSERVATIVE	complement	Human Gene Similar to SWISSPROT-ID:P01026 COMPLEMENT C3 PRECURSOR (CONTAINS: C3A ANAPHYLATOXIN) - RATTUS NORVEGICUS (RAT), 1663 aa.	1.7E-42
6595-6596	cg34407554	234	TCCGAACGGCC GCACGCGTAGC AGT/CJCTCGCG GATCAAGGTGTC GTACCG	T	C	Val (6811)	Ala (6812)	CONSERVATIVE	dehydrogenase	Human Gene Similar to TREMBLNEW-ID:E1202273 METHYLENETETRAHYDROFOLATE DEHYDROGENASE - MYCOBACTERIUM TUBERCULOSIS, 281 aa.	8.7E-39
6597-6598	cg29344427	445	CAGGACGCCAC CTACCGGTGGTG AA/C/GJCTTCGG GATCCGAGGTC GCCATCT	C	G	Glu (6813)	Asp (6814)	CONSERVATIVE	dehydrogenase	Human Gene Similar to SWISSPROT-ID:P20707 2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.2) (ALPHA-KETOGLUTARATE DEHYDROGENASE) - AZOTOBACTER VINELANDII, 943 aa.	9.4E-31
6599-6600	cg32128336	170	AGACCCGCACG GACTTCGCTATC GA/G/CJGTCTGT CACTCCGTGATG GACGTGT	G	C	Glu (6815)	Asp (6816)	CONSERVATIVE	eph	Human Gene Similar to SPTRMBL-ID:P96420 PUTATIVE ALPHA-ISOPROPYL MALATE SYNTHASE - MYCOBACTERIUM TUBERCULOSIS, 558 aa.	9.8E-47

6601-6602	cg42716656	214	TCCAGCTCATAC TCAGCAGCCACT A/C/TACTGTCCA CCTCTTCTAAAT AAATA	C	T	Val (6817)	Ile (6818)	CONSER VATIVE	glycoprotein	Human Gene Similar to SWISSPROT- ID:Q09332 UDP- GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT) - DROSOPHILA MELANOGASTER (FRUIT FLY), 1548 aa.	2.8E-43
6603-6604	cg20725546	453	AGCGGAAGGGT CTCGAGGTCGGT GA/C/G/TCCCTAC TTGACGAAGATT CGATCG	C	G	Asp (6819)	Glu (6820)	CONSER VATIVE	kinase	Human Gene Similar to SWISSPROT- ID:O06821 PHOSPHOGLYCERATE KINASE (EC 2.7.2.3) - MYCOBACTERIUM TUBERCULOSIS, 412 aa.	9.4E-42
6605-6606	cg29345567	449	GTTACCTGCGT CTGCTGGCAGG AC/G/A/CGACCC CCACCACATCTG CGAGGCC	G	A	Arg (6821)	His (6822)	CONSER VATIVE	phosphatase	Human Gene Similar to SWISSPROT- ID:P06987 IMIDAZOLEGLYCEROL- PHOSPHATE DEHYDRATASE (EC 4.2.1.19) (IGPD) / HISTIDINOL- PHOSPHATASE (EC 3.1.3.15) - ESCHERICHIA COLI, 355 aa.	1.4E-33
6607-6608	cg43083165	546	TTCTGTCAGCCT CTCACCCAGCGT G/G/A/CCAGCAC GTGGCGAAGCT CAGCAC	G	A	Ala (6823)	Val (6824)	CONSER VATIVE	struct	Human Gene Similar to SWISSPROT- ID:P08590 MYOSIN LIGHT CHAIN 1, SLOW-TWITCH MUSCLE BVENTRICULAR ISOFORM (MLC1SB) (ALKALI) - HOMO SAPIENS (HUMAN), 194 aa.	1.1E-36
6609-6610	cg44127439	43	AGACCATGCGC TTGAGGACCTCG A/C/T/GGTATCCA TCCTGTCTCTCGT AGGAG	C	T	Val (6825)	Ile (6826)	CONSER VATIVE	synthase	Human Gene Similar to SWISSPROT- ID:P19206 BIOTIN SYNTHASE (EC 2.8.1.6) (BIOTIN SYNTHETASE) - BACILLUS SPHAERICUS, 332 aa.	7.9E-45
6611-6612	cg32152874	167	CATGGCCATGCA CCTGCTCACGCA C/G/A/ACCTGCG CCACAAAGTGG GCGGTG	G	A	Asp (6827)	Asn (6828)	CONSER VATIVE	transcript factor	Human Gene Similar to SPTREMBL- ID:Q24140 NEURON SPECIFIC ZINC FINGER TRANSCRIPTION FACTOR - DROSOPHILA MELANOGASTER (FRUIT FLY), 664 aa.	1.5E-39
6613-6614	cg43103077	2229	CATGTAAATGT TTATAAGAAGCT A/C/T/TTTTCTT CATGGGAAGAAA TTCCC	C	T	Val (6829)	Ile (6830)	CONSER VATIVE	transferase	Human Gene Similar to TREMBLNEW- ID:G2804586 1,4- A -D-GLUCAN: 1,4-A - D-GLUCAN 6-A-D-(1,4-A-D-GLUCANO) TRANSFERASE (EC 2.4.1.18) - AGROBACTERIUM TUMEFACIENS, 734 aa.	3.5E-42

6615-6616	cg43287601	1507	ACCGTGTGGCCCA AGGCTGGTCTTG A/A/TCTCCTGAC CTCAAGTGATCC GCCCG	A	T	Thr (6831)	Ser (6832)	CONSERVATIVE	UNCLASSIFIED	Human Gene Similar to SWISSPROT-ACC:P39188 !!! ALU SUBFAMILY J WARNING ENTRY !!!! - Homo sapiens (Human), 591 aa.	2.70E-46
6617-6618	cg20297086	145	ACGACCCCTCACC GCGGCGATGTC CA/A/GJGGTGT GCACGACAAGTA CCCGGAG	A	G	Lys (6833)	Arg (6834)	CONSERVATIVE	UNCLASSIFIED	Human Gene Similar to SPTREMBL-ACC:P95543 ELONGATION FACTOR TU1 - PLANOBISPORA ROSEA, 397 aa.	9.00E-45
6619-6620	cg43129081	318	CTCCCGAGTAGC TGGGACTACAGG C/A/GJCGCGCCA CCACGCCCGGC TAATTTT	A	G	His (6835)	Arg (6836)	CONSERVATIVE	UNCLASSIFIED	Human Gene Similar to SWISSPROT-ACC:P39189 !!! ALU SUBFAMILY SB WARNING ENTRY !!!! - Homo sapiens (Human), 587 aa.	3.70E-41
6621-6622	cg43928088	647	TACTAAATATAC AAAATTAGCCAG G/C/TJGTGGTG CACACGCGCTGA ATCCCA	C	T	Arg (6837)	His (6838)	CONSERVATIVE	UNCLASSIFIED	Human Gene Similar to SPTREMBL-ACC:O60448 NEURONAL THREAD PROTEIN AD7C-NTP - HOMO SAPIENS (HUMAN), 375 aa.	5.20E-40
6623-6624	cg16836645	361	CGGCAAGGGCT TCGGCCACAGCT CG/G/AJCTTCAA GCGGCATCGGC GCACGCA	G	A	Asp (6839)	Asn (6840)	CONSERVATIVE	UNCLASSIFIED	Human Gene Similar to SPTREMBL-ACC:O35483 KRUPPLE-RELATED ZINC FINGER PROTEIN - MUS MUSCULUS (MOUSE), 812 aa.	7.50E-39
6625-6626	cg43963181	732	GCTTCTTTTCTT TCTTCTCTGGTA T/CJCTGAGGATT CCAACTGGATC TAGT	T	C	Ile (6841)	Val (6842)	CONSERVATIVE	UNCLASSIFIED	Human Gene Similar to TREMBLNEW-ACC:CAB43966 PUTATIVE ACYL-COA BINDING PROTEIN - ARABIDOPSIS THALIANA (MOUSE-EAR CRESS), 354 aa.	2.60E-38
6627-6628	cg29256713	97	TCCATTGCTCT CGCTGTCCGGA GG/T/CJCGGTTT GAGGTCGAACCT CATTACC	T	C	Val (6843)	Ala (6844)	CONSERVATIVE	UNCLASSIFIED	Human Gene Similar to SPTREMBL-ACC:O86812 HYPOTHETICAL 52.9 KD PROTEIN - STREPTOMYCES COELICOLOR, 493 aa.	8.70E-38
6629-6630	cg43090974	404	TCTCGAACTCCT GACCTCAAGATC C/A/GJCTGCCT CGGCCTCCCAAA GIGCTG	A	G	His (6845)	Arg (6846)	CONSERVATIVE	UNCLASSIFIED	Human Gene Similar to SWISSPROT-ACC:P39195 !!! ALU SUBFAMILY SX WARNING ENTRY !!!! - Homo sapiens (Human), 591 aa.	9.20E-36

6631-6632	cg43930764	465	GATGATGGAGAC GCCAAAGAGAA G/A/GCAAGTCG CATGTTCCAGAC GTC	A	G	Val (6847)	Ala (6848)	CONSERVATIVE	UNCLASSIFIED	Human Gene Similar to SPTREMBL-ACC:O09111 NEURONAL PROTEIN 15.6 - MUS MUSCULUS (MOUSE), 133 aa.	3.10E-35
6633-6634	cg42667624	935	CTGCATAGCTGG AAATGCTCTTAATT [C/G]ATCCTCAC ACTTAACGTGATA GTTT	C	G	Glu (6849)	Gln (6850)	CONSERVATIVE	UNCLASSIFIED	Human Gene Similar to SWISSPROT-ACC:P39195 !!! ALU SUBFAMILY SX WARNING ENTRY !!!! - Homo sapiens (Human), 591 aa.	5.00E-35
6635-6636	cg42667624	940	TAGCTGGAATG TCTTAATCTATC [C/T]TCACACTTA ACTGATAGTTTG GCTA	C	T	Arg (6851)	Lys (6852)	CONSERVATIVE	UNCLASSIFIED	Human Gene Similar to SWISSPROT-ACC:P39195 !!! ALU SUBFAMILY SX WARNING ENTRY !!!! - Homo sapiens (Human), 591 aa.	5.00E-35
6637-6638	cg39667665	280	CAAAAAATTAGCT GGCGTGGTGG CG[C/G]GCGCCT GTAATCCAGCT ACTTGGG	C	G	Ala (6853)	Gly (6854)	CONSERVATIVE	UNCLASSIFIED	Human Gene Similar to SWISSPROT-ACC:P39194 !!! ALU SUBFAMILY SQ WARNING ENTRY !!!! - Homo sapiens (Human), 593 aa.	1.40E-34
6639-6640	cg38821538	331	TCACGCCACTGT ACTCCAGCCTGG G[C/T]AACAGAG CAAGACTCTGTC TCTAAA	C	T	Ala (6855)	Val (6856)	CONSERVATIVE	UNCLASSIFIED	Human Gene Similar to SWISSPROT-ACC:P39195 !!! ALU SUBFAMILY SX WARNING ENTRY !!!! - Homo sapiens (Human), 591 aa.	3.50E-33
6641-6642	cg42657675	300	TGGCTCATGCCT GTAATCCAGCA T[T/C]TTGGGAGG CCGAGATGGGC GGATCA	T	C	Lys (6857)	Arg (6858)	CONSERVATIVE	UNCLASSIFIED	Human Gene Similar to SWISSPROT-ACC:P39192 !!! ALU SUBFAMILY SC WARNING ENTRY !!!! - Homo sapiens (Human), 585 aa.	1.80E-32
6643-6644	cg21632104	116	ACGGTCTGCGG CGGCTTCGTGCA CT[C/A]CCCCGAT GACCCCTCCCGT GGACAC	C	A	Gly (6859)	Val (6860)	CONSERVATIVE	UNCLASSIFIED	Human Gene Similar to TREMBLNEW-ACC:CAB38487 PUTATIVE HELICASE - STREPTOMYCES COELICOLOR, 815 aa.	3.00E-32
6645-6646	cg43926000	386	ATCCACGCACTT TGGGAGGCCAA GGT[C/G]GGGCGG ATCACTTGAGGT CAGGAGT	T	C	His (6861)	Arg (6862)	CONSERVATIVE	UNCLASSIFIED	Human Gene Similar to SWISSPROT-ACC:P39193 !!! ALU SUBFAMILY SP WARNING ENTRY !!!! - Homo sapiens (Human), 593 aa.	1.90E-31

6647-6648	cg37854509	79	TGTGTGTGCCGG TGCTCCAGCAGC GTATGGACAGG CGGCTGAAGCA GCAGCCA	T	A	Thr (6863)	Ser (6864)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to REMTREMBL- ACC:E1329909 DJ733D15.1 (ZINC- FINGER PROTEIN) - HOMO SAPIENS (HUMAN), 496 aa (fragment).	3.20E-31
6649-6650	cg29344427	243	TCCGTGACGTTG GTGTAAAGGCGCA AATGAAACCTCAG CCAACTCGTCGA CTGGT	A	G	Phe (6865)	Leu (6866)	NON- CONSER VATIVE	dhydrog enase	Human Gene Similar to SWISSPROT- ID:P20707 2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.2) (ALPHA- KETOGLUTARATE DEHYDROGENASE) - AZOTOBACTER VINELANDII, 943 aa.	9.40E-31
6651-6652	cg32128336	137	TCGGCTACGAGT ACTCTCCGGAGA TTCGJTATGCCA GACCCGCACGG ACTTCG	C	G	Ile (6867)	Met (6868)	NON- CONSER VATIVE	eph	Human Gene Similar to SPTREMBL- ID:P96420 PUTATIVE ALPHA- ISOPROPYL MALATE SYNTHASE - MYCOBACTERIUM TUBERCULOSIS, 558 aa.	9.80E-47
6653-6654	cg32128336	252	TAATCTGCCGGC TACCGTCGAGAT GGAJGCACTCC GAACACCTACGC CGACCA	G	A	Gly (6869)	Ser (6870)	NON- CONSER VATIVE	eph	Human Gene Similar to SPTREMBL- ID:P96420 PUTATIVE ALPHA- ISOPROPYL MALATE SYNTHASE - MYCOBACTERIUM TUBERCULOSIS, 558 aa.	9.80E-47
6655-6656	cg38912931	190	TAAGTTCACCTG CCTCTGGGAGTC TGTGTCCTGTA GGACCAACTAAC AACACC	G	T	Gly (6871)	Cys (6872)	NON- CONSER VATIVE	eph	Human Gene Similar to SWISSPROT- ID:P06759 APOLIPOPROTEIN C-III PRECURSOR (APO-CIII) - RATTUS NORVEGICUS (RAT), 100 aa.	5.50E-37
6657-6658	cg42716656	373	GGACCCCTTAGCA AAACTACTGTCT GATCAGTGAAA GAAATCTCTGGC TCTAAG	A	C	Ser (6873)	Ala (6874)	NON- CONSER VATIVE	glycoprot ein	Human Gene Similar to SWISSPROT- ID:Q09332 UDP- GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.) (DUGT) - DROSOPHILA MELANOGASTER (FRUIT FLY), 1548 aa.	2.80E-43
6659-6660	cg42512386	776	CCAAAGAGGGCT GGACAGTTACCA GATGAGATGA TGAGGATGGTGA TGATAT	A	G	Arg (6875)	Gly (6876)	NON- CONSER VATIVE	kinesin	Human Gene Similar to SPTREMBL- ID:O01349 KINESIN-73 - DROSOPHILA MELANOGASTER (FRUIT FLY), 1921 aa.	4.10E-36

6661-6662	cg42719442	411	AGCAAATACACC CAGGAGGAGTA GA[G/A]GGCAGG AAATAATCAAAC TCAGAGC	G	A	Gly (6877)	Arg (6878)	NON- CONSER VATIVE	nuclease	Human Gene Similar to SWISSNEW- ID:P11369 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - MUS MUSCULUS (MOUSE), 1300 aa. lpcds:SWISSPROT-ID:P11369 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - MUS MUSCULUS (MOUSE), 1300 aa	9.70E-47
6663-6664	cg43974178	1724	TGTGATTGTGGA GGAACAGACAGA G[G/A]AGACCCA AGTGACTGAAGA AGTGAC	G	A	Glu (6879)	Lys (6880)	NON- CONSER VATIVE	struct	Human Gene Similar to SPTREMBL- ID:Q10465 TITIN, SKELETAL MUSCLE ISOFORM (EC 2.7.1.-) (CONNECTIN) - HOMO SAPIENS (HUMAN), 7962 aa (fragment).	6.40E-40
6665-6666	cg38335527	439	ACGGCGTGCAA GGACAAGCAGCT GC[A/G]GATCTTT GACCCAGAACAA AAGCCG	A	G	Gln (6881)	Arg (6882)	NON- CONSER VATIVE	struct	Human Gene Similar to SWISSPROT- ID:Q92176 CORONIN-LIKE PROTEIN P57 - BOS TAURUS (BOVINE), 461 aa.	7.00E-37
6667-6668	cg39517733	271	CACTTGGGGTAG CAGCCTTCCAGG CT[C]ACGGAGAT CTGTAGGCACT GTCCA	T	C	Ser (6883)	Gly (6884)	NON- CONSER VATIVE	struct	Human Gene Similar to SPTREMBL- ID:Q14425 GASTRIC MUCIN - HOMO SAPIENS (HUMAN), 850 aa (fragment).	3.90E-36
6669-6670	cg44127439	163	GCCTCCTTGATG GAAGCCGCCTTC TT[C]GTCGTCGA CAAACCCCAAC AGACA	T	C	Lys (6885)	Glu (6886)	NON- CONSER VATIVE	synthase	Human Gene Similar to SWISSPROT- ID:P19206 BIOTIN SYNTHASE (EC 2.8.1.6) (BIOTIN SYNTHETASE) - BACILLUS SPHAERICUS, 332 aa.	7.90E-45
6671-6672	cg44127439	85	TCGTAGGAGTGG GTACTGCAGATC T[C/T]GCCGTAAT GAGACGAGCG GTATTG	C	T	Glu (6887)	Lys (6888)	NON- CONSER VATIVE	synthase	Human Gene Similar to SWISSPROT- ID:P19206 BIOTIN SYNTHASE (EC 2.8.1.6) (BIOTIN SYNTHETASE) - BACILLUS SPHAERICUS, 332 aa.	7.90E-45

6673-6674	cg43103077	2058	GAATGAGCTGTG TCTACCAGTTCT T[G/T]TAGCTCTT CAGGTGTTCCAT AACGG	G	T	Gln (6889)	Lys (6890)	NON- CONSER VATIVE	transfe se	Human Gene Similar to TREMBLNEW- ID:G2804586 1,4- A- D-GLUCAN: 1,4-A- D-GLUCAN 6-A-D-(1,4-A-D-GLUCANO) TRANSFERASE (EC 2.4.1.18) - AGROBACTERIUM TUMEFACIENS, 734 aa.	3.50E-42
6675-6676	cg43103077	2205	CCTTTGATTCTT GGTAGTACATTG C[A/T]TGTAATAA GTTTATAAGAAG CTACT	A	T	Cys (6891)	Ser (6892)	NON- CONSER VATIVE	transfe se	Human Gene Similar to TREMBLNEW- ID:G2804586 1,4- A- D-GLUCAN: 1,4-A- D-GLUCAN 6-A-D-(1,4-A-D-GLUCANO) TRANSFERASE (EC 2.4.1.18) - AGROBACTERIUM TUMEFACIENS, 734 aa.	3.50E-42
6677-6678	cg43103077	2298	CTTAGACTCCGT GGCTTCTTTGGT C[T/C]GGAATGCT TAAACTCATATG AGTGT	T	C	Arg (6893)	Gly (6894)	NON- CONSER VATIVE	transfe se	Human Gene Similar to TREMBLNEW- ID:G2804586 1,4- A- D-GLUCAN: 1,4-A- D-GLUCAN 6-A-D-(1,4-A-D-GLUCANO) TRANSFERASE (EC 2.4.1.18) - AGROBACTERIUM TUMEFACIENS, 734 aa.	3.50E-42
6679-6680	cg39433010	372	TCTAATGTACCT TCCTGCATAGTT A[C/T]CTAGTTGG GTAATGGGAGGT TGGAA	C	T	Gly (6895)	Asp (6896)	NON- CONSER VATIVE	transfe se	Human Gene Similar to SPTREMBL- ID:Q12630 TRANSKETOLASE (EC 2.2.1.1) (GLYCOALDEHYDE TRANSFERASE) - KLUYVEROMYCES LACTIS (YEAST), 679 aa.	3.70E-35
6681-6682	cg38434693	108	GATCCCGCGGA CCCAGACATGGA AA[T/C]GATCGCG AGGGCAAGGAT CCTGTCA	T	C	Met (6897)	Thr (6898)	NON- CONSER VATIVE	transport	Human Gene Similar to TREMBLNEW- ID:E1237464 ABC TRANSPORTER ATP BINDING PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 542 aa.	7.80E-34
6683-6684	cg38434693	26	CCGAACGCGTGT CTTGCCCGGTGA A[A/G]CCCTTCCC GCAGCAGGTTCA GTACG	A	G	Thr (6899)	Ala (6900)	NON- CONSER VATIVE	transport	Human Gene Similar to TREMBLNEW- ID:E1237464 ABC TRANSPORTER ATP BINDING PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 542 aa.	7.80E-34
6685-6686	cg42879031	195	GCCTCTGGGTTG TACTTATAATCCA [C/T]CTCAGATC TGTGGTGTGGC ACTG	C	T	Val (6901)	Met (6902)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14526 KIAA0290 - HOMO SAPIENS (HUMAN), 906 aa (fragment).	1.10E-47

6687-6688	cg39513248	426	GCAGCTTGCAAG ATCGGTGTTAGA C[G/T]GGGATTCA GTCAGAGCCAG GTGGAA	G	T	Gly (6903)	Trp (6904)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SP TREMBL- ACC:O75160 KIAA0672 PROTEIN - HOMO SAPIENS (HUMAN), 818 aa.	2.70E-47
6689-6690	cg44911957	940	AGAGGATAATAA AGAACATTCAAT T[G/T]AGGTTTCA TTGTTTGGGAA CTTT	G	T	Glu (6905)	End (6906)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB05201 Y37A1B.1 PROTEIN - CAENORHABDITIS ELEGANS, 1222 aa.	1.60E-46
6691-6692	cg43287601	1528	TTGAACCTCTGA CCTCAAGTGATC C[G/A]CCCGCCT CGGCCTCCAAA GTGCTG	G	A	Ala (6907)	Thr (6908)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39188 !!! ALU SUBFAMILY J WARNING ENTRY !!!! - Homo sapiens (Human), 591 aa.	2.70E-46
6693-6694	cg43967859	773	GTGTGATCAGC TGGCCCTTAAT C[C/T]CTGGAGAA AACCATCTTCAT TAAAA	C	T	Gly (6909)	Arg (6910)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q09315 HYPOTHETICAL 42.0 KD PROTEIN F25B5.3 IN CHROMOSOME III - Caenorhabditis elegans, 376 aa.	3.80E-46
6695-6696	cg39527289	295	CCGGCTCACCGA GGACAAAACGT T[C/T]GCGAGAAC GTCGAAGAGGC CGTCGG	C	T	Arg (6911)	Cys (6912)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SP TREMBL- ACC:O53204 ABC-TRANSPOTER ATP BINDING PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 558 aa.	4.80E-46
6697-6698	cg43923983	711	GCAATATCTTCT TGGGAGCACAG GG[C/G]AAAGGT AAGTGCTTCAGT GAAGCCA	C	G	Cys (6913)	Ser (6914)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD26855 PHENYLALANYL TRNA SYNTHETASE BETA SUBUNIT - MUS MUSCULUS (MOUSE), 589 aa.	6.30E-44
6699-6700	cg42920024	260	CAATGAGCCGAG ATCATGCCACTG C[G/A]CTCCAGC CTGGGCAACAG GGTGAGA	G	A	Ala (6915)	Thr (6916)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39194 !!! ALU SUBFAMILY SQ WARNING ENTRY !!!! - Homo sapiens (Human), 593 aa.	1.10E-43
6701-6702	cg43302383	507	CTGAACCCACAG GACTTCATTGGC T[G/C]CCTGAAC GTGAAGGCGACT TTTTAT	G	C	Cys (6917)	Ser (6918)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P56198 FAT-SPECIFIC PROTEIN FSP27 - Mus musculus (Mouse), 239 aa.	1.60E-43

6703-6704	cg42734969	63	AAGTGCACAACT CTCTGTCTGAT G A/G CCATGAT GAGAAATATGGA GTCCCT	A	G	Asp (6919)	Gly (6920)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q16526 PHOTOLYASE-LIKE 1 (PHOTOLYASE HOMOLOG) - HOMO SAPIENS (HUMAN), 586 aa (fragment).	3.40E-42
6705-6706	cg43989360	408	TGTCGCCCCAGG CTGGAGTGCAGT GGT C GCAATCT TGGCTCACTGCA ACCTCC	T	C	Cys (6921)	Arg (6922)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39193 !!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!! - Homo sapiens (Human), 593 aa.	4.60E-42
6707-6708	cg43989360	495	CCTGAGTAGCTG GGATTACAGGCA T G C CACCACCA CGCCCGGCTAAT TTTTT	G	C	Ala (6923)	Pro (6924)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39193 !!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!! - Homo sapiens (Human), 593 aa.	4.60E-42
6709-6710	cg43989360	504	CTGGGATTACAG GCATGCACCACC A C T GCCCGGC TAATTTTTTGAT TTTTA	C	T	Arg (6925)	Cys (6926)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39193 !!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!! - Homo sapiens (Human), 593 aa.	4.60E-42
6711-6712	cg43989360	536	CTAATTTTTTGT TTTTTAGTAGAG A G CGGGGTTTC GCCATGTTGGCC AGGC	A	G	Asp (6927)	Gly (6928)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39193 !!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!! - Homo sapiens (Human), 593 aa.	4.60E-42
6713-6714	cg43280136	1093	AAATATGTCATC GGCTGGAAGAAA T C T GGAGGGC AGCCACCGCC CGAGGAG	C	T	Ser (6929)	Leu (6930)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O35412 SPA-1 LIKE PROTEIN P1294 - RATTUS NORVEGICUS (RAT), 1822 aa.	3.40E-41
6715-6716	cg43129081	329	CTGGGACTACAG GCACGCGCCAC CA C T GCCCGG CTAATTTTTTGT TTTTTA	C	T	Arg (6931)	Cys (6932)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39189 !!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!! - Homo sapiens (Human), 587 aa.	3.70E-41
6717-6718	cg43928088	644	CTCTACTAAAA TACAAAAATTAGC C A G GGCGTGG TGGCACAGCCT GTAATC	A	G	Leu (6933)	Pro (6934)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60448 NEURONAL THREAD PROTEIN AD7C-NTP - HOMO SAPIENS (HUMAN), 375 aa.	5.20E-40

6719-6720	cg39732713	876	CTCACTTTGTCA CCCAGGCTGGA GT[A/G]CAGTGG TGTGATCATAGC TCACTGC	A	G	Thr (6935)	Ala (6936)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39189 !!!! ALU SUBFAMILY SB WARNING ENTRY !!!! - Homo sapiens (Human), 587 aa.	2.90E-39
6721-6722	cg44127437	206	CCCTCTTCGTAAC TATCGCGTGTGG A[G/A]CGCTATCG GGATTCCACGCC ACGAT	G	A	Ala (6937)	Thr (6938)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P95095 CARBON STARVATION PROTEIN A HOMOLOG - Mycobacterium tuberculosis, 758 aa.	4.40E-39
6723-6724	cg42868441	433	TCCCAGCTACTT GGGAGGCTGAG GC[A/G]GGAGAA TTGCTTGAACCC AGGAGGC	A	G	Gln (6939)	Arg (6940)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39194 !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! - Homo sapiens (Human), 593 aa.	6.40E-38
6725-6726	cg29256713	58	CGATTGGGTGAC GCTGAGTCGTTT CT[C/G]GAACATCA TCGATTCCATTC GCTCT	T	C	Leu (6941)	Pro (6942)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPREMBL- ACC:O86812 HYPOTHETICAL 52.9 KD PROTEIN - STREPTOMYCES COELICOLOR, 493 aa.	8.70E-38
6727-6728	cg43921362	1276	ATGGACGTTAAC TGACCTAAATAC TT[C/A]AACCTCCT TCTCAATATAGT CGCTC	T	C	Lys (6943)	Glu (6944)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BA081908 HRPET-3 - HALOCYNTHIA RORETZI (SEA SQUIRT), 680 aa.	1.70E-37
6729-6730	cg38213630	158	AGAAACCAATC CCCATTGAGCTT A[G/T]CCACATCG AGTTCCCTCTC GCGAA	G	T	Ala (6945)	Asp (6946)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPREMBL- ACC:Q63213 ALPHA-2U GLOBULIN (RAT SALIVARY GLAND (ALPHA)2(MU) GLOBULIN, TYPE 1) - RATTUS NORVEGICUS (RAT), 181 aa.	4.00E-37
6731-6732	cg41616497	214	TGTCGCCCCAGG CTGGAGTGCAAT GG[C/T]GTGATCT CAGCTCACTGCA AACTCC	C	T	Arg (6947)	Cys (6948)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39194 !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! - Homo sapiens (Human), 593 aa.	9.70E-37
6733-6734	cg43320455	830	AAGACTACTCAA TTACCCCTATTTTA [G/A]AGGGTTGG TTTGTTTGTGT TTTG	G	A	Glu (6949)	Lys (6950)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39188 !!!! ALU SUBFAMILY J WARNING ENTRY !!!! - Homo sapiens (Human), 591 aa.	1.80E-36

6735-6736	cg27927141	313	CTTGTTCTTTAC GATGTAGGCATC CT/CJCTGGTTCC AGCAGGAAGTGA GGCAG	T	C	Glu (6951)	Gly (6952)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SP TREMBL- ACC:008722 TRANSMEMBRANE RECEPTOR UNC5H2 - RATTUS NORVEGICUS (RAT), 945 aa.	5.80E-36
6737-6738	cg43929320	274	GAAGATCTCTCT GCAAGAGTAGAT G[C/A]JAGTTAAGG AAGAAAATCTGA AGCTA	C	A	Ala (6953)	Glu (6954)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD26690 SHORT COILED COIL PROTEIN SCOCO - MUS MUSCULUS (MOUSE), 82 aa.	1.90E-35
6739-6740	cg35929441	332	TGGACCATTTCC TTACACCATATTA [C/A]AAAAATTAA CTCAAGATGGAT TAAA	C	A	Tyr (6955)	End (6956)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SP TREMBL- ACC:000363 PUTATIVE P150 - HOMO SAPIENS (HUMAN), 1275 aa.	3.30E-35
6741-6742	cg35929441	339	TTTCCTTACACC ATATTACAAAAAT [T/C]AACTCAAGA TGGATTAAAGAC TTAA	T	C	End (6957)	Gln (6958)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SP TREMBL- ACC:000363 PUTATIVE P150 - HOMO SAPIENS (HUMAN), 1275 aa.	3.30E-35
6743-6744	cg35929441	457	GGGCAAGAGATT CATGACAAAAAC A[C/T]CAAAAAGCA ATTGCAACAAAA GCAAA	C	T	Thr (6959)	Ile (6960)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SP TREMBL- ACC:000363 PUTATIVE P150 - HOMO SAPIENS (HUMAN), 1275 aa.	3.30E-35
6745-6746	cg42667624	617	CTGGTCTGTATA TGGTTGTTAATT C[G/A]GTGCTCTCC ATGGGGTAACAA GGGCC	G	A	Arg (6961)	End (6962)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39195 !!! ALU SUBFAMILY SX WARNING ENTRY !!!! - Homo sapiens (Human), 591 aa.	5.00E-35
6747-6748	cg39667665	180	ATCCAGCACTT TGGGAGGCCGA GG[C/T]GGGCGG ATCACCTGAGGT CAGGAGT	C	T	Arg (6963)	Trp (6964)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39194 !!! ALU SUBFAMILY SQ WARNING ENTRY !!!! - Homo sapiens (Human), 593 aa.	1.40E-34
6749-6750	cg42481380	383	GGAGAAATGGTGT GAACCCAGGAG GC[G/A]GAGCTT GCAGTGAGCCAA TATCGCG	G	A	Gly (6965)	Arg (6966)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39189 !!! ALU SUBFAMILY SB WARNING ENTRY !!!! - Homo sapiens (Human), 587 aa.	1.50E-34

6751-6752	cg42208556	178	AGACACGCTG GCCAATGTAGCG AAIAGJCCCCATC TCTACTACAAAT ATAAAA	A	G	Phe (6967)	Leu (6968)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39193 !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! - Homo sapiens (Human), 593 aa.	1.60E-34
6753-6754	cg43261509	433	CTTTGGGAGGCT GAGCGGGCGG ATC/TACTTAAG GTCAGGAGTTCA AGACCA	C	T	Ser (6969)	Leu (6970)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39188 !!!! ALU SUBFAMILY J WARNING ENTRY !!!! - Homo sapiens (Human), 591 aa.	1.60E-34
6755-6756	cg25239778	299	AACCCGGGAAGT GGAGGCTGCAG TG[A/G]GCCAGG ATCATGCCCACTG CACTCCA	A	G	Glu (6971)	Gly (6972)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39194 !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! - Homo sapiens (Human), 593 aa.	1.80E-34
6757-6758	cg38629253	224	TGCCCCGGCTAAT TTTTGTATTTTA[A/G]TAGAGACGG GGTTTCACCATG TTGG	A	G	Asn (6973)	Ser (6974)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39194 !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! - Homo sapiens (Human), 593 aa.	3.90E-34
6759-6760	cg42894694	931	CGGGTTCAAGC GATTCTCCTGCC TCIA/GJCCCTCCT GAGTAGCTGGG ACTACAG	A	G	Ser (6975)	Gly (6976)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39194 !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! - Homo sapiens (Human), 593 aa.	8.30E-34
6761-6762	cg39710199	389	ACGTCCATCGTC AGTCCGACCCG GC[T/C]GCCAG GAAGCGCCCGG CGACGATG	T	C	Ser (6977)	Gly (6978)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB50754 PUTATIVE INTEGRAL MEMBRANE TRANSPORT PROTEIN - STREPTOMYCES COELICOLOR, 269 aa.	1.20E-33
6763-6764	cg43280209	268	GACTACAGATGC CCACAACACGCG CT[C]JAGCTAATT TTTGATTTTGTAG TAGA	T	C	Leu (6979)	Pro (6980)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39194 !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! - Homo sapiens (Human), 593 aa.	1.90E-33

6765-6766	cg43276863	779	CCTGATGGGCTA GCCATTCTGAC TTTCJGATGTGA CAGGGGATAAG GACGTG	T	C	Leu (6981)	Ser (6982)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD39637 F9L1.2 PROTEIN - ARABIDOPSIS THALIANA (MOUSE- EAR CRESS), 290 aa.	2.50E-33
6767-6768	cg38821538	172	GTTCAAGATCAG CCTGGCCAAACAT GJAGJTGAAACC CTATCTCTACTA AAATTA	A	G	Asp (6983)	Gly (6984)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39195 !!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!! - Homo sapiens (Human), 591 aa.	3.50E-33
6769-6770	cg38821538	246	TACACGCCTGTA ATCCCAGCTACT CJAGJGGAGGCT GAGGCAGGAGA ATTGTTT	A	G	Arg (6985)	Gly (6986)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39195 !!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!! - Homo sapiens (Human), 591 aa.	3.50E-33
6771-6772	cg43297632	433	GCCATGCCCTGT CTTTGTTCTCAT JAGJAAATAGTCAC TGGGGCCGGGC GCAGT	A	G	Tyr (6987)	His (6988)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39189 !!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!! - Homo sapiens (Human), 587 aa.	6.70E-33
6773-6774	cg43297632	456	ATAAATAGTCAC TGGGGCCGGGC GCJAGJGTGACT CACGCCTGTAAT CCCAGCA	A	G	Leu (6989)	Pro (6990)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39189 !!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!! - Homo sapiens (Human), 587 aa.	6.70E-33
6775-6776	cg43297632	623	GCGGGCGCCTG TAGCCCCAGCTA CTTCJGGGAGG CTGAGCGGGA GAATGGCA	T	C	Gln (6991)	Arg (6992)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39189 !!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!! - Homo sapiens (Human), 587 aa.	6.70E-33
6777-6778	cg43297632	636	GCCCCAGCTACT TGGGAGGCTGA GGCCTJGGGAGA ATGGCAATGGCG TGAACCC	C	T	Ala (6993)	Thr (6994)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39189 !!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!! - Homo sapiens (Human), 587 aa.	6.70E-33

6779-6780	cg42657675	301	GGTTCATGCCTG TAATCCCAGCAT TTTCTGGGAGG CCGAGATGGC GGATCAC	T	C	Lys (6995)	Glu (6996)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39192 !!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!! - Homo sapiens (Human), 585 aa.	1.80E-32
6781-6782	cg23333150	300	CGCCCGCCAGC ATGCCCGGCCAA TTCTTTTGTATT TTAGTAGAGAC GGGGT	C	T	Glu (6997)	Lys (6998)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39194 !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!! - Homo sapiens (Human), 593 aa.	4.00E-32
6783-6784	cg42475469	345	TCACCATGTTGG CCAGACTGGTCT C[G/A]AACTCCTG ACCTCAAGTGAT CCACC	G	A	Ser (6999)	Leu (7000)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39194 !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!! - Homo sapiens (Human), 593 aa.	5.70E-32
6785-6786	cg44126917	125	TTTCCATCAGCA GCCAGCGTCGC TGCTAGCAATG GCCAGATCAAAA TGCCTC	C	T	Ala (7001)	Thr (7002)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q10818 HYPOTHETICAL 52.9 KD PROTEIN CY274.28C - Mycobacterium tuberculosis, 503 aa.	5.90E-32
6787-6788	cg44126917	80	AGTTCTCCAATC AGAACCGTCGAT C[C/T]CAAGAGA GCCTGTGGGAC CTTTCCA	C	T	Gly (7003)	Arg (7004)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q10818 HYPOTHETICAL 52.9 KD PROTEIN CY274.28C - Mycobacterium tuberculosis, 503 aa.	5.90E-32
6789-6790	cg42286566	178	AATTGGTCTCG AACTCCTGAGCT C[A/G]AGTGATCC GCCCGCCTTGG CCTCCC	A	G	Lys (7005)	Glu (7006)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39194 !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!! - Homo sapiens (Human), 593 aa.	1.40E-31
6791-6792	cg43926000	384	TAATCCCAGCAC TTTGGGAGGCCA A[G/A]GTGGGCG GATCACTTGAGG TCAGGA	G	A	Leu (7007)	Phe (7008)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39193 !!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!! - Homo sapiens (Human), 593 aa.	1.90E-31
6793-6794	cg43926000	392	GCACCTTTGGGAG GCCAAGGTGGG CG[G/A]ATCACTT GAGGTCAGGAG TTCAAGA	G	A	Ser (7009)	Phe (7010)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39193 !!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!! - Homo sapiens (Human), 593 aa.	1.90E-31

6795-6796	cg43926000	419	TCACTTGAGGTC AGGAGTTCAAGA C/C/TJAGCCTAGC CAAAATGGTGAA ACCC	C	T	Trp (7011)	End (7012)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39193 !!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!! - Homo sapiens (Human), 593 aa.	1.90E-31
6797-6798	cg43967015	745	AGCCAGGCGTG GTGGCGCATGC CTGT/CJAATCTC AGTACTCGGGA GGCTGAG	T	C	Thr (7013)	Ala (7014)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39194 !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!! - Homo sapiens (Human), 593 aa.	2.60E-31
6799-6800	cg43967015	829	TTGCAGTGGAGC CGAGATTGCGCC AT/CJTGCACCTCA GCCTGGGTAACA AGTGC	T	C	Met (7015)	Val (7016)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39194 !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!! - Homo sapiens (Human), 593 aa.	2.60E-31
6801-6802	cg43999149	497	TGCTTGGTACA GGACAGGCACTT GT/CJAGCGCG GCCGAGCGCT TGAGCC	T	C	Tyr (7017)	Cys (7018)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q35483 KRUPPLE-RELATED ZINC FINGER PROTEIN - MUS MUSCULUS (MOUSE), 812 aa.	4.00E-31
6803-6804	cg20729392	317	GGCGACAAGTG AGGGTACCCACA TC/A/GJACAGGCT GGCCACCAGA ATTGCAG	A	G	Leu (7019)	Ser (7020)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q49800 LYSP - MYCOBACTERIUM LEPRAE, 244 aa.	7.30E-31
6805-6806	cg43273813	324	TATAAAAAATTAG CCAGGCATGGT G/G/AJCATATGCC TGTAAGTCCAGC TACTC	G	A	Gly (7021)	Asp (7022)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39188 !!!!! ALU SUBFAMILY J WARNING ENTRY !!!!! - Homo sapiens (Human), 591 aa.	7.80E-31
6807-6808	cg42487874	283	GTCAGGAGTTTG AGACCATCCTGG C/C/TJAGCACGG TGAAGCCCCGTC TCTACT	C	T	Gln (7023)	End (7024)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39194 !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!! - Homo sapiens (Human), 593 aa.	8.50E-31

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<210> 3951
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<223> 1 of 2 allelic variants (3952 is other entry)

<221> misc_feature
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<223> Accession number cg43925523

<400> 3951
taggggtgta aagcagtgag ttgtgttggg gggtattttt caaccaggg t 51

<210> 3952
<211> 51

<212> DNA
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<223> 2 of 2 allelic variants (3951 is other entry)

<221> misc_feature
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<223> Accession number cg43925523

<400> 3952
taggggtgta aagcagtgag ttgtgctggg gggtattttt caaccaggg t 51

<210> 3953
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (3954 is other entry)

<221> misc_feature
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<223> Accession number cg43925525

<400> 3953
tccacacctg tgattgttcc atggacctgt gttccgttct tcaattcaat g 51

<210> 3954
<211> 51
<212> DNA
<213> Homo sapiens

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<222> (26)...(0)
<223> 2 of 2 allelic variants (3953 is other entry)

<221> misc_feature
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<223> Accession number cg43925525

<400> 3954
tccacacctg tgattgttcc atggaactgt gttccgttct tcaattcaat g 51

<210> 3955
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (3956 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43925674

<400> 3955

aaaaactcct ccagagtcac caatctgtct ttgtagtat caacctcatt c

51

<210> 3956

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (3955 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43925674

<400> 3956

aaaaactcct ccagagtcac caatcggtct ttgtagtat caacctcatt c

51

<210> 3957

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (3958 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43925785

<400> 3957

acatcttata attcagatct gcattcggtta acaggagaat tgagagtttt g

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<210> 3958

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (3957 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43925785

<400> 3958
acatcttata attcagatct gcatttggta acaggagaat tgagagtttt g 51

<210> 3959
<211> 51
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<223> 1 of 2 allelic variants (3960 is other entry)

<221> misc_feature
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<223> Accession number cg43925785

<400> 3959
ttgttataga caaaaataaa agcattctgt aaacttctaa aagcatacac a 51

<210> 3960
<211> 51
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<213> Homo sapiens

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<223> 2 of 2 allelic variants (3959 is other entry)

<221> misc_feature
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<223> Accession number cg43925785

<400> 3960
ttgttataga caaaaataaa agcatcctgt aaacttctaa aagcatacac a 51

<210> 3961
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (3962 is other entry)

<221> misc_feature
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<223> Accession number cg43926022

<400> 3961
aaaaatccac ctacacacac agtctctctt tatctaagt gattcaagat g 51

<210> 3962
<211> 51
<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (3961 is other entry)

<221> misc_feature

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<223> Accession number cg43926022

<400> 3962

aaaaatccac ctacacacac agtctgtctt tatctaagtg gattcaagat g

51

<210> 3963

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (3964 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43926066

<400> 3963

ccaggtggct ggccatcctc ttctaggggc tccagggcgc cctgcactgg c

51

<210> 3964

<211> 50

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (3963 is other entry)

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<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43926066

<400> 3964

ccaggtggct ggccatcctc ttctagggct ccagggcgcc ctgcactggc

50

<210> 3965

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (3966 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43926066

<400> 3965
gtggctgccc cccggagaca tgtgtcagag aggcacgggt caggtgaccc a 51

<210> 3966
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3965 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43926066

<400> 3966
gtggctgccc cccggagaca tgtgtaagag aggcacgggt caggtgaccc a 51

<210> 3967
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (3968 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43926186

<400> 3967
ccccggggca ctggggaaca gaaaggaatg agacccaac aggcagaagc c 51

<210> 3968
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (3967 is other entry)

<221> misc_feature

<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43926186

<400> 3968
ccccggggca ctggggaaca gaaagaatga gacccaaca ggcagaagcc 50

<210> 3969
<211> 51
<212> DNA
<213> Homo sapiens

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<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3970 is other entry)

<221> misc_feature
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<223> Accession number cg43926292

<400> 3969
aagataaacc tttaagtctg agtatgcctg taattacaga agaagaagag a 51

<210> 3970
<211> 51
<212> DNA
<213> Homo sapiens

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<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3969 is other entry)

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<222> (0)...(0)
<223> Accession number cg43926292

<400> 3970
aagataaacc tttaagtctg agtattcctg taattacaga agaagaagag a 51

<210> 3971
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (3972 is other entry)

<221> misc_feature
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<223> Accession number cg43926292

<400> 3971
tgcctgtaat tacagaagaa gaagagaatg aaagtttgag tggaacagag t 51

<210> 3972
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (3971 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43926292

<400> 3972
tgcctgtaat tacagaagaa gaagaaaatg aaagtttgag tggaacagag t 51

<210> 3973
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3974 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43926326

<400> 3973
ggcaacttgt gttccatgtg tcaagcctac ttccaagcag aaaatgaaga a 51

<210> 3974
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3973 is other entry)

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<222> (0)...(0)
<223> Accession number cg43926326

<400> 3974
ggcaacttgt gttccatgtg tcaagtctac ttccaagcag aaaatgaaga a 51

<210> 3975
<211> 51

<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3976 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43926397

<400> 3975
tatttataaa ctgcaacaaa tcttccaccc tccgatgggc aacgacgctt t 51

<210> 3976
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3975 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43926397

<400> 3976
tatttataaa ctgcaacaaa tcttctaccc tccgatgggc aacgacgctt t 51

<210> 3977
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3978 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43926442

<400> 3977
ttgtgcaaaa cgtgcctcct tgtttgtggg taagtgaatc tgacagaggt t 51

<210> 3978
<211> 51
<212> DNA
<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (3977 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43926442

<400> 3978

ttgtgccaaa cgtgcctcct tgtttctggg taagtgaatc tgacagaggt t

51

<210> 3979

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (3980 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43926481

<400> 3979

acgtcttcag cagcgctttc tggagcttcg cgaagtcgga atagcgccgt t

51

<210> 3980

<211> 50

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (3979 is other entry)

<221> misc_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43926481

<400> 3980

acgtcttcag cagcgctttc tggagttcgc gaagtcggaa tagcgccgtt

50

<210> 3981

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (3982 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43926489

<400> 3981
gccagtactg ctgaagctcc cgcgtgggtca tgctggagtt ggagctcagg c 51

<210> 3982
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3981 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43926489

<400> 3982
gccagtactg ctgaagctcc cgcgtagtca tgctggagtt ggagctcagg c 51

<210> 3983
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3984 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43926603

<400> 3983
ttatttgtac tataagaaaa aaaaaatcct aaaaagtcca tacagattgg a 51

<210> 3984
<211> 50
<212> DNA
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<220>
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<223> 2 of 2 allelic variants (3983 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)

<223> Accession number cg43926603

<400> 3984

ttatttgtac tataagaaaa aaaaatccta aaaagtccat acagattgga

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<210> 3985

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (3986 is other entry)

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<222> (0)...(0)

<223> Accession number cg43926788

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51

<210> 3986

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (3985 is other entry)

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<223> Accession number cg43926788

<400> 3986

tctctggaca ctgccactct ccccatgggc accgcttctc agccacaaac c

51

<210> 3987

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (3988 is other entry)

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<400> 3987

ctttatggga cttaagtttt ttttttctcc tctccatctc taggatgtcg t

51

<210> 3988

<211> 50
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<223> 2 of 2 allelic variants (3987 is other entry)

<221> misc_feature
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<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43926788

<400> 3988
ctttatggga ctttaagtttt tttttctcct ctccatctct aggatgtcgt

50

<210> 3989
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (3990 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43926828

<400> 3989
tactaaatga gttacccatt tttttgttc atcctgagaa catgctaaca g

51

<210> 3990
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3989 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43926828

<400> 3990
tactaaatga gttacccatt tttttgttca tcctgagaac atgctaacag

50

<210> 3991
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (3992 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43926935

<400> 3991
ctgtagaggt acacaaaaag aaaaaggaaa aataactact agaaaaaagt

50

<210> 3992
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3991 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43926935

<400> 3992
ctgtagaggt acacaaaaag aaaaaggaaa aaataactac tagaaaaaag t

51

<210> 3993
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3994 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43926973

<400> 3993
ttttagcttc aaagttgaaa aacagattgg tactaacagt ccttctagag a

51

<210> 3994

<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3993 is other entry)

<221> misc_feature
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<223> Accession number cg43926973

<400> 3994
ttttagcttc aaagttgaaa aacaggttgg tactaacagt ccttctagag a

51

<210> 3995
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (3996 is other entry)

<221> misc_feature
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<223> Accession number cg43927077

<400> 3995
tggtcctagt gcacacgcgt gaaggacctg gtatcggctt tagcacaatc c

51

<210> 3996
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (3995 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43927077

<400> 3996
tggtcctagt gcacacgcgt gaagggcctg gtatcggctt tagcacaatc c

51

<210> 3997
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature

<222> (26)...(0)
<223> 1 of 2 allelic variants (3998 is other entry)

<221> misc_feature
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<223> Accession number cg43927077

<400> 3997
tggccaaaac caggtccttt ctcaggacag ggttgggcag atggacacat t 51

<210> 3998
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3997 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43927077

<400> 3998
tggccaaaac caggtccttt ctcagtacag ggttgggcag atggacacat t 51

<210> 3999
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (4000 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43928057

<400> 3999
ttggtctgga gaaagttctc cctttcttca tctaccttaa tttcatgtcc a 51

<210> 4000
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (3999 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43928057

<400> 4000
ttgggtctgga gaaagttctc cctttgttca tctaccttaa tttcatgtcc a 51

<210> 4001
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (4002 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43928063

<400> 4001
gtttggcatt caaaacagga cttcacgttt cagtggacag ctggggaaaag g 51

<210> 4002
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (4001 is other entry)

<221> misc_feature
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<223> Accession number cg43928063

<400> 4002
gtttggcatt caaaacagga cttcatgttt cagtggacag ctggggaaaag g 51

<210> 4003
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (4004 is other entry)

<221> misc_feature
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<223> Accession number cg43928063

<400> 4003
ctctcgagtc ttacttaacc taaaagacaa actgggtcaa cttggtaaatt g 51

<210> 4004
<211> 51

<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (4003 is other entry)

<221> misc_feature
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<223> Accession number cg43928063

<400> 4004
ctctcgagtc ttacttaacc taaaaaaca actgggtcaa cttggtaaat g 51

<210> 4005
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (4006 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43928177

<400> 4005
cagtcagtgt gatcagtttt tctgcgtgtg taataattta tcaaaataag t 51

<210> 4006
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (4005 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43928177

<400> 4006
cagtcagtgt gatcagtttt tctgcatgtg taataattta tcaaaataag t 51

<210> 4007
<211> 51
<212> DNA
<213> Homo sapiens

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<400> 4007

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51

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<211> 51

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<223> Accession number cg43928213

<400> 4008

ctcttatagt gcaaccatgg cagaccattc aacagtcct cccccctctt c

51

<210> 4009

<211> 51

<212> DNA

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<223> Accession number cg43928396

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tttttagacc atatagggtg acttctgat gttgccatgg catttgtaaa c

51

<210> 4010

<211> 51

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<223> 2 of 2 allelic variants (4009 is other entry)

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<223> Accession number cg43928396

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<210> 4011
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<223> Accession number cg43928430

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<210> 4012
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<210> 4013
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<223> 1 of 2 allelic variants (4014 is other entry)

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<223> Accession number cg43928432

<400> 4013
tggtgaggca gaagtcaatc ttaggatgtg gtctgtacat atctgcagat a 51

<210> 4014
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<223> 2 of 2 allelic variants (4013 is other entry)

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<223> Accession number cg43928432

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<210> 4015

<211> 51

<212> DNA

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<223> 1 of 2 allelic variants (4016 is other entry)

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<223> Accession number cg43928785

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51

<210> 4016

<211> 51

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<223> Accession number cg43928785

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<210> 4017

<211> 51

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<223> 1 of 2 allelic variants (4018 is other entry)

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<223> Accession number cg43928902

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<210> 4018
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<210> 4019
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<223> 1 of 2 allelic variants (4020 is other entry)

<221> misc_feature
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<223> Accession number cg43929221

<400> 4019
cttctaataa tttctgttat aaatttccag cattttaatg aaaatctaata g 51

<210> 4020
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<223> 2 of 2 allelic variants (4019 is other entry)

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cttctaataa tttctgttat aaattgccag cattttaatg aaaatctaataat g

51

<210> 4021

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<213> Homo sapiens

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<223> Accession number cg43929415

<400> 4021

atggtagaat tactagttca gaattggcat agattctggt gttaaaatag a

51

<210> 4022

<211> 51

<212> DNA

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<223> 2 of 2 allelic variants (4021 is other entry)

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<223> Accession number cg43929415

<400> 4022

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51

<210> 4023

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<212> DNA

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<223> 1 of 2 allelic variants (4024 is other entry)

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<223> Accession number cg43929536

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ggaagaggag gaaggcgacg gcaacagtga ccagctcatg ggcttcgaga g

51

<210> 4024

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<400> 4024
ggaagaggag gaaggcgacg gcaacggtga ccagctcatg ggcttcgaga g 51

<210> 4025
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<223> 1 of 2 allelic variants (4026 is other entry)

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<223> 1 of 2 allelic variants (4028 is other entry)

<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
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<400> 4027
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<210> 4028
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<210> 4029
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<400> 4029
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<210> 4030
<211> 51
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<223> 2 of 2 allelic variants (4029 is other entry)

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<223> Accession number cg43929652

<400> 4030

cctgaaataa gtgaagttac tagctactaa ataaatgtca ctcaaaagca g

51

<210> 4031

<211> 51

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51

<210> 4032

<211> 51

<212> DNA

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<223> 2 of 2 allelic variants (4031 is other entry)

<221> misc_feature

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<223> Accession number cg43929652

<400> 4032

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<210> 4033

<211> 51

<212> DNA

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<223> 1 of 2 allelic variants (4034 is other entry)

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<400> 4033

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51

<210> 4034

<211> 51
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<223> 2 of 2 allelic variants (4033 is other entry)

<221> misc_feature
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<400> 4034
taaataaatg tcactcaaaa gcagtttctt ggctttttct tacacagcgg g 51

<210> 4035
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (4036 is other entry)

<221> misc_feature
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<223> Accession number cg43929652

<400> 4035
tttttcttac acagcgggca acttttcttt taaattctcc atttctatct t 51

<210> 4036
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (4035 is other entry)

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<223> Accession number cg43929652

<400> 4036
tttttcttac acagcgggca acttttcttt taaattctcc atttctatct t 51

<210> 4037
<211> 51
<212> DNA
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<222> (26)...(0)
<223> 1 of 2 allelic variants (4038 is other entry)

<221> misc_feature
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<223> Accession number cg43929652

<400> 4037
cttttctttt aaattctcca tttctatctt ccctccattc tttcgagca t 51

<210> 4038
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (4037 is other entry)

<221> misc_feature
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<400> 4038
cttttctttt aaattctcca tttctgtctt ccctccattc tttcgagca t 51

<210> 4039
<211> 51
<212> DNA
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<223> 1 of 2 allelic variants (4040 is other entry)

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<223> Accession number cg43929652

<400> 4039
cttccctcca ttctttogca gcatcaacat tagcaggtga gtctccatta g 51

<210> 4040
<211> 51
<212> DNA
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<223> 2 of 2 allelic variants (4039 is other entry)

<221> misc_feature
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<223> Accession number cg43929652

<400> 4040
cttccctcca ttctttcgca gcatctacat tagcaggtga gtctccatta g 51

<210> 4041
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (4042 is other entry)

<221> misc_feature
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<223> Accession number cg43929652

<400> 4041
tccattcttt cgcagcatca acattagcag gtgagtctcc attagggctct g 51

<210> 4042
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (4041 is other entry)

<221> misc_feature
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<400> 4042
tccattcttt cgcagcatca acatttgcag gtgagtctcc attagggctct g 51

<210> 4043
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (4044 is other entry)

<221> misc_feature
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<223> Accession number cg43929652

<400> 4043
cattagcagg tgagtctcca ttagggctctg ccagcataga aatgacacta a 51

<210> 4044
<211> 51

<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (4043 is other entry)

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<223> Accession number cg43929652

<400> 4044
cattagcagg tgagtctcca ttaggatctg ccagcataga aatgacacta a

51

<210> 4045
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (4046 is other entry)

<221> misc_feature
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<400> 4045
tccggatcat gttgtgctat gtacaggtct ttacaattct tcttgaaggt t

51

<210> 4046
<211> 51
<212> DNA
<213> Homo sapiens

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<222> (26)...(0)
<223> 2 of 2 allelic variants (4045 is other entry)

<221> misc_feature
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<400> 4046
tccggatcat gttgtgctat gtacaagtct ttacaattct tcttgaaggt t

51

<210> 4047
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (4048 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43929880

<400> 4047
acatcgaaga tttgtttata ataggaaaaa aaaaagctac ccactgtcat g 51

<210> 4048
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (4047 is other entry)

<221> misc_feature
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<221> misc_feature
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<223> Accession number cg43929880

<400> 4048
acatcgaaga tttgtttata ataggaaaaa aaaagctacc cactgtcatg 50

<210> 4049
<211> 51
<212> DNA
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<222> (26)...(0)
<223> 1 of 2 allelic variants (4050 is other entry)

<221> misc_feature
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<223> Accession number cg43929880

<400> 4049
atttgtttat aataggaaaa aaaaaagcta cccactgtca tgcgctggga a 51

<210> 4050
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (4049 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43929880

<400> 4050
atttgtttat aataggaaaa aaaaagctac ccactgtcat gcgctgggaa 50

<210> 4051
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (4052 is other entry)

<221> misc_feature
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<400> 4051
catcctcagc ggcccctctg cagggcagag tctcgtctc actctcccag c 51

<210> 4052
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 2 of 2 allelic variants (4051 is other entry)

<221> misc_feature
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<223> Accession number cg43929880

<400> 4052
catcctcagc ggcccctctg cagggtagag tctcgtctc actctcccag c 51

<210> 4053
<211> 51
<212> DNA
<213> Homo sapiens

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<223> 1 of 2 allelic variants (4054 is other entry)

<221> misc_feature
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<223> Accession number cg43929880

<400> 4053

actccacctt gcataagtgc ttgaggatca cacaaccaga tacgtagatc a

51

<210> 4054

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (4053 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43929880

<400> 4054

actccacctt gcataagtgc ttgagaatca cacaaccaga tacgtagatc a

51

<210> 4055

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (4056 is other entry)

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<222> (0)...(0)

<223> Accession number cg43930022

<400> 4055

gccattcagg acctaattga acaatcgcta ccattccttc cacttttagg c

51

<210> 4056

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (4055 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43930022

<400> 4056

gccattcagg acctaattga acaattgcta ccattccttc cacttttagg c

51

<210> 4057

<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (4058 is other entry)

<221> misc_feature
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<223> Accession number cg43930314

<400> 4057
ccccagagca tctgcggcct tcaggcgcac ccccggttg gagtcctgca g 51

<210> 4058
<211> 50
<212> DNA
<213> Homo sapiens

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<223> 2 of 2 allelic variants (4057 is other entry)

<221> misc_feature
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<221> misc_feature
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<223> Accession number cg43930314

<400> 4058
ccccagagca tctgcggcct tcagggcacc ccccggttgg agtcctgcag 50

<210> 4059
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> 1 of 2 allelic variants (4060 is other entry)

<221> misc_feature
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<223> Accession number cg43930314

<400> 4059
gatcacagcc tgacaattgg ccattctccag ctgctcatct ggggtcccaa g 51

<210> 4060
<211> 51
<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (4059 is other entry)

<221> misc_feature
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<223> Accession number cg43930314

<400> 4060
gatcacagcc tgacaattgg ccatcaccag ctgctcatct ggggtcccaa g 51

<210> 4061
<211> 51
<212> DNA
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<220>
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<222> (26)...(0)
<223> 1 of 2 allelic variants (4062 is other entry)

<221> misc_feature
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<223> Accession number cg43930342

<400> 4061
cagggctcag ttgggaccag tgtggagaaa gacaggaaag tggaaaagct t 51

<210> 4062
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (4061 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43930342

<400> 4062
cagggctcag ttgggaccag tgtgggaaa gacaggaaag tggaaaagct t 51

<210> 4063
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (4064 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43930456

<400> 4063
ctgggtgcac actggacgct tagacgtgaa catctttctc agtcatcac c 51

<210> 4064
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (4063 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43930456

<400> 4064
ctgggtgcac actggacgct tagacatgaa catctttctc agtcatcac c 51

<210> 4065
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (4066 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43930460

<400> 4065
taaagggtta aagaaaaaag ggaggggctt tcttacaagc tttttcacia g 51

<210> 4066
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (4065 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43930460

<400> 4066

taaagggttta aagaaaaaag ggaggagctt tcttacaagc tttttcacaa g

51

<210> 4067

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (4068 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43930652

<400> 4067

tgacatacaa gtacaagaag agcaaattgt gctcaaaata ctttattctt a

51

<210> 4068

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (4067 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43930652

<400> 4068

tgacatacaa gtacaagaag agcaatttgt gctcaaaata ctttattctt a

51

<210> 4069

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (4070 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43930652

<400> 4069

tggacatgtg atgagcacat gtctagtatt gcagcaagga aatcacatca g

51

<210> 4070

<211> 51

<212> DNA

<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> 2 of 2 allelic variants (4069 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43930652

<400> 4070
tggacatgtg atgagcacat gtctattatt gcagcaagga aatcacatca g 51

<210> 4071
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (4072 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43930874

<400> 4071
caacccaaat taacagtatt attaacttcc taccccaagc tggctctccc c 51

<210> 4072
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (4071 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43930874

<400> 4072
caacccaaat taacagtatt attaaattcc taccccaagc tggctctccc c 51

<210> 4073
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (4074 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43930919

<400> 4073
acatggctag acacagagcc cgggagggca aaggaaaatt ggaggcccct t 51

<210> 4074
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (4073 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43930919

<400> 4074
acatggctag acacagagcc cgggatggca aaggaaaatt ggaggcccct t 51

<210> 4075
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (4076 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43931240

<400> 4075
ggaaggagga aacaccagta agacacgaaa gggcaaata tagtcagaa t 51

<210> 4076
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (4075 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43931240

<400> 4076
ggaaggagga aacaccagta agacatgaaa gggcaaata tagtcagaa t 51

<210> 4077

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (4078 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43931447

<400> 4077

tttaaacctt ggtttggtat tttcctgggg tgatggtgac tttggaaaat t

51

<210> 4078

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (4077 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43931447

<400> 4078

tttaaacctt ggtttggtat tttcccgggg tgatggtgac tttggaaaat t

51

<210> 4079

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (4080 is other entry)

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43931447

<400> 4079

gatggtgact ttggaaaatt gggccggggc ggaagtgaag gctgcaacat t

51

<210> 4080

<211> 51

<212> DNA

<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (4079 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43931447

<400> 4080
gatggtgact ttggaaaatt gggccagggc ggaagtgaag gctgcaacat t 51

<210> 4081
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (4082 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43931671

<400> 4081
caaaaaggaa aaacaaacaa aaaaaacagt aattctgaac acatgaagag t 51

<210> 4082
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (4081 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43931671

<400> 4082
caaaaaggaa aaacaaacaa aaaaacagta attctgaaca catgaagagt 50

<210> 4083
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature

<222> (26)...(0)
<223> 1 of 2 allelic variants (4084 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43931755

<400> 4083
acttgaaaat aaaaagattt ttttttccaa aggaatgctg cacccatttc a 51

<210> 4084
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (4083 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43931755

<400> 4084
acttgaaaat aaaaagattt ttttttccaaa ggaatgctgc acccatttca 50

<210> 4085
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (4086 is other entry)

<221> misc_feature
<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43932129

<400> 4085
tgactcttcc aaatccccac atgttaaaaa aacctgttgg tacaggctca 50

<210> 4086
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (4085 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43932129

<400> 4086
tgactcttcc aaatccccac atgttaaaaa aaacctgttg gtacaggctc a 51

<210> 4087
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (4088 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43932330

<400> 4087
gttaaaacat tctaaaatgt tgtaataat ttaatgtgaa tactgttaaa c 51

<210> 4088
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (4087 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43932330

<400> 4088
gttaaaacat tctaaaatgt tgtaactaat ttaatgtgaa tactgttaaa c 51

<210> 4089
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (4090 is other entry)

<221> misc_feature

<222> (0)...(0)
<223> Accession number cg43932388

<400> 4089
tatgtattca ggggttcaga taaggactgg aagcaacccc aaaattagac g 51

<210> 4090
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (4089 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43932388

<400> 4090
tatgtattca ggggttcaga taaggctctgg aagcaacccc aaaattagac g 51

<210> 4091
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 1 of 2 allelic variants (4092 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43932459

<400> 4091
gtagcagggc ccgggtggaa gggtcaggca ccgacctcat cagggccacg a 51

<210> 4092
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (26)...(0)
<223> 2 of 2 allelic variants (4091 is other entry)

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43932459

<400> 4092
gtagcagggc ccgggtggaa gggtcgggca ccgacctcat cagggccacg a 51